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SYMPOSIA AND ORAL SESSIONS

Late-Breaking Original Research

LB1 Performance of Illumina and Affymetrix bovine high-density genotyping platforms in Holsteins and Jerseys. G. Rincon[1], K. Weber[1], A. Van Eenennaam[1], B. L. Golden[2], and J. F. Medrano*[1], *[1]Department of Animal Science, University of California Davis, Davis, [2]Dairy Science Department, California Polytechnic State University, San Luis Obispo.*

Two high-density single nucleotide polymorphism (SNP) genotyping arrays have recently become available for bovine genomic analyses, the Illumina High-Density Bovine BeadChip Array (777,962 SNP) and the Affymetrix Axiom Genome-Wide BOS 1 Array (648,855 SNP). These products each have unique design and chemistry attributes, and the extent of marker overlap and their potential utility for QTL fine mapping, detection of copy number variation, and multi-breed genomic selection are of significant interest to the cattle community. This study compares the performance of these 2 arrays using DNA samples from 16 dairy cattle (10 Holstein, 6 Jersey). Data were analyzed with SVS7 software (Golden Helix) filtering to remove SNP having a call rate less than 90% and linkage disequilibrium (LD) pruning was used to remove linked SNP ($r^2 \geq 0.9$). Maximum, average, and median gaps were calculated for each analysis based on genomic position of SNP on the bovine UMD3.1 genome assembly. The Illumina and Affymetrix arrays include 49,345 and 47,741 SNP from the widely used Bovine Illumina SNP50, respectively. All samples were successfully genotyped (≥98% SNP genotyped) with both platforms. Average number of genotyped SNP in the Illumina platform was 775,681 and 637,249 for the Affymetrix platform. Only 96,640 SNP were shared between the 2 platforms, and the average SNP concordance at these loci was 99.9%. Despite fewer total SNP on the Affymetrix array, 19% more SNP remained (480,196) after LD pruning resulting in a smaller average gap size of 5,159 bp relative to the Illumina array where 388,263 SNP remained resulting in a 6,881 bp average gap size. However, only 224,115 Illumina and 241,038 Affymetrix SNP remained following removal of SNP with a minor allele frequency (MAF) of zero in these Holstein and Jersey samples, resulting in an average gap size of 11,887 bp and 11,018 bp, respectively. Combining the 354,348 informative ($r^2 \geq 0.9$), polymorphic (MAF ≥ 0), unique SNP data from both platforms reduced the average gap size to 7,560 bp. This marker density of informative SNP has been projected to be sufficient to obtain consistent marker effects across breeds.

Key Words: SNP, genomics, cattle

LB2 Independent assessment of commercial DNA tests for beef cattle production traits. K. L. Weber* and A. L. Van Eenennaam, *Department of Animal Science, University of California, Davis.*

Two commercial companies offer DNA tests to improve the accuracy of selection in Angus cattle. The American Angus Association (AAA) national cattle evaluation incorporates DNA test information using genetic correlations estimated from the genetic relationship between DNA test results and phenotypic data in their database. The genetic correlation between the target trait and test results is expected to decrease as the relationship between the training and evaluation populations becomes more distant. The objective of this study was to estimate the genetic correlation between DNA test results and target traits in typical commercial ranch bulls (born 2003–2007) sourced from the Angus seedstock sector. Molecular breeding values (MBV) from Igenity (Duluth, GA) and HD 50K molecular value predictions (MVP) from Pfizer Animal Genetics (Kalamazoo, MI) were obtained for 29 registered Angus bulls that had sired 1852 progeny with commercial cows on 3 northern California ranches. Each bull had at least 20 progeny weaning weight records or 10 carcass records. Traits evaluated were weaning weight (WW; n = 1734), ADG (n = 341) from feedlot entry to estimated feedlot final weight (derived from HCW/0.63), HCW (n = 455), ribeye area (RE; n = 455), and marbling score (MS; n = 455). DNA test results were correlated with the target trait using a bivariate animal model with the DNA test treated as a second trait. REML estimates of the genetic correlation ± SE estimated in this data set (and those estimated by AAA where available) for Igenity MBV were WW 0.12 ± 0.22 (0.45), ADG −0.01 ± 0.42, HCW 0.33 ± 0.27 (0.54), RE 0.35 ± 0.24 (0.58), and MS 0.61 ± 0.19 (0.65). For Pfizer MVP, genetic correlations were WW 0.51 ± 0.17 (0.52), ADG 0.10 ± 0.39, HCW 0.08 ± 0.28 (0.48), RE 0.57 ± 0.21 (0.60), and MS 0.71 ± 0.17 (0.57). Genetic correlation estimates were generally positive and somewhat lower than the AAA value, although estimates had large SE. Incorporating the DNA test information as a correlated trait to improve the low accuracy AAA EPD associated with yearling bulls did not consistently improve rank order correlation with commercial ranch estimated breeding values based on observed progeny performance.

Key Words: genomic selection, beef, accuracy

LB3 Multivariate factor analysis of genomic correlation matrices in three US dairy cattle breeds. N. P. P. Macciotta*[1] and J. B. Cole[2], *[1]Dipartimento di Scienze Zootecniche, Università di Sassari, Sassari, Italy, [2]Animal Improvement Programs Laboratory, Agricultural Research Service, USDA, Beltsville, MD.*

High-density marker maps allows the prediction of genomic values both genome-wide (GW) and for each chromosome (CHR). The comparison of correlations between traits on the GW and CHR levels may be of great help for understanding the genetic architecture of single or groups of traits. Multivariate factor analysis (MFA) models the (co) variance of a multivariate system by extracting latent variables able to reconstruct the common (co)variance structure. In this work, GW and CHR (*Bos taurus* autosomes (BTA) 6, 14, and 18) correlation matrices for 3 US dairy cattle breeds were analyzed with MFA. Data refer to 2,038 Brown Swiss (BS), 63,615 Holstein (HO) and 8,084 Jersey (JE) cattle, respectively. A total of 23 productive and functional traits were considered. About 80% of the (co)variance was explained by 6 or 7 latent factors. The comparison of correlations between the factors and the traits highlighted some similarities between breeds at the GW level. Latent factors associated (r > = 0.60) with milk yield

traits, milk composition, udder morphology, strength, and functional traits (productive life, SCS, daughter pregnancy rate) were extracted. Some differences were observed at CHR level. On BTA6 BS showed an overlapping of yield and composition with a single factor, whereas they tend to remain distinct in HO and JE. However, in HO and JE there are 2 latent factors associated with functional traits on BTA6, which harbors genes affecting milk production and reproduction. The analysis of BTA14 highlighted in the JE a factor associated with both milk yield and composition traits, except for protein percentage, and differences between GW and CHR was noted, which is consistent with the presence of genes known to affect selected traits (DGAT1). Results for GW and CHR were similar for BTA18, which is known to harbor a QTL affecting calving traits and conformation in Holsteins. Multivariate factor analysis is capable of identifying differences in genetic correlations among traits across the genome and on individual chromosomes, and may be a useful tool to identify regions of the genome affecting multiple traits for further study.

Key Words: genomic selection, chromosome, factor analysis

LB4 Transcriptional profiling during pig fetal skeletal muscle development using direct high-throughput sequencing and cross-platform comparison with gene expression microarrays. C. W. Ernst*[1], J. P. Steibel[1], B. P. Sollero[1,2], G. M. Strasburg[1], S. E. F. Guimarães[2], and N. E. Raney[1], *[1]Michigan State University, East Lansing, [2]Federal University of Viçosa, Viçosa, MG, Brazil.*

§%§Skeletal muscle fiber formation is under genetic control, but little is known about the specific genes involved or how their expression patterns are coordinated. The aim of this study was to identify differentially expressed genes in *longissimus dorsi* muscle of Yorkshire × Landrace pigs at 40 and 70 d of gestation (encompassing the transition from primary to secondary fibers). Total RNA was pooled from 3 fetuses from gilts at each gestational age (n = 3). Transcriptional profiling was performed by direct sequencing (RNaseq) with an Illumina GAIIx revealing 6,299 differentially expressed tags (FDR <0.10). The same samples were previously evaluated using the Pig-oligoarray microarray comprised of 20,400 70-mers, and qPCR was completed for a subset of genes. To perform a cross-platform comparison between RNaseq and microarray analyses, microarray results were expressed as log-fold change (FC) with associated p-value and q-value (FDR), and comparisons filtered with FDR <0.10 (n = 1,218). Microarray oligonucleotides were matched to RNaseq tags based on HGNC annotation resulting in 1,410 matching pairs of oligonucleotides and sequenced transcripts (with multiple transcripts mapping to the same oligonucleotide). Correlation of log-FC between the technologies was 0.72. Expression patterns obtained with RNaseq for 11 genes assayed by qPCR (annotated in Build 9) were validated. These included 4 non-differentially expressed genes (FDR >0.10 in both assays; CTNNB1, HPRT1, STAT1, TIMP3), 6 genes more highly expressed at 70 d (FDR <0.10; CA3, DLK1, FBXO32, MYOZ1, NRAP, USP13), and 1 gene more highly expressed at 40 d (FDR <0.10; TNC). Relative FC from RNaseq and qPCR for all genes agreed in both direction and magnitude. As expected, RNaseq identified additional differentially expressed transcripts over the microarray results. However, this analysis demonstrated that the microarray results were repeatable, and results of both technologies were comparable to qPCR. Thus, both microarrays and RNaseq are reliable and RNaseq may complement and extend microarray studies.

Key Words: RNAseq, microarray, skeletal muscle

LB5 Growth, DXA skeletal traits, and spinal curvature are compromised within four weeks in pigs fed diets with no supplemental vitamin D. L. A. Rortvedt*, Z. Hassen, and T. D. Crenshaw, *University of Wisconsin, Madison.*

Recent necropsies from commercial operations implied vitamin D (D) deficiencies in young pigs, which are not typical. In 2010, we reported that kyphosis, an abnormal spine curvature, was induced in young pigs fed D-limited diets for 9 or 13 wk. The current objective was to evaluate relationships among dietary D, Ca, and P on skeletal traits and assess methods for early detection of kyphosis. In 2 trials (n = 72 ea) pigs weaned at ~3 wk were fed diets with no supplemental D for 1 wk then 1 of 8 diets (corn-SBM) for 4 wk. Treatments included supplementation with D, 0 (-D) or 280 (+D) IU/kg; Ca, 75% (0.53%) or 150% (1.05%); P, 95% (0.57%) or 120% (0.72%) of requirements. On d 28 pigs were killed and scanned using DXA (GE Lunar Prodigy) to determine bone mineral content (BMC, g/pig) and density (BMD, g/cm^2). Gain was depressed ($P < 0.01$) in pigs fed -D and tended ($P < 0.12$) to be altered by interactions between D, Ca, and P. Differences in BMC were detected due to D ($P < 0.01$). Expected responses to Ca and P ($P < 0.01$) were observed, but dependent on D ($P < 0.01$). Differences in BMD, which accounts for size, were also detected. Pigs fed -D had reduced BMD ($P < 0.01$). Excess P suppressed BMD in pigs fed -D, but increased BMD in pigs fed +D ($P < 0.07$). Differences were detected in serum Ca and P at 4 wk due to D, Ca, and P ($P < 0.01$). Two methods to assess spinal curvature involved angle measurements from digital images versus a polynomial fit derived from lateral DXA scans. No differences among treatments were detected using angle measurements. Differences ($P < 0.02$) due to D were detected in all polynomial coefficients. Thus, a polynomial fit of the spine offers a method to detect differences due to D within 4 wk.

Table 1.

Vit D, IU/kg	0	0	0	0	280	280	280	280	
Ca, %	75	75	150	150	75	75	150	150	
P, %	95	120	95	120	95	120	95	120	SEM
Gain, kg/d[a]	0.407	0.375	0.348	0.353	0.567	0.572	0.542	0.619	0.023
Serum Ca, mg/dL[a,b,e]	8.18	7.39	9.07	9.71	11.01	11.64	14.02	12.49	0.87
Serum P, mg/dL[a,b,c]	8.40	10.25	8.21	10.07	11.40	12.53	9.28	12.36	0.67
BMD, g/cm^2 [a,d]	0.428	0.398	0.500	0.410	0.615	0.654	0.662	0.753	0.048

a. D, $P < 0.01$; b. Ca, $P < 0.02$; c. P, $P < 0.01$; d. D × P, $P < 0.05$; e. D × Ca × P, $P < 0.02$.

Key Words: kyphosis, calcium, phosphorus

LB6 Effect of *trans*-palmitoleic acid (*trans*-16:1 n-7) on lipid metabolism and cellular proliferation in primary bovine adipocytes. A. K. G. Kadegowda*, T. A. Burns, M. Miller, and S. K. Duckett, *Clemson University, Clemson, SC.*

Trans-palmitoleic acid (*t*-16:1) has been suggested to have beneficial effects on human health including lower adiposity. Objectives were to quantify the amounts of *t*-16:1 in meat samples and to determine the effect of *t*-16:1 on cellular proliferation and lipid metabolism in bovine primary adipocytes. For the first objective, *t*-16:1 in LM samples from steers finished on 2 different forage-finishing systems were analyzed by GC. For the second objective, bovine primary preadipocyte cultures were isolated from intermuscular fat of 18 mo-old Angus

crossbred heifers (n = 2). Preadipocytes were differentiated (D0) in differentiation media [DMEM containing 10% fetal calf serum, 2.5 μg/mL insulin, 0.25 μ*M* dexamethasone (DEX), 20 μ*M* troglitasone, 0.5 m*M* isobutylmethylxanthine (IBMX), and 10 m*M* acetate] for 2 d. Cells were further differentiated from D2 to D6 in media without DEX and IBMX. From D0 to D6, cells were treated with 1 of 4 levels (0, 50, 150, or 300 μ*M*) of *t*-16:1 and for fatty acid analysis by GC and gene expression by RT-qPCR. The effect of *t*-16:1 on cell proliferation of pre-differentiated and differentiated cells was assayed using Cell Counting Kit-8. The treatment effects were analyzed by ANOVA using Proc Mixed (SAS). The *t*-16:1 content in meat samples varied from 0.56 to 1.18 g/100 g total FA. Increasing *t*-16:1 supplementation linearly increased ($P < 0.05$) total cellular FA, decreased ($P < 0.01$) C18:1c9, increased *t*-16:1 ($P < 0.01$), its elongation product t11 18:1($P < 0.01$) which was desaturated to c9t11 CLA ($P < 0.01$). Decreased C18:1c9 was probably due to increased availability of alternative FA (*t*11–18:1) for desaturation. *Trans* 16:1 increased ($P < 0.01$) FASN and ELVOL6 (at 50 μ*M*) but did not affect SCD1. *t*16:1 affected cell proliferation of pre-differentiated cells ($P < 0.05$) but did not affect the differentiated cells. Results showed that meat samples are a source of *t*-16:1and the effects of *t*-16:1 are probably mediated through c9t11 CLA in the differentiated adipocytes.

Key Words: *trans*-palmitoleic acid, adipocyte, lipid metabolism

LB7 Ferric citrate decreases ruminal hydrogen sulfide production in feedlot cattle fed diets high in sulfate. M. E. Drewnoski*[1], P. H. Doane[2], and S. L. Hansen[1], *[1]Iowa State University, Ames, [2]ADM Research, Decatur, IL.*

Sulfate content of ethanol co-products often limits inclusion in cattle diets. Dissimilatory reduction of sulfate by sulfate-reducing bacteria in the rumen produces sulfide, which can lead to a buildup of the toxic gas hydrogen sulfide (H_2S) in the rumen, resulting in reduced performance and occasionally toxicosis. We hypothesized that adding ferric ions would competitively inhibit ruminal sulfate reduction. The objectives of these studies were to determine the effects of ferric citrate on ruminal fermentation, ruminal sulfate reduction, and DMI of cattle. The effects of 5 levels (0, 25, 50, 100, 150, 200 mg/kg of additional Fe in the in vitro fluid) and 2 sources (ferric citrate or ferric ammonium citrate) of ferric ions on in vitro H_2S production, IVDMD, total gas production, and fluid pH were examined (n = 6 per treatment). Rumen fluid was collected from a steer that was adapted to a high concentrate, high sulfate diet (0.51% S) and mixed with an equal volume of McDougall's buffer, without the reducing solution. Addition of either source of ferric ions decreased ($P < 0.01$) H_2S concentration without affecting gas production ($P = 0.38$), fluid pH ($P = 0.80$), or IVDMD ($P = 0.38$) after a 24 h incubation. An in vivo experiment was conducted using 8 ruminally fistulated steers (455 kg) in a replicated Latin square design with 4 periods and 4 treatments. The treatments included a high concentrate, high S control diet (0.46% S) or the control diet plus ferric ammonium citrate at 200, 300, or 400 mg Fe/kg diet DM. Each period lasted 11 d with a 3 d washout period where all cattle were fed the control diet, and an 8 d period in which steers were fed their experimental diet. Intake was determined during the last 4 d in a period. Inclusion of ferric ions in the diet of steers did not affect DMI ($P = 0.21$) or ruminal pH ($P = 0.48$). There was a linear ($P < 0.01$) decrease in the concentration of ruminal H_2S as ferric ion addition increased. Ferric citrate appears to be an effective way to decrease ruminal production of H_2S, which could allow producers to safely increase inclusion of co-products containing elevated sulfate.

Key Words: distillers grains, iron, sulfur

LB8 Adding an anti-inflammatory lactic acid bacteria to a *Bacillus*-based direct-fed microbial improves calf performance. M. Duersteler*[1], K. N. Novak[1], C. A. Wehnes[1], M. E. Davis[1], D. R. Shields[2], and A. H. Smith[1], *[1]Danisco USA Inc., Waukesha, WI, [2]Merrick's Inc., Union Center, WI.*

Enhanced immune development in calves was observed when scouring calves were treated with an electrolyte containing a *Bacillus*-based direct-fed microbial (DFM) selected for reducing bacterial pathogens. The objective of this experiment was to determine the effect of adding anti-inflammatory lactic acid bacteria (LAB) to the *Bacillus*-based DFM on immunity and calf performance. *Enterococcus faecium* ID7 was selected for anti-inflammatory activity from a library of LAB isolated from healthy calves. Rat intestinal epithelial IEC-6 cells (3×10^5) were treated with *Bacillus* spores (10^7 cfu), high and low dose *E. faecium* ID7 (10^8 cfu, 10^7 cfu), or *Bacillus* spores with high and low dose *E. faecium* ID7 for one hour. *Bacillus* spores increased ($P < 0.05$) expression of inflammatory cytokines (IL-1β, IL-6, TNF-α and MIP-2). High and low dose ID7 reduced ($P < 0.05$) expression of inflammatory cytokines caused by *Bacillus* spores. Calves (72) were randomly assigned to 3 treatments; control, *Bacillus*-based DFM (2×10^9 cfu/head/day) or *Bacillus*-based DFM plus *E. faecium* ID7 (2×10^9 *Bacillus*, 1×10^9 ID7 cfu/head/day). Treatments were administered in non-medicated 20:20 all milk replacer fed at 1.25 lbs/day until weaning at 6 weeks, and calves were given starter feed ad libitum throughout the 8 weeks of the trial. The *Bacillus* DFM plus *E. faecium* ID7 increased average daily gain over wk 5–6, 7–8 and over all 8 weeks ($P = 0.03$) compared with the control calves. These results indicate that providing a balanced immune response by adding an anti-inflammatory LAB to a pathogen reducing *Bacillus*-based DFM improves calf performance.

Table 1. Average daily gain (kg) per period and over trial

Week	Control ± SE	*Bacillus* DFM	*Bacillus* DFM plus ID7
1-2	0.23 ± 0.03	0.26 ± 0.03	0.31 ± 0.03
3-4	0.58 ± 0.04	0.60 ± 0.04	0.63 ± 0.04
5-6	0.78 ± 0.03^{a}	0.86 ± 0.03^{ab}	0.91 ± 0.04^{b}
7-8	1.01 ± 0.05^{a}	1.06 ± 0.05^{ab}	1.16 ± 0.05^{b}
Overall ADG	0.65 ± 0.03^{a}	0.70 ± 0.03^{ab}	0.75 ± 0.03^{b}
Total Gain	36.39 ± 1.49^{a}	38.94 ± 1.52^{ab}	42.18 ± 1.56^{b}

Means with different letters are significantly different ($P < 0.05$) within rows; means separation by least square difference. Statistical analysis by Proc Mixed procedure (SAS 9.1.3).

Key Words: direct-fed microbial, calf, immunity

Sunday, July 10, 2011

SYMPOSIA AND ORAL SESSIONS
Triennial Lactation Symposium: Lactation Biology Training for the Next Generation—A Tribute to Dr. H. Allen Tucker

1 Bovine mammary epithelial cell lineages and parenchymal development. S. Ellis*[1], R. M. Akers[2], A. V. Capuco[3], and S. Safayi[1], *[1]Clemson University, Clemson, SC, [2]Virginia Polytechnic Institute, Blacksburg, VA, [3]USDA-ARS, Beltsville Agricultural Research Center, Beltsville, MD.*

Mammary development proceeds from an aggregation of cells in the ventral ectoderm to the establishment of an elaborate tree of alveoli, ducts, and cisternae. However, despite abundant data on endocrine regulation of ruminant mammary growth, we know comparatively little about cell lineages, expression of differentiation markers, and plasticity in mammary cell phenotype. Histologic analyses have revealed cell populations with distinct histochemical profiles, but functional assessment of the cell populations during development has been limited to analysis of proliferation and frequency estimations of morphotypes. The lack of transplantation models, limited availability of validated antibodies with reactivity to bovine antigens, and similar technical challenges have generally hindered the pace of discovery, but the application of new technologies like laser microdissection, transcriptional profiling, and multispectral image analysis are yielding important cues into bovine mammary cell ontogeny and developmental regulation. Our analyses have shown that prepubertal ovariectomy affects epithelial architecture, increases the proportion of cells expressing the estrogen receptor, and increases myoepithelial cell development, all concomitant with dramatic reduction in the mass of parenchymal tissue. Our observations point to a dual role for ovarian secretions in the control of not only the rate of epithelial development, but also the nature of the parenchymal development. The balanced stimulus and inhibition pathways are likely to cooperatively regulate mammary growth. The increased reliance on objective staining analyses and quantitative approaches will ensure broader repeatability, application, and extension of the findings. Advances in the understanding of mammary epithelial cell ontogeny, coupled with the established knowledge of endocrine factors affecting mammary development may yield intervention strategies to improve dairy profitability.

Key words: mammary development, cell lineage, prepubertal mammary growth

2 Prolactin—The multi-faceted potentiator of mammary growth and function. R. C. Hovey*, J. F. Trott, A. Schennink, W. K. Petrie, and M. K. VanKlompenberg, *University of California, Davis.*

Prolactin (PRL) confers numerous biological effects including its principle actions on the mammary glands during growth and lactation. These effects are mediated by dimers of the transmembrane PRL receptor (PRLR) and subsequent activation of numerous downstream signaling cascades. Traditional interpretations of how PRL acts on the mammary glands have generally built upon the concept that PRL acts directly, and independently, on the target epithelium during periods of mammary gland growth and lactation. In this presentation we will first review PRL action during mammary gland growth and lactation in several species with a focus on similarities and differences across PRLR and the control of its expression. We will then outline several lines of evidence to support the notion that many effects of PRL are mediated by additional mechanisms intrinsic to the mammary glands. Specifically, the effects of PRL on mammary gland growth are tightly coordinated by concomitant changes in the circulating levels of estrogen and progesterone, which in turn can modulate both PRLR expression and downstream gene expression. Furthermore, PRL not only acts on the epithelial population, but also modifies the stromal microenvironment by facilitating processes such as tissue remodeling and angiogenesis. Taken together, these modes of action highlight the many pathways by which PRL coordinately regulates and facilitates mammary gland growth during gestation before it initiates and regulates lactation.

Key words: prolactin, mammary gland, lactation

3 The lactocrine hypothesis: Programming reproductive tract development. F. F. Bartol*[1], J. C. Chen[2], D. J. Miller[1], A.-L. Frankshun[2], A. A. Wiley[1], A. J. Silva[1], M. E. Camp[2], K. M. Ferio[2], and C. A. Bagnell[2], *[1]Auburn University, Auburn, AL, [2]Rutgers University, New Brunswick, NJ.*

For eutherian mammals, a continuum of maternal support insures that development of progeny follows an optimal program. Beginning in utero, such support extends into the early neonatal period when nutrients and bioactive factors are communicated from mother to offspring in colostrum/milk. Defined as lactocrine signaling, communication of milk-borne bioactive factors (MbFs) from mother to offspring as a consequence of nursing is important for development of many somatic tissues, including the female reproductive tract. Endometrial development in the neonatal pig is estrogen receptor (ESR1) dependent. Disruption of ESR1-dependent, estrogen-sensitive developmental events shortly after birth (postnatal day = PND 0) that alter tissue developmental trajectory as determined on PND 14 can have long-term consequences for uterine function and reproductive capacity in adults. The lactocrine hypothesis for maternal programming of porcine endometrial development was proposed initially to explain how bioactive colostral relaxin (a porcine MbF), acting via its cognate receptor which is expressed in uterine tissues at birth, induces uterine expression of ESR1 and the parallel expression of other morphoregulatory factors such as vascular endothelial growth factor (VEGFA). This, it was proposed, insures propagation of down-stream signaling events essential to the success of endometrial development. To test the lactocrine hypothesis, patterns of uterine and endometrial gene expression and morphogenesis were evaluated at PND 2 and PND 14 in gilts that either nursed normally or were maintained in a lactocrine-null state on porcine milk replacer for defined periods from birth. Imposition of the lactocrine-null state for 48h from birth suppressed endometrial expression of morphoregulatory factors, including ESR1 and VEGFA, inhibited endometrial cell proliferation and retarded uterine gland development

by PND 14. Results provide the first evidence of cell compartment-specific, lactocrine-mediated endometrial morphogenesis and indicate that lactocrine signaling contributes to the palette of factors affecting reproductive tract development in the neonate.

Key words: lactocrine, uterus, development

4 Opportunities for improving milk production efficiency in dairy cattle. E. E. Connor*[1], J. L. Hutchison[2], K. M. Olson[2], and H. D. Norman[2], *[1]USDA-ARS, Bovine Functional Genomics Laboratory, Beltsville, MD, [2]USDA-ARS, Animal Improvement Programs Laboratory, Beltsville, MD.*

Increasing feed costs and the desire to improve environmental stewardship have stimulated interest in improving feed efficiency of livestock, including that of US dairy herds. For instance, USDA cost projections for corn and soybean meal suggest a 20% increase over 2010 pricing for a 16% protein mixed dairy cow ration in 2011, which may lead to a reduction in cow numbers to maintain profitability of dairy production. Furthermore, an October 2010 study by The Innovation Center for US Dairy to assess the carbon footprint of fluid milk found that the efficiency of feed conversion is the single greatest factor contributing to variation in the carbon footprint, due to its effects on methane release during enteric fermentation and from manure. Thus, we are conducting research to identify the most efficient dairy cattle at conversion of feed to milk using residual feed intake (RFI), a measure used successfully to identify the most efficient beef cattle at conversion of feed to gain. Residual feed intake is calculated as the difference between predicted and actual feed intake to support maintenance and production (e.g., growth in beef cattle, or milk in dairy cattle). Selection for a lower RFI phenotype can reduce feed intake, methane production, nutrient losses in manure, and visceral organ weights substantially in beef cattle. We have evaluated RFI measures during the first 90 d of lactation for the USDA-Beltsville Holstein herd and found the heritability of RFI to be 0.16 (n = 254). A difference in net feed intake of 8.3 kg/d DM was found between the least and most efficient animals. Mean actual DMI differed by 3.7 kg/d ($P < 0.0001$) between the efficient and inefficient groups (±0.5 SD from the mean RFI of 0), with no differences ($P > 0.20$) in mean BW, ADG, or ECM exhibited between the 2 groups. These results suggest promise for using RFI in dairy cattle to improve feed conversion to milk. Previous and current research on the use of RFI in lactating dairy cattle will be discussed, as well as opportunities to improve production efficiency of dairy cattle using RFI for milk production.

Key words: dairy cow, feed efficiency, residual feed intake

5 Lactational imprinting: The mechanism underlying the mammary response to changes in milking frequency? E. H. Wall*[1], J. P. Bond[2], and T. B. McFadden[3], *[1]Department of Animal Science, University of Vermont, Burlington, [2]Vermont Genetics Network Bioinformatics Core, University of Vermont, Burlington, [3]Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Alberta, Canada.*

Regular removal of milk from the mammary gland is critical to maintaining milk secretion. Early studies in rodents demonstrated that changes in milking frequency influenced mammary cell number, DNA content and cell activity, and blood flow. Later studies in ruminants confirmed these observations, and confirmed that the response was regulated locally within the mammary gland. In addition, it was discovered that frequent milk removal during early lactation stimulated an increase in milk production that partially persisted through late lactation, indicating long-term effects on mammary function. The local mechanisms regulating the mammary response to changes in milking frequency are poorly understood, although several have been proposed. To gain insight into the mechanisms underlying the mammary response to changes in milking frequency, and to identify genes associated with the response, we used a functional genomics approach and conducted experiments on dairy cows exposed to unilateral frequent milking (UFM; twice daily milking (2X) of the left udder half, 4-times daily milking (4X) of the right udder half). Across multiple experiments, we were unable to detect an effect of UFM on mammary cell proliferation or apoptosis. We have identified, however, distinct transcriptional signatures associated with the mammary response to milk removal, milk stasis, and UFM during early lactation. Sequential sampling of mammary tissue revealed that when UFM was imposed during early lactation, a group of genes was coordinately regulated with changes in differential milk production. Moreover, some genes were persistently differentially expressed after UFM and were associated with the long-term increase in milk yield. We conclude that a coordinated transcriptional response underlies the increase in milk yield elicited by frequent milking during early lactation, and that the transcriptional signature may be a marker for the autocrine regulation of milk production. Moreover, we propose that we have identified a novel form of imprinting associated with long-term alteration of mammary function, which we term "lactational imprinting."

Key words: gene expression, imprinting, mammary gland

6 Mammary metabolism of amino acids in dairy cows. H. Lapierre*[1], L. Doepel[2], G. Raggio[3], and S. Lemosquet[4], *[1]Agriculture and Agri-Food Canada, Sherbrooke, QC, Canada, [2]University of Calgary, Calgary, AB, Canada, [3]College Alfred, Guelph University, Guelph, ON, Canada, [4]UMR1080 Dairy Production, INRA, Saint-Gilles, France.*

The mammary gland (MG) is the major net user of essential AA (EAA) supply. The MG metabolism of AA is not, however, a straightforward process. In the late 70s, 2 major groups of EAA were identified: Grp 1 [His, Met, Phe (+Tyr), Trp] for which MG uptake was similar to MP output, and Grp 2 (Ile, Leu, Val, Lys) for which uptake was greater than MP output. To confirm this and to expand our knowledge of MG metabolism, we have adapted and refined techniques including: measuring net flux with AA concentrations determined by isotopic dilution on individual rather than pooled samples, and measuring total flux using AA labeled with stable isotopes. Mammary net fluxes indicate that the stoichiometric transfer of Grp 1 AA is maintained under changing supply: the uptake to output ratio (U:O) is not different from 1. Using labeled Phe, we observed that doubling Phe supply did not result in any mammary oxidation of Phe + Tyr, indicating no alteration of the U:O. For Grp 2 AA, not only does the MG remove them in excess of MP secretion, but this excess increases with increasing supply. Using labeled Leu, we observed that Leu taken up in excess of MP secretion is oxidized within the MG, and that oxidation increased further with increased Leu excess induced by duodenal casein infusion. It is hypothesized that the excess uptake of Leu (and other Grp 2 AA) can provide ATP to support increased protein synthesis induced by increased protein supply or supply carbon skeleton for the synthesis of non-EAA or both. Using labeled Lys, we observed that under normal feeding conditions, Lys U:O averaged 1.37 with the N of Lys taken up in excess mainly transferred to Glx, Asx, Ser and Ala; with Lys depletion, lower Lys mammary excess (12%) was also transferred to other AA, but at lower rates. Arg is a unique EAA

as its U:O varies between 2 and 3. Deletion of Arg from an abomasal infusate decreased the U:O from 2.5 to 2.1 but did not alter MP output, suggesting that other sources of N can cover Arg deficiency. The MG metabolism of EAA is coordinated with splanchnic metabolism: the liver removes a large fraction of the portal absorption of Grp 1 AA whereas it removes, on a net basis, little if any Grp 2 AA.

Key words: dairy cow, amino acid, mammary

7 Stress effects on postpartum reproduction in dairy cows. M. A. Crowe* and E. J. Williams, *Veterinary Sciences Centre, University College Dublin, School of Agriculture, Food Science and Veterinary Medicine, Belfield, Dublin 4, Ireland.*

The objective of the presentation is to review the effects of production stressors on reproductive performance of dairy cows. It has been well documented that genetic selection for milk yield over the last 50 years has been associated with reduced fertility. In addition to negative associations between yield and conception rate, there is also an association between milk production and expression of behavioral estrus. Stress caused by production diseases in high yielding dairy cows also contributes to the problems of poor fertility. Lameness results in reduced intensity of estrus, and can contribute to ovulation failure, which is largely due to reduced pre-ovulatory estradiol secretion and failure of the LH surge. Mastitis has been associated with prolonged intervals to dominant follicle selection, and in animals with uterine infection the dominant follicle grows slower and produces less estradiol. In a recent study we identified that milk yield was associated with an increased incidence of uterine infection, which is known to contribute to reduced fertility and prolonged calving to conception intervals. The incidence of uterine disease was 73% in high yielding, compared with 45% in low yielding cows. As well as effects at the ovary, various models of stress have also been shown to perturb endocrine secretion in the hypothalamus and anterior pituitary. In conclusion, the adverse affects on fertility associated with genetic selection for yield in dairy cows is in part associated with increased incidences of production disease induced stress but is also associated with high milk yield. Funded by SFI (07/SRC/B1156).

Key words: production disease, fertility, dairy cow

Monday, July 11, 2011

POSTER PRESENTATIONS

Animal Behavior and Well-Being

M1 Validation of an automated method for recording the feeding behavior of dairy cows using a Calan Broadbent Feeding System. L. M. Klaiber*, P. D. Krawczel, S. S. Thibeau, and H. M. Dann, *William H. Miner Agricultural Research Institute, Chazy, NY.*

Assessing feeding behavior is important in understanding the effects of nutrition and management on the well-being of dairy cows. Historically, collection of behavioral data from cows fed with a Calan Broadbent Feeding System required the labor-intensive practices of direct observation or video review. The objective of this study was to validate the output of a HOBO change-of-state datalogger, mounted to the door shell and latch plate, against video data summarized with continuous sampling. Data (number of feed bin visits per day and feeding time in minutes per day) were recorded with both methods from 26 lactating cows and 10 nonlactating cows for 3 d per cow (n = 108). The agreement (established by non-significant R^2) of the datalogger and video methods was evaluated using the REG procedure of SAS to compare the mean response of the methods against the difference between the methods. The maximum allowable difference (MAD) was set at ± 3 for bin visits and ± 20 min for feeding time. Ranges for feed bin visits (2 to 140 per d) and feeding time (28 to 267 min per d) were established from video data. Using all the data, agreement was established between the datalogger and video methods for feed bin visits (P = 0.47; $R^2 < 0.005$), but was not established for feeding time ($P < 0.001$; $R^2 = 0.25$; $y = -0.64x + 92.5$). The complete data set was screened to remove visits of a duration ≤ 3 s reflecting a cow unable to enter a feed bin (7% of all data) and ≥ 5400 s reflecting a failure of the door to close properly (<1% of all data). Using the screened data set, agreement was established for feed bin visits ($P = 0.57$; $R^2 < 0.003$) and feeding time ($P = 0.13$; $R^2 = 0.01$). For bin visits, 4% of the data were outside of the MAD. For feeding time, 3% of the data were outside of the MAD and 83% of the data were within ± 3 min. The agreement between the 2 methods indicates that the use of a datalogger is a viable method for the assessment of feeding behavior for cows using the Calan Broadbent Feeding System. Use of the screening criteria before analyzing data resulting from the datalogger method is recommended.

Key words: validation, feeding behavior, Calan

M2 Animal welfare assessment of intensive dairy farms from central zone of Chile under confinement with different housing systems. M. J. Castro, C. Kobrich, and M. S. Morales*, *Departamento Fomento de la Produccion Animal, Facultad de Ciencias Veterinarias y Pecuarias, Universidad de Chile, Santiago, RM, Chile.*

The objective was to evaluate dairy welfare in 2 types of confinement systems in central Chile. Nineteen dairy farms were free stall (FS, n = 9) or California corral (CC, n = 10). Herd size ranged from 40 to 1100 lactating cows; animal welfare was assessed using the Welfare Quality® protocol for dairy cattle which considers animal based measures to evaluate the overall welfare (OW) at the farm, using 4 welfare principles: good feeding, good housing, good health and appropriate behavior, and 11 welfare criteria, giving a score (excellent, enhanced, acceptable and not classified) to each. Results from the scores by criteria, principles and OW were statistically described and analyzed by Kruskal-Wallis ANOVA using Minitab. No differences between housing systems for OW and the different principles were observed; while among the 11 welfare criteria considered in the evaluation; only absence of prolonged hunger, expression of social behavior (ESB) and good human-animal relationship (GHAR) showed statistical differences ($P \leq 0.05$) between FS and CC, where FS had higher scores for ESB and GHAR than observed for CC. The OW ranged between acceptable and enhanced, no farm showed an excellent level, and only one was nonclassified. The welfare principles good feeding and good housing among dairy farm systems ranged excellent to enhanced, while good health was acceptable and appropriate behavior ranged between acceptable and not classified. Results reflect that animal behavior generally is not considered a productive issue, whereas nutrition and feeding, housing and health management do receive more attention because of their direct effects on production. Confinement systems did not differ in measures of animal welfare quality and both systems had acceptable welfare quality. Funded by European Union-Latin American cooperative project (Nº FOOD-CT-2004–506508) and CONICYT.

Key words: animal welfare, dairy cows, housing systems

M3 Effect of dietary starch on the behavior of early postpartum dairy cows. P. D. Krawczel*[1], B. H. Nelson[1,2], H. M. Gauthier[1], L. M. Klaiber[1], R. E. Clark[1], R. J. Grant[1], and H. M. Dann[1], *[1]William H. Miner Agricultural Research Institute, Chazy, NY, [2]Department of Animal Science, The University of Vermont, Burlington.*

Propionate, a product of starch fermentation, may be the signal for satiety in ruminant species, which suggests that altering the starch content of a ration may alter feeding behavior. The objective of this study was to evaluate the feeding and lying behavior of multiparous dairy cows (n = 13/treatment) fed a total mixed ration containing L (21.0 ± 0.3% of DM), M (23.2 ± 0.3% of DM), or H (25.5 ± 0.3% of DM) dietary starch levels from 1 to 14 d in milk (DIM). Housing consisted of sand-bedded freestalls and a Calan Broadbent Feeding System. Following a completely randomized design, behavioral data from 8 to 14 DIM were captured using dataloggers (feeding recorded continuously and lying recorded at 1-min intervals). The bimodal distribution of intervals between visits to feed bins was used to calculate a meal criterion, which was used to establish the mean meals per day, the mean duration of each meal, and the meal time per day (active feeding time plus additional within-meal time). Lying behavior consisted of mean lying time per day and the mean daily bouts. Data were analyzed by ANOVA with the MIXED procedure of SAS using treatment and day as fixed factors and cow within treatment as a random factor. Dry matter intake increased from d 8 (19.7 ± 0.6 kg/d) to d 14 (20.7 ± 0.6 kg/d; $P < 0.001$), but no treatment or treatment by day interaction was evident ($P \geq 0.55$). Meals (10.4 ± 0.5 n/d), meal duration (17.1 ± 0.9 min/meal), and lying (696 ± 37 min/d) did not differ by treatment ($P \geq 0.36$), day ($P \geq 0.18$), or treatment by day interaction ($P \geq 0.31$). Feeding and meal times had treatment by day interactions ($P \leq 0.04$)

with the response of the L cows on d 14 (172 ± 10 min/d and 202 ± 12 min/d), relative to H (138 ± 10 min/d and 164 ± 12 min/d) and M (140 ± 10 min/d and 157 ± 12 min/d) cows, most likely responsible for this effect. A treatment by day interaction was evident ($P = 0.05$) for lying bouts, but the range of the mean of bouts (from 10 to 14) did not suggest a biologically meaningful effect. Treatment-by-day interactions suggest the possibility of behavioral responses in early postpartum dairy cows to dietary starch that merit further evaluation.

Key words: behavior, starch, transition cow

M4 Effects of a high forage prepartum diet on feeding behavior of 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, BC, Vancouver, British Columbia, Canada, [2]Agriculture and Agri-Food Canada, Agassiz, British Columbia, Canada.*

Feeding higher forage diets prepartum is known to reduce energy intake before calving and improve postpartum health in dairy cows, but the effects of these diets on feeding behavior has not been described. The aim of this study was to compare the feeding behavior of cows fed either a traditional close up diet (NEL = 1.46 Mcal/kg; 24.3% concentrate, 76.8% forage) or a higher forage diet (NEL = 1.41 Mcal/kg; 13.4% concentrate, 86.6% forage) prepartum. Treatments were assigned to cow (n = 20 healthy multiparous Holsteins) within the same pen. Alternate electronic Insentec feeders provided access to feed and were programmed to allow access only to cows assigned to that diet. The number, duration and intake for each feeder visit was recorded electronically, and these data were used to calculate daily DMI, feeding time, and the number and duration of meals (with meals defined using the distribution of intervals between feeder visits). Time spent ruminating was measured using an electronic collar. All measures were recorded from 2 wk before calving until the day of calving. Cows fed the higher forage diet had lower DMI before calving (13.2 ± 0.6 vs. 16.0 ± 0.6 kg/d; $P = 0.003$), but spent more time ruminating (517 ± 12 vs. 411 ± 12min/d; $P < 0.0001$) compared with cows fed the traditional pre-calving diet. Cows on the higher forage diet ate fewer meals (9.4 ± 0.4 vs. 10.9 ± 0.4 meals/d; $P = 0.02$), but spent more time consuming meals (388.3 ± 13.8 vs. 324.3 ± 13.8 min/d; $P = 0.005$) than those on the traditional pre-calving diet. The number of separate visits to the assigned feeder (where cows were allowed access to feed) averaged (±SD) 70 ± 23 visits/d and did not differ between treatments. Cows also attempted to enter feeders assigned to the alternate treatment diet; these attempts were recorded but access to feed was denied. The number of attempted visits was higher for cows fed the higher forage vs. traditional diet (17.4; 95% CI = 17.0–22.9 vs. mean = 4.3; 95% CI = 3.5–5.2; $P = 0.02$). In conclusion, cows fed higher forage diets prepartum period consumed less DM, but ruminated more, consumed fewer and longer meals and made more attempts to access feed from the alternate treatment.

Key words: forage, dairy cow, behavior

M5 Diurnal grazing behavior of cattle fed a concentrate supplement during the dry-rainy transition season in tropical conditions. H. J. Fernandes*[1], V. Siqueira[1], L. O. Tedeschi[2], G. C. Coelho[1], L. M. Paiva[1], C. Guaraldo[1], and J. C. Souza[3], *[1]State University of Mato Grosso do Sul, Aquidauana, MS, Brazil, [2]Texas A&M University, College Station, [3]Federal University of Mato Grosso do Sul, Aquidauana, MS, Brazil.*

The objective of this study was to evaluate the effect of a concentrate supplementation on the grazing behavior of cattle under tropical conditions. Twenty-four Nellore bulls, with average initial BW of 384 ± 28.8 kg were divided into 4 groups and grazed Mombaça grass (*P. maximum*, Jacq.) pastures in the beef cattle center of the State University of Mato Grosso do Sul, in Aquidauana, Brazil, at the beginning of the transition of the dry to the rainy season. Two groups received concentrate supplementation and other 2 received only mineral supplementation. After 28 d of adaptation, animals were individually identified and their grazing behavior was observed using binoculars from 0600 to 1800 h, every 5 min, during 6 consecutive day. At each observation, the animals' behavior was classified as standing in leisure, standing ruminating, lying in leisure, lying ruminating, walking, grazing, consuming supplement, or drinking water. The total time ruminating was calculated as the sum of time standing and lying while ruminating. The total time of leisure was calculated as the sum of time standing and lying in leisure. The daily time spent in each behavior was analyzed considering the effect of the type of the supplement. The diurnal time standing in leisure in animals receiving concentrate was greater than those receiving mineral supplement (Table 1). Also the time spent on diurnal period to consume supplement was greater for those animals. The diurnal grazing time was greater for animals that received mineral supplement. The other observed behaviors were not affected by the type of supplement provided.

Table 1. Means of diurnal behavior (min/d) of cattle during the dry-rainy transition season

Behavior	Type of Mineral	Supplement Concentrate	SE	*P*-value
Standing in leisure	51.3	59.6	3.00	0.054
Standing ruminating	4.35	4.38	0.88	0.976
Lying in leisure	191	191	11.3	0.982
Lying ruminating	43.7	42.7	5.90	0.901
Total time ruminating	48.0	47.1	6.31	0.918
Total time of leisure	242	251	12.6	0.628
Walking	20.8	22.8	1.70	0.423
Grazing	392	354	7.99	0.001
Consuming supplement	9.47	37.6	1.46	<0.001
Drinking water	7.13	7.52	0.629	0.664

Key words: behavior, grazing animals, supplementation

M6 Competition and feed restriction affect feeding and competitive behavior of group-housed dairy cows. L. K. M. Collings*[1], D. M. Weary[1], N. Chapinal[1,2], and M. A. G. von Keyserlingk[1], *[1]University of British Columbia, Vancouver, BC, Canada, [2]University of Guelph, Guelph, ON, Canada.*

The effects of overstocking at the feed bunk are known, but no research has focused on the effects of restricting feed access time, or feeding to a slick bunk in group-housed cows. Our aim was to determine the effects of temporal and spatial competition on the feeding behavior of group-housed cows. Using a replicated Latin square design 48 Holstein cows were randomly assigned to groups of 6 cows; groups were assigned to either a competitive (2:1 cows:bin) or non-competitive (1:1 cow:bin) treatment and provided feed access for either 14 or 24 h/d. DMI, feeding time and rate were measured for 24 h and 2 h following fresh feed delivery for the last 4 d of the 7 d periods. Displacements were recorded for 2 h after the delivery of morning feed (peak

feeding period) and 2 h following afternoon milking. DMI tended to decline when feed access was restricted (27.0 vs. 25.7 ± 0.5 kg/d, P = 0.06), but was not affected by competition (26.4 ± 1.9, mean ± SD). Feed restricted cows had lower daily feeding times (190.9 vs. 207.9 ± 6.1 min, P = 0.005). When fed competitively restricted access cows had increased feeding rates during the day (136.9 vs. 155.6 ± 3.8 g/min, P < 0.0001) and during the peak feeding period (146.5 vs. 175.2 ± 4.3 g/min, P < 0.0001). In the peak feeding period, competitive cows had lower DMI (6.1 vs. 6.9 ± 0.3 kg/2 h, P = 0.02) and feeding times (41.5 vs. 51.6 ± 2.1 min/2 h, P = 0.0001) and increased feeding rates (160.9 vs. 137.8 ± 3.9 g/min, P < 0.0001). In contrast, feed restricted cows had higher DMI (7.8 vs. 5.2 ± 0.3 kg/2 h, P < 0.0001) and feeding time (54.7 vs. 38.5 ± 2.1 min/2 h, P < 0.0001). Restricting feed access in conjunction with limited feed bunk access resulted in the greatest increase in daily displacements (15.0 vs. 7.4 ± 1.4, P < 0.0001), with the majority of these occurring during the peak feeding period (11.2 vs. 4.8 ± 1.1, P < 0.0001). Adequate space and time to access feed is essential to minimize the welfare concerns that can arise with indoor group housing systems.

Key words: feeding behavior, competition, dairy

M7 Effect of residual feed intake in reactivity of Nellore heifers. T. L. Sobrinho[1], L. T. Egawa[2], R. H. Branco[2], E. Magnani[2], S. F. M. Bonilha[2], and M. E. Z. Mercadante*[2], *[1]Faculdade de Ciências Agrárias e Veterinárias, Jaboticabal, São Paulo, Brazil, [2]Instituto de Zootecnia, Sertãozinho, São Paulo, Brazil.*

Residual feed intake (RFI) is the difference between DMI observed and predicted by regression equation as function of mid metabolic BW and ADG. This study aimed to evaluate reactivity of Nellore heifers classified as high, medium and low RFI. The experiment was conducted at Instituto de Zootecnia - Sertãozinho/São Paulo/Brazil. Fifty-six Nellore heifers with averages of 282 kg for BW and 9 mo for age were evaluated during 6 weighings. Reactivity score was obtained using qualitative behavioral measure (temperament score), based on movement, posture, breathing, stress level and presence or absence of kicks and vocalisation being classified on scale from 1 (docile) to 5 (aggressive). High RFI animals and the low RFI ones consumed, respectively, on average, 7.13 and 6.32 kg of DM/d, corresponding to a difference of 0.810 kg of DM/d between less and more efficient animals. There was no significant difference (P = 0.4943) in reactivity among RFI levels. Docile animals when compared with the agitated ones use less energy, but the relationship between reactivity and ADG is not always antagonistic, depending of each animal. Reactivity not always defines temperament, that is a measure of complex expression, which justifies differences in physiological and productive traits.

Table 1. Performance, DMI and reactivity of Nellore heifers classified for RFI

Traits	High RFI	Medium RFI	Low RFI	P-value
n	18	21	17	
DMI, kg/d	7.13[a]	6.63[b]	6.32[c]	<0.0001
RFI, kg/d	0.406[a]	0.010[b]	−0.442[c]	<0.0001
ADG, kg/d	0.832[a]	0.858[a]	0.861[a]	0.7508
Reactivity	2.06[a]	2.47[a]	2.29[a]	0.4943

[a-c]Means within a row followed by the same letter do not differ (P > 0.05) by Tukey test.

Key words: behavior, efficiency, temperament

M8 Effect of different short- and long-term heat stress exposure periods and fescue toxicosis on the immune system. P. A. Eichen*[1], D. K. Kishore[1], M. R. Waldron[1], T. J. Evans[2], K. L. Fritsche[1], and D. E. Spiers[1], *[1]University of Missouri, Division of Animal Sciences, Columbia, [2]University of Missouri, Department of Veterinary Pathobiology, Columbia.*

Fescue toxicosis and heat stress have each been shown to independently impact immune function of animals. The primary objective of this study was to investigate how heat stress, in combination with fescue toxicosis, affects the immune system. A secondary objective was to assess the effect of length of exposure to these stressors. Rats (n = 144) were housed at thermoneutrality (TN; 21°C) and fed diets containing ergopeptine alkaloids (E+), no alkaloids (E-), or pair-fed (PF to E+) for one week. They were then divided into TN or heat stress (HS; 33°C) groups and exposed for a 3-d short-term (ST) or 21-d long-term (LT) period. Blood samples, collected at the end of the trial, were analyzed by flow cytometry for various lymphocyte subpopulations, including: T cells, natural killer (NK) cells, B cells, CD4+ and CD8+ T cell subsets. In both ST and LT, daily food intake (FI) was reduced as a result of consumption of E+ diet (50% and 40%, respectively) with additional decrease during HS. During LT HS, there was partial recovery of FI by Day 4. Individually, neither E+ nor HS in ST affected proportions of NK, T- or B-lymphocytes present in the circulation. However, acute exposure to both stressors elevated NK cells % (P < 0.05), while diminishing B-cell % in turn (P < 0.05). These changes in lymphocyte subpopulations were clearly not a consequence of FI reduction from E+ and HS, because PF to E+ rats fed to the same intake failed to show these immune cell profile shifts. In contrast to ST effects, LT exposure to HS alone elevated NK cells % (P < 0.05). However, it took the combination of LT HS and E+ exposures to reduce T-lymphocyte % in the blood (P < 0.05). In summary, acute- and long-term exposures to HS and/or E+ can lead to alterations in circulating immune cell subpopulations. Additional studies are needed to determine if such shifts in circulating lymphocytes might affect host response to infection.

Key words: heat stress, immune, fescue toxicosis

M9 Intake and feeding behavior in growing heifers fed a high concentrate diet and offered a total mixed ration or dietary components separately. S. P. Iraira, M. Rodríguez-Prado, X. Manteca, J. L. Ruíz de la Torre, S. Calsamiglia*, and A. Ferret, *Universitat Autònoma Barcelona, Bellaterra, Barcelona, Spain.*

Calves fed high concentrate diets consume low amounts of forage when dietary components are offered separately. Total mixed ration could be a good approach to promote a greater intake of roughage. Eight Simmental heifers (118 ± 3.8 kg initial BW) were used to study the effects of feeding method on intake and animal behavior in a cross-over design experiment. Treatments consisted of feeding concentrate and chopped barley straw as: 1) choice (CH; concentrate and straw in separate feed bunks), or 2) as total mixed ration (TMR; concentrate and straw mixed in one feed bunk). Feeds were offered on an ad libitum basis, but always maintaining a concentrate to straw ratio of 90 to 10. The experiment was performed in 2 21-d periods, and sampling was carried out in the last week of each period. At the end of each period, heifers changed treatment, so the final number of animals per treatment was 8. Intake was recorded over 7 consecutive days. Barley straw was coarsely chopped with a chopping machine. Animal behavior was video-recorded for 24-h on d 2 and d 6 of each sampling week. Differences were analyzed by using the MIXED procedure of SAS, for

intake variables, and the GLIMMIX procedure of SAS, for behavior variables. Concentrate intake and total DMI of heifers fed with the CH feeding method were higher than when fed with the TMR (5.1 and 5.3 kg vs. 4.7 and 5.0 kg, for CH and TMR; $P = 0.002$ and $P = 0.021$, respectively). Conversely, intake of barley straw was higher in heifers fed with the TMR feeding method than in heifers fed CH (0.21 vs. 0.31 kg, for CH and TMR; $P = 0.001$). Total NDF intake was similar in both treatments. In contrast, NDF intake from barley straw was higher in heifers fed with the TMR feeding method than in heifers fed with CH (0.16 vs. 0.23 kg, for CH and TMR; $P = 0.001$). Feeding method did not affect eating and drinking behaviors but it did affect ruminating behavior and heifers fed TMR spent more time ruminating than heifers fed concentrate and barley straw separately (287 vs. 376 min, for CH and TMR; $P = 0.007$).

Key words: feeding behavior, feeding method, high-concentrate diet

M10 Validation and cross-prediction of a single or dual accelerometers for the prediction of grazing, standing/walking, and lying behavior of beef cattle using linear discriminant analysis. M. S. Gadberry[1], W. Whitworth*[2], G. Montgomery[2], and K. Simon[1], *[1]University of Arkansas, Cooperative Extension Service, Little Rock, [2]University of Arkansas, Southeast Research and Extension Center, Monticello.*

The objective of this study was to evaluate Hoboware's Pendant G 3-axis accelerometer data logger for the prediction of grazing (G), standing/walking (SW), and lying (L) behavior in beef cattle. Three mature, nonlactating Beefmaster cows (C1, C2, and C3) of mild temperament were monitored. On Jun 28, accelerometers were halter mounted, aligned posterior to the poll (P1) or placed within a patch and adhered to the hide, caudal to the shoulder and centered over the thoracic vertebrae (P2). Data logging was programmed to begin Jun 30 at 0700 for 1 s intervals. Cattle behavior was recorded by 3 observers using a spreadsheet with a timestamp script, recording the change in cow behavior from G, SW, and L. Linear discriminant analysis (LDA) was used to predict behavior within cow using a 50% random sample as the training data set and the remaining observations as a test data set. The prediction of one cow's behavior using another cow's prediction coefficients was also examined. At 1 s intervals, logger capacity (16,270 obs) was reached at 1130. Observed time G, SW, and L differed among cows ($P < 0.001$). Among cows, the percentage of accurate predictions for G tended to differ ($P = 0.06$) for P1, P2 and combined position (P1P2), 85.5%, 81.9%, and 93.1%, respectively. Percent accuracy for L activity differed ($P < 0.001$) for P1, P2 and (P1P2), 76.4%, 97.6%, and 98.1%, respectively. Percent accuracy for SW activity differed ($P = 0.002$) for P1, P2 and (P1P2), 63.5%, 84.0%, and 91.9%, respectively. For C1 and C2, G and L could be cross-predicted with >90% accuracy. However, SW was less predictable at 36% and 67% accuracy when C1 was used as the predictor of activity for C2 and vice versa, respectively. C3 coefficients could not predict C1 or C2 and vice versa for G and SW (less than 10% accuracy). These results indicate LDA, based on 2 positions of a 3-axis accelerometer, can predict G, SW, and L with greater than 90% accuracy, however, prediction of one cow's behavior from another cow's prediction coefficients does not appear viable.

Key words: accelerometer, beef cattle, behavior

M11 Comparison of logging intervals for accelerometer predicted grazing, standing/walking, and lying behavior of beef cattle. M. S. Gadberry*[1], W. Whitworth[2], G. Montgomery[2], and K. Simon[1], *[1]University of Arkansas, Cooperative Extension Service, Little Rock, [2]University of Arkansas, Southeast Research and Extension Center, Monticello.*

Because extending logging interval for a fixed capacity data logger increases the total observation time, the objective of this study was to evaluate logging interval of Hoboware's Pendant G 3-axis accelerometer data logger for the prediction of grazing (G), standing/walking (SW), and lying (L) behavior in beef cattle. One mature, nonlactating Beefmaster cow (C1) of mild temperament was monitored. On Jun 28, an accelerometer was halter mounted and aligned posterior to the poll and another placed within a patch and adhered to the hide, caudal to the shoulder and centered over the thoracic vertebrae. Data logging began Jun 30 at 0700 for 1 s intervals. Logger capacity was reached at 1130. Cattle behavior was recorded by a single observer using a spreadsheet with a timestamp script, recording the change in behavior from G, SW, and L. Using the C1 data set, linear discriminant analysis (LDA) was used to predict behavior using separate training and test observations. Five replications of training and test samples were drawn at 60, 30, or 15 s intervals and a t-test was used to determine if the percentage of predicted time differed from actual. Training sets were >90% accurate at predicting G and L at all 3 intervals. Training sets were 83%, 91%, and 88% accurate for predicting SW using 60, 30, and 15 s intervals, respectively. Actual percentage time G, SW, and L was 27, 22.5, and 50.5%. Percentage of time predicted G at 60, 30, and 15 s intervals was 29.8 ($P = 0.03$), 23.4 ($P = 0.002$), and 31% ($P = 0.001$), respectively. Percentage of time predicted SW using 60, 30, and 15 s intervals was 25.2 ($P = 0.04$), 24 ($P = 0.05$), and 22.4% ($P = 0.88$), respectively. Percentage of time predicted L using 60, 30, and 15 s intervals was 45 ($P = 0.002$), 52.6 ($P = 0.001$), and 46.4% ($P = 0.001$), respectively. No interval produced a best match to the actual observed G and L activity. As a result, prediction inaccuracies resulting from extended logging intervals must be considered in using this technology for estimating behavior on pasture.

Key words: accelerometer, beef cattle, behavior

M12 A comparison of lipopolysaccharide-induced febrile responses across heat-tolerant and -sensitive *Bos taurus* cattle in different thermal environments. R. E. Chaffin*[1], B. Scharf[1], J. S. Johnson[1], J. K. Bryant[1], D. K. Kishore[1], P. A. Eichen[1], J. A. Carroll[2], C. C. Chase[3], S. W. Coleman[3], N. C. Burdick[2], R. L. Weaber[1], and D. E. Spiers[1], *[1]University of Missouri, Columbia, [2]USDA-ARS, Livestock Issues Research Unit, Lubbock, TX, [3]USDA-ARS, SubTropical Agricultural Research Station, Brooksville, FL.*

Accurate detection of fever in cattle is an important step in maintaining health of a herd. There is little information on several fronts regarding the differences in febrile response to a lipopolysaccharide (LPS) challenge. These include differences in hot (HS) and thermoneutral (TN) environments and between heat-tolerant and -sensitive cattle. Likewise, there has been no comparison of febrile responses across different regions of the body. Eighteen–month–old Angus (ANG; n = 11; 306.7 ± 25.87 Kg BW) and Romosinuano (RO; n = 10; 312.9 ± 31.96 Kg BW) heifers, all derived from Florida, were fitted with ruminal telemetric transmitters (Tru; SmartStock, Pawnee, OK), rectal temperature dataloggers (Tre; Reuter et al., JAS 88:3291), and vaginal temperature dataloggers (Tvg; iButton, Maxim, Sunnyvale, CA). Animals were housed in separate stanchions in 4 temperature-controlled environmental chambers (Brody Environmental Center, University of Missouri). Ambient temperature was within cycling thermoneutral

range (TN; 18.5–23.5°C) for a one wk adjustment period, followed by an increase in 2 chambers to cycling heat stress level (HS; 18.5–38°C) for another 2 wks. On Day 20 of study, an *Escherichia coli* (O111:B4; Sigma-Aldrich, St Louis, MO) LPS (0.5 µg/Kg BW) was administered intravenously to all heifers at approximately 1000 h. Although LPS effect on Tru showed no differences ($P > 0.05$) across breed or environment, there was an approximate 1°C increase in HS animals within 5 h following injection. Tre increased by over 2.0°C within 5 h of injection, with higher values (~0.4°C; $P < 0.05$) for ANG versus RO and HS versus TN. During HS, RO heifers appeared to exhibit the largest increase in Tre. Although Tvg increased by over 2°C 6 h post-LPS injection ($P < 0.05$), there were no general breed or environment differences. These results show that there are regional differences in thermal response to LPS injection, with Tre providing the greater separation across breed and environment. Additional studies are needed to verify a heat-induced increase in the febrile response following an LPS challenge.

Key words: heat stress, cattle, LPS

M13 Effects of alternative housing and feeding systems on the performance of dairy heifer calves. J. A. Pempek*, M. L. Eastridge, N. A. Botheras, C. C. Croney, and W. S. Bowen, *The Ohio State University, Columbus.*

This study investigated the effects of housing and milk feeding method on the production performance of dairy calves. Eighty-two female Holstein calves were allocated to treatments at 6 ± 3 d of age and monitored for approximately 9 wk. Treatments were as follows: individual housing fed with a bucket, individual housing fed with a bottle, paired housing fed with a bucket, or paired housing fed with a bottle. Two experimental sites were utilized. Calves were housed in hutches (non-tethered, wire pen) at Site 1 (n = 34) and in wire-panel pens in a feed commodity shed at Site 2 (n = 48). Calves allocated to the individual treatment were housed in a single hutch at Site 1, whereas calves assigned to the paired treatment were housed by joining 2 adjacent hutches with doubling of the pen size. Pasteurized whole milk was fed via bucket or bottle twice a day (6 L/d). Calves had ad libitum access to calf-starter (same at both sites) and water. Gradual weaning commenced at wk 6 by reducing the calves' milk allowance by 2 L/wk. Calves were weaned at the beginning of wk 8. Grain consumption and body weight were monitored on a weekly basis and wither height measured at the beginning and end of the experiment. Data were analyzed using the MIXED model procedure of SAS. Total DM intake (grain and milk solids) was higher for calves housed in pairs compared with those housed individually (1764 ± 28 versus 1686 ± 27 g/d; $P = 0.04$). Average daily gain (ADG) was higher for Site 1 compared with Site 2 (1.6 ± 0.05 versus 1.4 ± 0.05 kg/d; $P = 0.001$). Bottle feeding also increased ADG compared with bucket feeding (1.6 ± 0.04 versus 1.4 ± 0.05 kg/d; $P = 0.01$). Change in wither height was greater at Site 1 (13.5 ± 0.5 versus 9.5 ± 0.4 cm; $P < 0.0001$) and for calves housed individually (12.2 ± 0.4 versus 10.8 ± 0.5 cm; $P = 0.03$). In conclusion, housing young calves in pairs may enhance performance due to social facilitation.

Key words: dairy calves, paired housing, performance

M14 Environmental enrichment influence on feedlot cattle performance. B. J. Howell*[1], J. R. Brethour[2], and J. R. Jaeger[2], *[1]Fort Hays State University, Hays, KS, [2]Kansas State University, Hays.*

Feedlot cattle are able to consume feedstuffs rapidly, quickly meeting DM intake requirements, and therefore have much more idle time in a confined space compared with grazing animals. The objective of 2 experiments was to investigate the effects of providing an environmental enrichment device consisting of a large brush on live and carcass performance in steers in a feed yard environment. In Exp. 1, yearling crossbred steers (n = 156) were allotted by weight to 2 treatments, no brush (control) or access to a brush (brush). Steers were fed for 73 d using 3 replications per treatment (n = 26 hd/replication). Steers were implanted with Synovex Plus and were not treated for parasites. In Exp. 2, yearling crossbred steers (n = 165) were blocked by weight and projected harvest date to 3 replications per treatment (n = 25 to 33 hd/replication). Steers had been previously implanted with Synovex-S, and were treated with Atroban for lice. Replication 1 was harvested (48 d), replication 2 (80 d), and replication 3 (110 d). All cattle were fed a high-energy finishing ration comprised primarily of dry-rolled milo and included sorghum silage, soybean meal, urea, ammonium sulfate and 300 mg Rumensin, 90 mg Tylan, and 30,000 IU Vitamin A per head. The brush treatment increased 12th rib fat thickness in Exp. 1 ($P < 0.05$), but not in Exp. 2 ($P > 0.05$). No differences ($P > 0.05$) were observed between treatments for average daily gain, dressing percentage, calculated yield grade, marbling, proportion grading Choice, kidney, or pelvic and heart fat. Daily dry matter intake was not different between treatments in Exp. 1 ($P > 0.10$), but was greater ($P = 0.03$) in Exp. 2 for steers housed with a brush compared with control steers (13.02 vs. 12.73 kg, respectively). Continual interaction occurred with the brush device in all brush replications throughout both trials, indicating it did provide a stimulus for the cattle.

Key words: environmental enrichment, beef cattle, feedlot

M15 Lack of the expressive associations between temperament, aggression and weight gain in finishing weight feedlot cattle. D. R. Soares*[1], K. Schwartzkopf-Genswein[2], A. C. Sant'anna[1], T. da Silva Valente[1], P. M. Rueda[1], J. N. dos Santos Gonçalves Cyrilo[3], and M. J. R. P. da Costa[4], *[1]Sao Paulo State University, Animal Science Posgraduation, Jaboticabal, Sao Paulo, Brazil, [2]Agriculture and Agri–Food Canada, Lethbridge Research Centre, Lethbridge, Alberta, Canada, [3]Animal Science Institut of Sertaozinho, Sertaozinho, Sao Paulo, Brazil, [4]Animal Science Department, Sao Paulo State University, Jaboticabal, Sao Paulo, Brazil.*

The aim of this study was to determine the relationship between temperament, aggressive behavior and average daily gain (ADG), in feedlot cattle. Behavioral observations were conducted for 10 d (0700 to 1800) using a continuous sampling method. Fifty–3 bulls (35 Nelore and 18 Nelore cross with an average age of 30 ± 3 mo.) were observed in one feedlot pen. The frequencies of 2 types of aggressive behavior were recorded: displacement (DISP; physical contact where the initiator pushed with his head, horn or body resulting in a change in the receivers position) and non-displacement (NDISP; as described above, without any change of the receivers position). Temperament was assessed, in the pen during at weights registers on d 1, d 29 and d 54 at the end of fattening period, using flight distance (FD: proximity (m) to which a stock person could come to an individual animal before it would move away) and flight speed (FS: speed (m/s) at which the animal exited a handling chute). Average daily gain was calculated using animal weights obtained on d 1 and d 54 at the end of the fattening period and Pearson correlation coefficients were estimated for all variables. There were significant positive correlations ($P < 0.05$) between FD and FS (r = 0.58), DISP and NDISP (r = 0.74) and negative correlations between NDISP and FS (r = –0.29). No correlations

($P > 0.05$) were observed between NDISP and FD (r = –0.17), DISP and FD (r = –0.06), DISP and FS (r = –0.13), or between ADG and any of the other variables (NDISP: r = 0.07, DISP: r = 0.03, FD: r = 0.09 and FS: r = –0.03). Based on these results we conclude that there is no expressive association between temperament, intra-specific aggression, or ADG. Financial support: CNPq and ETCO Group.

Key words: behavior, confinement, reactivity

M16 Relationship between temperament, blood flow and area in the external jugular vein, and body temperature in crossbred beef calves. H. L. Sanchez-Rodriguez*, R. C. Vann, E. Baravik-Munsell, S. T. Willard, and P. L. Ryan, *Mississippi State University, Mississippi State, MS.*

The relationship between temperament, blood flow and dimension of the external jugular vein, and body temperature was assessed in Angus crossbred calves [223.4 ± 33.2 kg BW; 262.72 ± 24.94 d old (mean ± SD)] during December, 2010. An average between exit velocity and pen score was used to classify the calves according to their temperament (calm, intermediate, and temperamental). Calves (n = 91) were weighed and the hair of the neck over the jugular vein was clipped. Pulsatility Index (PI) and area of the lumen of the external jugular vein were measured via Duplex Doppler and B mode ultrasound, respectively. The luminal area of the jugular vein was standardized by body weight. Rectal and superficial temperatures of the neck region (over the hair and over the skin) were also recorded. Blood samples were collected for future plasma cortisol analysis. There was a tendency for higher PI values ($P = 0.09$) in temperamental than in calm calves [1.78 ± 0.16, 1.87 ± 0.15, and 2.28 ± 0.18 for the calm (n = 31), intermediate (n = 32), and temperamental (n = 28) groups, respectively]. Luminal areas of the jugular vein were not affected by temperament ($P = 0.65$; 0.254 ± 0.016, 0.242 ± 0.015, and 0.263 ± 0.018 mm^2/kg BW for the calm, intermediate, and temperamental groups, respectively). Rectal temperatures were greatest ($P = 0.01$) in temperamental than in calm and intermediate calves (39.38 ± 0.13, 38.92 ± 0.12, and 38.90 ± 0.11°C, respectively). There was no effect of temperament on the superficial temperature of the hair ($P = 0.10$; 24.08 ± 0.65, 26.00 ± 0.61, and 25.15 ± 0.72°C) or the skin ($P = 0.84$; 33.23 ± 0.55, 33.59 ± 0.51, and 33.17 ± 0.61°C) in the neck region for the calm, intermediate, and temperamental calves, respectively. In this study there was a relationship between temperament and some important indicators of the animal′s physiological status (internal body temperature and Pulsatility Index). The effect of these physiological changes can influence the performance of beef cattle and therefore these markers may be beneficial in developing better tools for selection of beef cattle.

Key words: beef calves, temperament, blood flow

M17 Pre-separation behavior of calves being weaned by different methods. H. T. Boland*[1,5], S. T. Willard[2], K. Umemura[3], G. Scaglia[4], J. A. Parish[5], and T. F. Best[1], *[1]Mississippi State University, Prairie Research Unit, Prairie, [2]Mississippi State University, Department of Biochemistry and Molecular Biology, Mississippi State, [3]National Agricultural Research Center for Hokkaido Region, Toyohira, Sapporo, Japan, [4]Louisiana State University Agricultural Center, Iberia Research Station, Jeanerette, [5]Mississippi State University, Department of Animal and Dairy Sciences, Mississippi State.*

Two-stage weaning can potentially reduce stress associated with abrupt weaning of calves. British crossbred beef cattle (n = 96 cow-calf pairs) were used to evaluate 3 weaning methods: "one-size fits all" nose-clips (ONE), adjustable size nose-clips (ADJ), and fence-line weaning (FL). In a fourth control treatment group (CTRL) calves remained in pastures with their dams. Nose-clips were placed on ONE and ADJ calves on d −4 and FL calves were placed in pastures adjacent to their dams on d −4. All calves were completely separated from cows the morning of d 0. Calves wore bite counters and IceTag sensors to evaluate pre-separation grazing behavior and locomotor activity. Three trial periods were conducted in sequential weeks in Fall 2010. There were 2 replicate groups (4 cow-calf pairs per group) of each treatment per wk and each group grazed an area of 2.0 ha. Pasture assignment was randomized for treatment each week to minimize effects of differently shaped paddocks on behavior. A standard stride length of 65 cm was used to estimate distance traveled. Data were analyzed using PROC MIXED of SAS. There was no effect of weaning method on number of bites and steps, distance traveled, and time spent standing or lying per day ($P > 0.05$). On d −4, bites/d were less while steps/d and distance traveled/d were greater compared with d −3, −2, and −1 ($P < 0.05$). This was likely due to cattle being handled the morning of d −4 to start the experimental treatments and being introduced to new pastures. Unseasonably high ambient temperatures during wk 1 may have led to an effect of wk ($P < 0.05$) on bites/d with values being less in wk 1 than wk 2. Average high temperatures during wk 1, 2, and 3 were 36, 27, and 25°C, respectively. Time spent standing was greater, and consequently time spent lying was less in wk 1 compared with wk 3 ($P < 0.05$). On d −4 FL calves spent more time standing ($P < 0.05$) than CTRL calves, but only tended ($P = 0.07$) to stand more than ONE calves. The data indicate that use of these gradual weaning methods did not greatly alter behavior of calves during the first stage of the weaning process compared with calves that continued to nurse.

Key words: weaning methods, grazing behavior, pedometers

M18 Predictors of body thermal status in heat-tolerant and -sensitive *Bos taurus* cattle exposed to different temperature loads under controlled conditions. D. E. Spiers*, H. L. Vellios, P. A. Eichen, B. Scharf, J. S. Johnson, D. K. Kishore, and R. L. Weaber, *University of Missouri, Columbia.*

There have been attempts to derive predictors of thermal status for cattle, with the ultimate goal of developing practical models. There have been few studies under controlled conditions that have compared cattle with different sensitivities to thermal stress. There has been little attempt to identify shifts in predictors of thermal strain that occur with adaptation to heat stress. The present study evaluated multiple potential determinants of thermal status over repeated exposures to heat stress to determine shifts in correlation coefficients (R). Heat-sensitive Angus steers from Oklahoma (n = 6 per trial) and Missouri (n = 6 per trial) were compared against heat-tolerant Romosinuano steers (n = 5 per trial) from Florida in the Brody Environmental Center (University of Missouri). Air temperature (Ta), rectal temperature (Tre) and respiration rate (RR), as well as skin temperatures for ear, shoulder, rump, upper tail and lower tail were measured hourly for 24 h during one day midway through each temperature interval. Two different groups of animals were used in 2 separate trials. Cattle were exposed to a constant 20–22°C (TN) for 8 d, followed by 2 separate 7 d cyclic heat stress (HS) periods. Ta in Trial 1 cycled 26–36 then 28–37°C for the 2 cycles, and in Trial 2 cycled 28–38 then 30–40°C. In no case was Ta a reliable predictor of Tre or RR. Likewise, there was no skin temperature or Tre that served as a reliable determinant ($P > 0.05$) of RR. All additional comparisons examined skin temperature predictions of Tre. Trunk sites were closely related ($P < 0.05$) across breed and environment (TN and HS), with lower R between extremities. Rump and

shoulder sites were better Tre predictors under all conditions. Shift from TN to HS environments generally increased R from ~0.50 to 0.60. Use of only times when daily Ta increased (0500 to 1500) further improved R (~0.70) for many sites. Trial 2 with higher Ta did not increase R. Trunk temperature, and not RR or Ta, during the daily temperature rise is the best predictor of rectal temperature across heat-tolerant and -sensitive breeds.

Key words: cattle, heat stress, model

M19 Sexual behavior of Nellore cattle in the Pantanal. J. C. DeSouza*[1], U. G. P. Abreu[2], J. R. B. Sereno[3], C. H. M. Malhado[4], J. A. Freitas[5], P. B. Ferraz Filho[6], H. J. Fernandes[7], R. L. Weaber[8], and W. R. Lamberson[8], *[1]Mato Grosso do Sul Federal University – UFMS/ Animal Science, Aquidauana, Brazil, [2]Empresa Brasileira de Pesquisa Agropecuária - CPAP-EMBRAPA, Corumbá, Brazil, [3]Empresa Brasileira de Pesquisa Agropecuária - CPAC - EMBRAPA, Brasília, DF, Brazil, [4]South of Bahia State University - UESB, Bahia, Brazil, [5]Parana Federal University - UFPR, Palotina, Brazil, [6]Mato Grosso do Sul Federal University - UFMS, Tres Lagoas, Brazil, [7]State University of Mato Grosso do Sul, Aquidauana, Brazil, [8]Animal Sciences, University of Missouri, Columbia.*

The objective of this study was to evaluate the sexual behavior of Nellore bulls and cows by observing the duration of courtship, the hierarchy of bulls, the distance maintained between bulls, and the behavior of Nellore cows with respect to the choice of bull in a natural service mating system in the Pantanal Region of Mato Grosso do Sul, Brazil. Behavior was observed between 6:00 a.m. to 7:00 p.m. for a total of 380 h over 2 years. Thirty-six bulls were observed, of which 9 were more than 60 mo old, (GE5); 15 were 24 to 30 mo in year one (GE2_3) with 12 of these retained for a second year (GE2_4). The bull to cow ratio was 1:20 (average). All bulls from GE5 group maintained 10 M separation from each other, with one being the leader in a clear hierarchy. When GE2_3 bulls, in lots of 3, were exposed to cows, they spent the first days together, interacting through touching, licking and smelling each others' testicles. From the third day on, they started to exhibit the Flehmen response and mounting cows, but without completing sexual intercourse. The first service was observed on d 5. The hierarchical ranking among GE2_3 bulls was established only in the second year. Bulls from GE2_4 group were more precocious, completing sexual intercourse by the third day. A total of 32 matings were observed with 6 being repeated. Only 5 of the 26 serviced cows were observed to choose the male to mate. Among the 26 first matings, 11 took place before 10:00 a.m., 8 occurred from 10:00 a.m. to 4:00 p.m., and 13 occurred after 4:00 p.m. The mean duration of courtship was 68.45 min; and ranged from 17 to 186 min. Of the observation courtship, 75.76% lasted 60 min or less, 15.15% lasted between 60 and 120 min, and 3.0% lasted more than 120 min (Chi-Square = 26.91; $P < 0.0001$). It was observed in many cases that the bull and cows copulation once and then part with no further courtship or copulation. The presence of hierarchical (dominant) bulls may hinder fertility rate since it results in uneven distribution of matings among bulls.

Key words: courtship, ethology, Nellore

M20 Behavioral reactivity to psychosocial stress determines the effects of lavender oil on anxiety in sheep. P. Hawken[1], C. Fiol*[2], and D. B. Blache[1], *[1]UWA Institute of Agriculture (Animal Production), The University of Western Australia, Perth, Western Australia, Australia, [2]Departamento de Bovinos, Facultad de Veterinaria, Universidad de la República, Montevideo, Uruguay.*

The aim was to determine the effects of lavender (*Lavendula augustofolia*) oil on individuals that innately differ in their reactivity to stress. Merino ewes (n = 24) selected for high (nervous) and low (calm) expression of behavioral reactivity to isolation were allocated to 1 of 4 groups: Calm Lav; Calm Con; Nerv Lav; Nerv Con. Ewes were fitted with a mask that contained wool scented with 10% lavender (Lav) or peanut (Con) oil for 30 min before entering an isolation box for 5 min. Agitation score and activity in the box were recorded using a video camera and calibrated agitation meter. Blood was sampled before fitting the mask; before entering and after exiting the box, and 30 min after exiting the box. Behavioral and cortisol data were analyzed with 2-way and repeated measures ANOVA, respectively. Agitation score, central line crosses, vocalizations, and cortisol after exiting the box were lower for calm than nervous ewes, irrespective of exposure to Lav (Table 1; $P < 0.001$). Exposure of calm ewes to Lav decreased vocalizations, central line crosses (Table 1; $P < 0.05$), and cortisol before entering the box compared with calm control (14.6 ± 0.9 vs. 24.4 ± 3.4 ng/mL; $P < 0.05$). Among the nervous ewes, exposure to Lav increased vocalizations, escape attempts (Table 1; $P < 0.05$), and cortisol 30 min after exiting the box (37.1 ± 5.8 vs. 14.8 ± 3.0 ng/mL; $P < 0.05$). In conclusion, lavender decreased anxiety in sheep selected for calm temperament but increased some measures of anxiety in sheep selected for nervous temperament. Differences in behavioral reactivity to psychosocial stress appear to determine the effect of lavender oil on anxiety in sheep.

Table 1.

	Calm Con	Calm Lav	Nerv Con	Nerv Lav
Agitation score	67.8±20.0^{a}	28.1±7.46^{a}	299±43.8^{b}	374±72.0^{b}
Central line crosses	16.6±4.23^{a}	3.42±0.81^{b}	53.8±4.38^{c}	57.2±6.18^{c}
Vocalizations (bleats/min)	1.95±0.86^{a}	0.34±0.19^{b}	5.60±1.01^{c}	9.2±1.13^{d}
Escape attempts	1^{ab}	0^{ac}	0^{ac}	4^{b}
Mean cortisol after exiting box (ng/mL)	32.0±2.8^{a}	34.6±1.0^{a}	58.5±4.2^{b}	53.3±1.5^{b}

$^{a-d}$Different superscripts indicate significant differences between treatments (at least $P < 0.05$).

Key words: stress, lavender, temperament

M21 Characteristics and welfare of horses used for transportation in northeast Ohio. K. Bennett-Wimbush*, M. Amstutz, and D. Willoughby, *Ohio State University Agricultural Technical Institute, Wooster.*

Horse transportation is common in some geographical locations, often dictated by cultural beliefs and practices. However, little information is available on welfare issues concerning this sub-segment of the US equine population. The purpose of this study is to characterize factors that influence travel speed and document welfare and safety concerns of horses used as primary modes of transportation. Horse drawn vehicles/riders (n = 306) were observed at 8 different locations, representing 3 distinct communities in northeast Ohio during summer 2010. Environmental conditions (slope, heat index), gait characteristics (hitch, gait, speed, lameness) and driver/rider factors (gender, vehicle type, safety equipment) were recorded. Differences between variables

were determined by Least Square Means, GLM and Fisher's Exact Test, SAS. Travel speed was correlated with terrain slope ($P < 0.01$), community ($P < 0.001$), heat index ($P < 0.05$), gait ($P < 0.001$) and lameness grade ($P < 0.05$). Most notably, horses traveled slower uphill (slope > 1.0), during periods of high (>25°C.) heat index and when exhibiting a grade 3 lameness, using the AAEP 0–5 lameness scale. Overall, there was a trend ($P = 0.10$) for double hitches to travel slower than single hitches. Travel speed within vehicle type was observed. Wagons (4.63 ± 0.25 m/sec) traveled slower ($P < 0.01$) than buggies (5.00 ± 0.10 m/sec) which traveled slower ($P < 0.05$) than open buggies (5.35 ± 0.13 m/sec). This was most likely due to the vehicle and cargo weight. Pacing accounted for 2.6% of the observations at 5.14 ± 0.38 m/sec while 92.8% of the horses trotted (5.14 ± 0.07 m/sec), although speeds were not different. Grade 3 lameness was observed in 4.1% of the horses which slowed ($P < 0.05$) travel speed to 4.23 ± 0.35 m/sec compared with non-lame horses (5.07 ± 0.07 m/sec). Youth drivers were more likely to drive lame horses than women or adult men. The frequency of displayed slow-moving vehicle signs on horse drawn vehicles varied by community from 41.3 to 94.6%. This is a safety concern for both the occupants and animals. In this study, lameness was minimal and appropriate animal welfare allowances were observed.

Key words: equine, welfare

M22 Female mate choice in the domesticated goat (*Capra hircus*). K. M. Longpre* and L. S. Katz, *Rutgers University, New Brunswick, NJ.*

Female mate choice is the tendency for females to distinguish among and mate selectively with one specific phenotype. In promiscuous species such as the goat, in which males contribute genes only, females should choose to mate with high quality males. This sexual selection can account for the display of dimorphic characteristics not attributed to Darwin′s theory of natural selection. Female mate choice has not been studied in most domesticated species, in part due to single-male breeding programs and the use of artificial insemination. Both of these practices inhibit the opportunity for mate choice. Therefore, the appearance of mate choice in a domesticated species, when the environment or management system allows it to be expressed, suggests that the underlying mechanisms of mate choice are robust. We find that female goats are able to distinguish among and show preference for males with higher serum testosterone (T) concentrations ($P < 0.05$). Our studies indicate that morphological cues, specifically T-dependent neck and shoulder musculature are not used to distinguish among males. Instead, females use T-dependent physiological and/or behavioral cues, which increase in frequency and intensity during the breeding season, to assess potential mates. Specifically, males that emit potent chemical cues ($P < 0.001$) and high frequency courtship cues ($P < 0.001$) are preferred by estrous females. It is males with higher circulating T concentrations that emit more potent chemical cues ($P < 0.05$), and display higher frequency courtship cues ($P < 0.01$). Furthermore, high circulating T concentrations impose high energetic costs as males with higher T concentrations lose more body weight during the breeding season ($P < 0.05$), likely due to the increased frequency of T-dependent behavior expression. We conclude that female mate choice exists in the domestic goat, and circulating T concentrations and the resulting T-dependent behaviors in males may serve as an honest indicator of a male′s overall quality.

Key words: goats, sexual selection, mate choice

M23 Effects of spray-dried porcine plasma (SDPP) administered as an oral gavage on indicators of health, welfare, and performance in pigs transported after weaning. L. M. Wittish* and M. J. Estienne, *Virginia Polytechnic Institute and State University, Blacksburg.*

Transportation of swine is an emerging welfare issue, especially for pigs weaned and then transported to other farms for grow-finish. Weaned pigs fed starter diets containing SDPP show improved growth performance. The objective of this study was to determine the effects of SDPP, administered as an oral gavage during suckling, on indicators of health, welfare, and performance in transported weaned pigs. At weaning (4 wk of age), pigs were assigned to one of 4 treatments: I. SDPP (0.375 g/mL) + transport, II. Water + transport, III. SDPP + no transport, and IV. Water + no transport (n = 10 barrows and 10 gilts per treatment). Pigs received 25 mL of the assigned gavage 2x/d for 5 d before weaning. Pigs were moved from the farrowing barn, loaded on a livestock trailer and transported on a 5-h roundtrip or were moved directly to the on-site wean-to-finish barn. Rectal temperatures and blood samples were obtained at weaning and after relocation. Pig BW was determined at weaning, after relocation and at weekly intervals for 5 wk thereafter. Rectal temperature increased in all groups, but the magnitude of increase was greatest for groups I and II (treatment x time, $P < 0.01$). Effects of treatment x time ($P < 0.01$) were detected for several blood measures. Creatinine levels increased in all groups, but the magnitude was greatest for groups I, II, and III. Circulating concentrations of cortisol, urea nitrogen, and chloride increased, and calcium decreased, in groups I and II only. Potassium increased in group I only. That levels of phosphorous and sodium increased in group II only suggests a protective effect of prior treatment with SDPP in transported pigs. There was a trend ($P = 0.08$) for an effect of treatment x time for BW, and BW were greater at wk 4 and 5 after weaning for group I compared with group IV. In summary, transportation impacted physiological indicators of health and welfare in weaned pigs. Providing SDPP before weaning prevented transportation-induced changes in blood levels of phosphorous and sodium.

Key words: pig, spray-dried porcine plasma, transportation

M24 Castration is no laughing matter, nitrous oxide can′t even help. J. L. Rault*[1] and D. C. Lay[2], [1]*Department of Animal Sciences, Purdue University, West Lafayette, IN,* [2]*USDA-ARS-Livestock Behavior Research Unit, West Lafayette, IN.*

Surgical castration is performed on all male pigs in the United States. However, castration is painful and analgesics are being considered to relieve pain. Inhalant gases with analgesic properties allow for a fast induction, short-term and reversible effects, and are a needle-free option. Isofluorane, halothane and carbon dioxide have been tested to alleviate castration-induced pain in pigs with variable success. The use of those gases also raises practical or ethical concerns. Nitrous oxide (N_2O) or "laughing gas" has been widely used in human surgery and dental offices as an analgesic, sedative and anxiolytic drug. Yet, N_2O has not been thoroughly investigated for use in farm animals. N_2O possesses appealing features for the animal industry: It is not regulated as a drug, it is widely available, relatively inexpensive, and harmless. We hypothesized that the analgesic effect of N_2O may reduce the pain induced by castration. We used 24 piglets from 12 litters, one piglet receiving N_2O (N) and a littermate receiving air as a control (C). After 150 s under the gas, castration was performed while the piglet remained under the gas. Behaviors and squeal lengths were recorded during castration. Behavioral observations were continued for 3 d

using a scan-sampling interval recording method, and weight gain was measured. Data were analyzed using a mixed model in SAS. N_2O successfully induced anesthesia in all N pigs, as validated by a skin pinch test and the loss of palpebral reflex. Squeal length was shorter in N pigs during the induction phase ($P < 0.001$) but not different during castration itself as N pigs awoke and squealed as much as C pigs. Agitation scores during the whole procedure were reduced in N pigs, in both frequency ($P = 0.02$) and intensity ($P = 0.02$). For 2 h following castration, N pigs displayed less huddling behavior than C pigs ($P < 0.05$). Over the 3 d, N pigs performed more tail wagging ($P < 0.01$) and slept less ($P < 0.05$) than C pigs. N_2O was effective in inducing anesthesia in neonatal pigs. Nonetheless, its anesthetic effect seemed ineffective in preventing castration-induced pain.

Key words: castration, analgesic

M25 The effect of using carbon dioxide gas and/or a NSAID to reduce the pain associated with castration in pigs. B. L. Davis*[1] and M. A. Sutherland[1,2], *[1]Texas Tech University, Lubbock, [2]Ruakura Research Centre, AgResearch, Hamiliton, New Zealand.*

Surgical castration is routinely conducted on commercial swine farms to prevent boar taint and reduce aggressive behaviors. However, the procedure of castration causes acute pain which is an animal welfare concern. The objective of this study was to evaluate the effect of general anesthesia (carbon dioxide: CO2) and a non-steroidal anti-inflammatory drug (NSAID) either singularly or combined on the pain caused by castration in pigs. Pigs were allocated to one of 7 treatments (n = 10 pigs per treatment): 1) sham castration (CON), 2) administration of CO2 only (CO2), 3) administration of NSAID only (NSAID), 4) castration (CAS), 5) castration while the pig was anaesthetized with CO2 gas (CAS+CO2), 6) castration plus NSAID administered at the time of castration (CAS+N), and 7) castration conducted while the pig was anesthetized with CO2 plus NSAID administered at the time of castration (BOTH). Blood samples were collected before (0), and 30, 60, 120, 180 min after administration of treatments for analysis of cortisol concentrations. Behavior was recorded (live observations) in the farrowing crates using 1-min scan sampling for up to 180 min after castration. Body weight was measured before and 24 h after experiment. Data were analyzed using the MIXED procedures of SAS. Cortisol concentrations were elevated ($P < 0.005$) in all castrated pigs 30 min after castration regardless of pain relief treatment. Cortisol concentrations remained elevated ($P < 0.05$) in CAS pigs for up to 180 min after castration, but were lower in CAS-CO2 pigs at 60, 120, and 180 min after castration as compared with pigs castrated without pain relief. Pigs castrated without pain relief spent more ($P < 0.05$) time lying without contact compared with non-castrated pigs and CAS+N and BOTH pigs spent less ($P < 0.06$) lying without contact compared with CAS pigs. Change in body weight did not differ ($P > 0.05$) among treatments 24 h after castration. Pain relief in the form CO2 and/or a NSAID appeared to have some beneficial effects on the physiological and behavioral response to castration in pigs.

Key words: pigs, castration, welfare

M26 The effects of group size on aggression when mixing unacquainted sows in outdoor paddocks. J. N. Marchant-Forde*[1], J. P. Garner[2], A. K. Johnson[3], R. M. Marchant-Forde[2], and D. C. Lay[1], *[1]USDA-ARS, West Lafayette, IN, [2]Purdue University, West Lafayette, IN, [3]Iowa State University, Ames.*

Aggression is a challenge when pigs are kept in groups. Sows fight at mixing when space is limited but this project sought to determine the amount and type of aggression observed when unacquainted Berkshire sows were mixed in pairs or in 2 established sub-groups of 3 in outdoor paddocks. Treatment 1 (PR) used 16 pairs of sows mixed into a 5000 m^2 paddock. Treatment 2 (GP) used 28 unacquainted groups of 3 sows, with 2 groups mixed into a 5000 m^2 pen. Behavior was recorded continuously for 60 min post-mixing and all-occurrences sampling was used to extract social interactions. The data were analyzed to determine the number of social interactions that did or did not contain aggressive components (i.e., pushing, knocking or biting) and fighting defined as interactions that contained 10 or more reciprocated, aggressive component actions. Within each interaction, data were analyzed to determine the number of component actions and the number of aggressive component actions. The data were compared using a GLM, with treatment as a fixed effect. The number of social interactions was similar in GP (15.7 ± 2.7) and in PR (14.4 ± 2.5, $P < 0.001$). The number of interactions that contained aggression was also similar (6.9 ± 1.4 v. 5.6 ± 1.2, $P > 0.05$), but GP interactions contained more aggressive components (26.8 ± 2.5) than PR interactions (16.6 ± 1.4, $P < 0.05$). Twelve of the 16 PR pairs fought and aggression occurred quickly, beginning with biting after 2.1 ± 0.4 interactions and 17.3 ± 6.9 components. In GP mixing, 8.5 ± 0.3 of the 15 possible pair combinations per group interacted, of which 5.6 ± 0.4 interacted aggressively and 1.5 ± 0.4 fought. A higher proportion of unacquainted pairs interacted aggressively (0.57 ± 0.07) and fought (0.17 ± 0.05) than acquainted pairs (0.10 ± 0.04 and 0 respectively, $P < 0.01$). Bites were delivered quickly after 2.2 ± 1.7 interactions and 9.2 ± 2.6 components. Mixing pairs or groups of sows in paddocks did not prevent aggression. Aggression occurred quickly but reduced rapidly, with sows using space for avoidance. The results further our understanding of aggression at mixing and will help to identify best practice for producers.

Key words: aggression, pigs, mixing

M27 Association of sow fear with prolactin and cortisol concentrations pre- and post-farrowing. C. E. Phillips*[1], Y. Z. Li[2], L. J. Johnston[2], G. C. Shurson[1], J. Deen[4], and C. Farmer[5], *[1]University of Minnesota, St. Paul, [2]West Central Research and Outreach Center, Morris, MN, [3]University of Minnesota-Morris, Morris, [4]College of Veterinary Medicine, St. Paul, MN, [5]Agriculture and Agri-Food Canada, Dairy and Swine R & D Centre, Sherbrooke, Quebec, Canada.*

A study was conducted to investigate associations among sow fear and circulating concentrations of prolactin and cortisol peripartum. Multiparous sows (n = 63) were subjected to human approach and novel object fear tests on wk 12 post-breeding. A fear score for each sow was calculated using Principal Component Analysis. Fear scores ranged from 0 to 7.88. Sows were classified as fearful (n = 31, scores = 7.32 ± 0.42) or less fearful (n = 32, scores = 4.36 ± 1.83). A subset of sows (7 fearful; 7 less fearful) from 2 winter farrowing groups were chosen to collect blood samples. Two days before the expected farrowing date of the first sow, sows were moved into the farrowing facility, anesthetized, and had an indwelling ear vein catheter inserted. The farrowing facility housed 8 sows, where sows shared a communal area and farrowed in individual pens. A blood sample was collected from each sow 2 d pre-farrowing, the day of farrowing, and 2 d post-farrowing between 1000 and 1100h. Catheters in 11 sows (5 fearful and 6 less fearful) remained functional for the sampling period. Serum samples were analyzed for prolactin and cortisol concentrations using RIA. Data were analyzed using repeated measures for day with the Glimmix

Procedure of SAS. There was no association ($P > 0.60$) of sow fear with prolactin (fearful 37.7 ± 3.8 ng/ml, less fearful 37.8 ± 3.7 ng/ml) or cortisol (fearful 4.2 ± 0.5 ug/dL, less fearful 4.5 ± 0.5 ug/dL) concentrations on any day. Prolactin concentrations 2 d before farrowing were lower ($P < 0.01$) than on all other days. Cortisol concentrations 1 d before farrowing and the day of farrowing were greater than 1 d post-farrowing ($P < 0.05$) and 2 d post-farrowing ($P < 0.01$). Results corroborate an increase in prolactin concentrations in sows on the day before farrowing to initiate the lactogenic process. They also suggest that cortisol concentrations are indicative of a greater stress level closest to the time of farrowing. Nevertheless, sow fearfulness as measured in this study, was not related to circulating concentrations of prolactin or cortisol pre- and post-farrowing.

Key words: sow, fear, parturition

M28 Molecular basis of virulence in *Staphylococcus aureus* ovine mastitis. C. Le Maréchal[1,2], N. Seyffert[1,4], J. Jardin[1,2], D. Hernandez[5], G. Jan[1,2], V. Azevedo[4], P. François[5], J. Schrenzel[5], S. Even[1,2], N. Berkova[1,2], R. Thiéry[3], J. R. Fitzgerald[6], S. Lortal*[1,2], and Y. Le Loir[1,2], *[1]INRA STLO, Rennes, France, [2]AGROCAMPUS OUEST STLO, Rennes, France, [3]ANSES, Sophia-Antipolis, France, [4]ICB/UFMG, Belo Horizonte, MG, Brazil, [5]University of Geneva Hospitals (HUG), Geneva, Switzerland, [6]University of Edinburgh, Edinburgh, Scotland, United Kingdom.*

Staphylococcus aureus is one of the main pathogens involved in ruminant mastitis worldwide. The severity of staphylococcal infection is highly variable, ranging from subclinical to gangrenous mastitis and is dependent on host as well as bacterial factors. This work represents an in-depth characterization of *S. aureus* mastitis isolates to identify bacterial factors involved in severity of mastitis infection. We employed genomic, transcriptomic and proteomic approaches to comprehensively compare 2 clonally related *S. aureus* strains that were responsible for severe (strain O11) and milder (strain O46) mastitis in ewes, respectively. Variation in the content of mobile genetic elements, iron acquisition and metabolism, transcriptional regulation and exoprotein production was observed. In particular, O11 produced relatively high levels of exoproteins, including toxins and proteases known to be important in virulence. A characteristic we observed in other *S. aureus* strains isolated from clinical mastitis cases. Our data are consistent with a dose-dependent role of some staphylococcal factors in the hypervirulence of strains isolated from severe mastitis. Mobile genetic elements, transcriptional regulators, exoproteins and iron acquisition pathways constitute good targets for further research to define the underlying mechanisms of mastitis severity.

Key words: *Staphylococcus aureus*, mastitis, omic approaches

M29 Serological proteome analysis of *Staphylococcus aureus* strains isolated from gangrenous and subclinical ewe mastitis reveals core and accessory seroproteomes. C. Le Maréchal[1,2], J. Jardin[1,2], G. Jan[1,2], S. Even[1,2], D. Hernandez[4], P. Francois[4], J. Schrenzel[4], D. Demon[5], E. Meyer[5], N. Berkova[1,2], R. Thiéry[3], E. Vautor[3], S. Lortal*[1,2], and Y. Le Loir[1,2], *[1]INRA STLO, Rennes, France, [2]AGROCAMPUS OUEST STLO, Rennes, France, [3]ANSES, Sophia-Antipolis, France, [4]University of Geneva Hospitals (HUG), Geneva, Switzerland, [5]Ghent University, Faculty of Veterinary Medicine, Merelbeke, Belgium.*

Staphylococcus aureus is a major cause of mastitis in ruminants. In ewe mastitis, symptoms range from subclinical to gangrenous mastitis. *S. aureus* factors or host-factors contributing to the different outcomes are not completely elucidated. In this study, experimental mastitis was induced on primiparous ewes using 2 *S. aureus* strains, isolated from gangrenous (strain O11) or subclinical (strain O46) mastitis. Strains induced drastically distinct clinical symptoms when tested in ewe and mice experimental mastitis. Notably, they reproduced mild (O46) or severe (O11) mastitis in ewes. Ewe sera were used to identify staphylococcal immunoreactive proteins commonly or differentially produced during infections of variable severity and to define core and accessory seroproteomes. Such SERological Proteome Analysis (SERPA) allowed the identification of 89 immunoreactive proteins, of which only 52 (58.4%) were previously identified as immunogenic proteins in other staphylococcal infections. Among the 89 proteins identified, 74 appear to constitute the core seroproteome. Among the 15 remaining proteins defining the accessory seroproteome, 12 were specific for strain O11, 3 were specific for O46. Distribution of one protein specific for each mastitis severity was investigated in 10 other strains isolated from subclinical or clinical mastitis. We report here for the first time the identification of staphylococcal immunogenic proteins common or specific to *S. aureus* strains responsible for mild or severe mastitis. These findings open avenues in *S. aureus* mastitis studies as some of these proteins, expressed in vivo, are likely to account for the success of *S. aureus* as a pathogen of the ruminant mammary gland.

Key words: *Staphylococcus aureus*, mastitis, seroproteome

M30 Changes of plasma fatty acid and metabolites during the transition period in dairy cows with or without subclinical mastitis after calving. Y. Yang[1,2], J. Wang*[1], S. Li[1], D. Bu[1], T. Yuan[1], L. Zhou[1], and P. Sun[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.*

The transition period is especially critical and present considerable physiological challenges to homeostasis that may contribute to the onset of most health disorders, and the biggest challenge is mastitis. To explore specific blood metabolic markers as risk factors for the development of mastitis during early lactation. Thirty-two Holstein primiparous cows were selected and separated into healthy cows (n = 18) and subclinical mastitic cows (n = 14) in 7–21 DIM according to the veterinary treatment records and milk somatic cell counts with 500,000 cells/mL. Blood samples were collected from the tail vein of the cows at 21, 14 and 7 d prepartum, and 1, 4, 7, 14 and 21 d postpartum. Distribution of fatty acids in plasma and metabolic parameters (glucose, blood urea nitrogen, total bilirubin, cholesterol and β-hydroxybutyrate, as well as aspartate aminotransferase) of serum are observed and presented identical profile in the transition cows that were healthy and developed subclinical mastitis. Plasma 18:2 *cis*-9,*cis*-12 was the main fatty acid and its weight percentage increased significantly during early lactation compared with values before calving and during the first week after calving, while stearic acid values gradually decreased from 21 d before parturition through early lactation. Oleic acid increased around the calving and then gradually decreased, 18:3 significantly decreased after calving and then gradually increased. Glucose, blood urea nitrogen, total bilirubin, cholesterol, high density lipoprotein and β-hydroxybutyrate, as well as aspartate aminotransferase activity of serum metabolites around the time of calving in cows were abruptly altered. During the gestation period and calving, no difference was observed in fatty acids and metabolic parameters in the transition cows with or without subclinical mastitis after calving. However, the multiplication product of aspartate aminotransferase at 21 and 14 d before calving from the subclinical mastitic cows was significantly higher than healthy cows and may have value as a potential marker for risk of mastitis during early lactation.

Key words: metabolites, fatty acid, cow

M31 iTRAQ quantitative analysis of changes of serum protein from the cows in the periparturient period. S. S. Li, J. Q. Wang*, H. Y. Wei, Y. X. Yang, D. P. Bu, T. J. Yuan, and P. Sun, *State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China.*

Serum potentially carries an archive of important histological information whose determination could serve important source of immune-related biomarkers. The objective of this study was to elucidate the molecular mechanisms of immune system suppressed in the periparturient cows. In this study, blood samples were collected at 21 d before expected calving and 1 d after calving from healthy Chinese Holstein heifers (n = 8) considered free of mastitis, milk fever and endometriosis based on the somatic cell count and clinical diagnosis. Developmental changes were examined using an integrated proteomic approaches consisting of minor abundance protein enrichment by ProteoMiner, protein label by isobaric tags for relative and absolute quantification (iTRAQ), protein identification by liquid chromatography coupled with tandem mass spectrometry (LC–MS/MS). In total, 78 serum proteins were identified and 19 proteins showed to be differentially expressed at 1 d after calving compared with 21 d before calving. In particular, 4 proteins including conglutinin, apolipoprotein A-II, deoxyhemoglobin and ECM1 protein were downregulated 11.24-, 2.27-, 2.17- and 1.68-fold at 1d postpartum, respectively, while 15 proteins were up-regulated, such as haptoglobin and lipopolysaccharide binding protein. Western blotting validated the relative increases of haptoglobin, which was in agreement with the LC–MS/MS data. These results may provide valuable information to elucidate immune system response at the protein level during the transition period.

Key words: periparturient, dairy cow, isobaric tags for relative and absolute quantification

M32 Prevalence, transmission and impact of bovine leukosis in Michigan dairies. T. M. Byrem*[1], J. T. Houseman[1], R. J. Erskine[2], P. C. Bartlett[2], C. Render[2], C. Febvay[2], D. H. Norman[3], and J. R. Wright[3], *[1]Antel BioSystems Inc., Lansing, MI, [2]Michigan State University, College of Veterinary Medicine, East Lansing, [3]Animal Improvement Programs Laboratory, ARS, USDA, Beltsville, MD.*

Bovine leukosis, caused by infection with the bovine leukemia virus (BLV), has been characterized as a benign disease of the immune system. Previous National Animal Health Monitoring Surveys indicate complacency has resulted in high BLV prevalence in US dairies (89%) and cows (40%). Recent evidence that BLV affects immunological responses to both pathogenic challenges and vaccination increases the importance of BLV monitoring and control programs to improve overall health and productivity of dairy cows. A herd profiling index utilizing Dairy Herd Improvement (DHI) milk samples was designed to determine the estimated BLV prevalence (EBP) and its relationship to herd management practices and productivity. Management surveys were conducted in Michigan dairies (113) and on DHI test date, milk samples from a subset of animals ($8 \leq n \leq 10$) in each of 1st, 2nd, 3rd, and ≥4th lactations were tested for antibodies to BLV by ELISA. Correlation between testing all lactating animals and the herd profiling index to determine BLV prevalence in 4 herds was 0.997 ($P < 0.01$). Infection with BLV was detected in 88% of the herds. Average EBP within herd was 29% (0–76%) and within lactation, increased from 20% in 1st lactation cows to 45% in ≥4th lactation cows ($P < 0.05$). Multivariate analysis of management variables identified recent animal purchases, bull breeding, palpations per pregnancy diagnosis in heifers, and straw bedding use for breeding heifers as significant ($P < 0.05$) practices associated with EBP. For every 10% increase in EBP, rolling herd average decreased by 115 ± 60 kg. Individual mature-equivalent lactation records were available for 3899 study animals. Significant effects of leukosis on milk, fat and protein yields were evident within all lactation groups. Across all lactation groups, BLV positive cows had lower milk (−488 kg), fat (−15 kg), and protein (−16 kg) than negative cows ($P < 0.001$). Infection with BLV reduces cow productivity and is associated with purchasing replacements and breeding practices for heifers. Herd profiling using DHI milk samples is an effective strategy to determine and monitor the prevalence of infection in BLV control programs.

Key words: bovine leukosis, milk ELISA, DHI

M33 Relationship between test-day somatic cell count with test-day milk yields in Iranian Holstein cows. A. Laki, S. Babai, and M. Dehghan-Banadaky*, *Department of Animal Sci., Campus of Agriculture and Natural Resources, University of Tehran, Karaj, Tehran, Iran.*

Mastitis is considered worldwide the most costly production disease in dairy herds. The assessment of the economic worthiness of control plans for mastitis has to be anal supported by reliable evaluations of the economic losses caused by the disease. Decrease in milk production is one of the largest components of the economic losses due to clinical and subclinical mastitis. Previous study showed that there is a negative relationship between somatic cell count and test day milk yield. So, the aim of the current study was to determine relationship between somatic cell count and test day milk yield in Iranian Holstein dairy herds. Ten Tehran large commercial Holstein dairy herds were involved in the investigation from October 2005 to September 2008. All test day milk compositions (n = 36433) analyzed by infrared test method at the Tehran milk quality laboratory. Test day milk yield of individual cows was collected from each dairy herd. Milk composition and yield data analyzed by SAS and procedure Correlation (SAS institute 2003). The result of this research showed that relationship between test day somatic cell count and milk yield is negative (−0.14). Also, average somatic cell count in this study was 401.66 × 103 cell/mL. It can be concluded that a large amount of milk in Iranian dairy herds wasted by subclinical mastitis.

Key words: test-day milk yield, somatic cell count, Holstein cows

M34 Effects of drying the udder using paper versus cloth towels on bacterial contamination of teat ends of lactating dairy cattle. C. N. Baloun*, S. I. Kehoe, and L. E. Baumann, *University of Wisconsin-River Falls, River Falls.*

Milking cows are prepared for milking with a standard routine of cleaning and wiping to remove dirt and bacteria as well as stimulate milk letdown. A typical routine consists of using a sanitizing agent and wiping it off with either a paper towel or cloth towel before attaching the milking unit. There are many reasons why producers would choose to use either paper or cloth towels however there is no previous research evaluating whether one is better than the other in drying teats after sanitation. Therefore, the objective of this experiment was to determine whether paper towels are better than cloth towels at reducing bacterial contamination at the teat end. Eight cows were chosen and sampled over 4 weeks (total number of samples used for analysis ranged from 150 to 190 depending on bacterial species) where half of the udder was dried with a paper towel and the other half was dried with a cloth towel after sanitation. Immediately after drying, premoistened swabs were wiped over the teat ends in a repeated circular manner and transported back to the lab in a transport broth (Zadoks et al., 2003). Swabs were vigorously swirled in the broth before plating onto Petrifilm plates (3M Petrifilm) to quantify aerobic, coliform, and staphylococcus spp. Statistical analysis was done using SAS 9.2 (2009) where bacterial counts were log-transformed and a proc mixed procedure with cow as the repeated measure was used. Results indicated no

significant differences between cloth and paper towels for coliform or staphylococcus species ($P > 0.05$). The least squares means for log counts of coliform spp. for cloth towels were 1.75 ± 0.5 and paper towels were 1.78 ± 0.05; log counts of staphylococcus spp. for cloth towels were 2.05 ± 0.04 and paper towels were 2.02 ± 0.04. There was a trend ($P < 0.10$) for log counts of aerobic spp. to be higher for cloth towels (2.93 ± 0.04) than for paper towels (2.85 ± 0.04). These results showed little difference between using either a cloth or paper towel to dry udders after sanitation, however, the trend for aerobic counts to be higher in cloth towels should be further evaluated.

Key words: teat, bacteria, milking preparation

M35 Metabolic and clinical responses of dairy cows to increasing oral doses of lipoteichoic acid. S. Iqbal*, Q. Zebeli, D. A. Mansmann, S. M. Dunn, and B. N. Ametaj, *University of Alberta, Edmonton, AB, Canada.*

Lipoteichoic acid (LTA), a cell wall component of gram-positive bacteria (GPB), might be involved in the patholphysiologic and metabolic responses observed in dairy cows during infections by GPB. This study aimed at establishing metabolic and clinical responses to increasing oral doses of LTA and the oral dose that will initiate clinical symptoms in dairy cows. Seven late lactating Holstein dairy cows of an average BW of 800 ± 30 kg were randomly allocated to an oral administration of 2 mL saline solution containing one of the following LTA doses 20, 40, 70, 100, 120, 150, and 200 μg to each cow, respectively. Blood samples were collected from the tail vein at −15 min, 1, 3, and 5 h, whereas clinical responses were observed at −15 min, 1, 2, 3, 4, 5, and 6 h after the oral administration of each dose of LTA. Blood data demonstrated that oral administration of LTA increased concentration of glucose in the plasma with the highest doses (150 and 200 μg) having the highest plasma glucose ($P < 0.01$). Furthermore, plasma glucose linearly increased with time after oral administration of LTA ($P < 0.01$). Interestingly, cows also showed greater concentrations of plasma cholesterol at the highest doses of 150 and 200 μg ($P < 0.01$). Also, concentrations of nonesterified fatty acid in the plasma were found higher at 150 and 200 μg doses ($P < 0.01$). No effect of any of the doses of LTA used was observed on the concentration of β-hydroxybutyric acid in the plasma ($P > 0.05$). On the other hand, clinical data indicated that oral LTA influenced rectal temperatures and respiration rates, although the variations were within the normal ranges ($P < 0.01$ and $P < 0.01$, respectively). Interestingly, the highest doses of LTA (150 and 200 μg) lowered rumen contractions ($P < 0.01$), whereas all other doses did not have an effect on this variable. Overall, oral administration of increasing doses of LTA modulated plasma patterns of selected metabolites and clinical responses of late lactating dairy cows. It was also determined that the clinical safe dose of oral LTA to be used in future experiments was 120 μg.

Key words: oral lipoteichoic acid, plasma metabolites, dairy cows

M36 Repeated oronasal application of lipopolysaccharide affected milk yield and composition in transition dairy cows. A. Hosseini*, D. A. Mansmann, Q. Zebeli, S. Iqbal, S. M. Dunn, and B. N. Ametaj, *University of Alberta, Edmonton, Alberta, Canada.*

Previously we showed that ruminal endotoxin was associated with depression of milk fat content and lowering of milk energy efficiency (MEE) in mid-lactation dairy cows. In this study, we tested the hypothesis that repeated oronasal application of lipopolysaccharide (LPS) during the transition period might affect milk yield and composition, MEE, and feed intake in transition dairy cows. One hundred primiparous (PP) and multiparous (MP) Holstein dairy cows, with average body weights of 620 and 720 kg, respectively, were randomly assigned into control (CTR; PP = 18; MP = 32) and treatment (TRT; PP = 19; MP = 31) groups. Either carrier alone (3 mL of 0.85% saline) or 3 increasing doses (0.01, 0.05, and 0.1 μg/kg BW) of LPS from *E. coli* 0111:B4 were applied oronasally (1 mL nasally and 2 mL orally) twice a week on wk −4, −3, and −2. Milk fat, protein, lactose, urea nitrogen (UN), somatic cell counts (SCC), and total solids (TS) and milk fat, protein, and lactose yields were determined weekly during wk 1–4 postpartum. Milk energy efficiency was calculated as milk fat yield over DMI consumed. Dry matter intake was recorded daily starting at 4 wk before and up to 4 wk after parturition, whereas milk yield data were recorded daily during the first 4 wk after parturition. All data were processed statistically by the MIXED procedure of SAS. Overall data indicated that TRT tended to increase milk yield in all cows ($P < 0.1$) with higher impact on MP cows ($P < 0.01$) during 4 wk postpartum. Milk fat, fat yield, TS, and MEE tended to decrease ($P \leq 0.07$) in relation with TRT × parity × week, although TRT did not affect ($P > 0.1$) milk fat, protein, lactose, UN, SCC, TS and MEE. The overall DMI was affected ($P \leq 0.001$) by parity with higher levels in MP cows. An effect of parity was obtained in relation with fat ($P < 0.01$), protein ($P < 0.001$), and lactose yields ($P < 0.01$) with greater levels in MP cows. In conclusion results of this study showed potential involvement of LPS in modification of milk yield and composition, and that the oronasal treatment with LPS might be used to increase milk yield in dairy cows.

Key words: LPS, oronasal application, milk metabolites

M37 Mortality patterns in Midwest DHIA herds. M. Q. Shahid*, M. I. Endres, J. K. Reneau, R. Chebel, and H. Chester-Jones, *University of Minnesota, St. Paul.*

The objective of this study was to describe the mortality patterns and identify risk factors for mortality in Midwest dairy herds. A total of 5,080,849 lactation records for cows that calved between January 2006 and December 2009 from 10 Midwest states were used. Overall mortality rate was 6.4 per 100 cow years with an increasing trend from 6.2 in 2006 to 6.7 in 2009. Herd level mortality rate was 5.6 ± 2.0 (mean ± SD). The distribution of mortality rates were estimated by categories of parity, stage of lactation and season. The association between mortality rate and different risk factors was investigated by using proportional hazards regression. Low first test day milk, parity, somatic cell score (SCS), fat to protein ratio (FPR), previous lactation dry period length, and breed were significantly associated with mortality ($P < 0.001$). Within herd, cows with higher 1st test day milk yield (>mean plus 1SD) had 0.95 times (5% less) hazard rate of mortality than cows with average milk yield (mean plus 1SD); however, cows with lower 1st test day milk yield (mean minus 1SD) had 1.49 times (49%) higher hazard rate of mortality than cows with average milk yield. Similarly, cows with FPR > 1.7 and < 1.0 at first test had 48 and 18%, respectively higher hazard rate of mortality than cows with FPR between 1.0 and 1.7. Every 1 unit increase in SCS was associated with a 6% increase in hazard rate of mortality. Cows with dry period >70 and <30 d had 1.38 and 1.22 times higher hazard rate of mortality, respectively than cows with dry period between 30 and 70 d. Crossbred cows had 14% less hazard rate of mortality than Holsteins; however, Jersey cows had 19% higher hazard rate of mortality than Holsteins. These results indicate that first test day records could be a useful tool to identify

cows at high risk of mortality. In addition, higher milk yield was not associated with higher mortality.

Key words: mortality, risk factors

M38 Cost analysis of feeding varying doses of *Saccharomyces cerevisiae* fermentation product on a commercial dairy. C. M. Shriver-Munsch*[1], E. M. Ramsing[1], J. R. Males[1], W. K. Sanchez[2], I. Yoon[2], and G. Bobe[1], *[1]Department of Animal Science, Oregon State University, Corvallis, [2]Diamond V, Cedar Rapids, IA.*

Feeding 56 g/d of *Saccharomyces cerevisiae* fermentation product (Diamond V Original XP; XP) improves milk production in most studies, suggesting increased profit margin. A double dose of XP may further increase profit. This study focused on the cost benefits associated with feeding a single or double dose of XP on a commercial dairy. Multiparous Holstein cows were fed a supplementation mixture of 0 (n = 32), 56 (n = 33), or 112 g/d (n = 31) of XP, corn, and molasses, provided as a top dressing starting at 28 d before the expected calving date and ending 28 d postpartum. During the supplementation period, milk yield and composition were measured twice weekly from the afternoon milking on non-consecutive days. The incurred cost included expenses for XP, medical treatment, and milk profit lost due to discarded milk and culling. Income was calculated from milk and cow sales. The difference between incurred costs and income was defined as net gain. Because we could not measure feed intake or hours of labor, general feed and labor costs were not included in the calculation. Overall, supplementation with XP did not significantly increase net profit, however, a double versus a single dose of XP decreased total daily cost by $2.00/cow ($P = 0.06$) and tended to increase daily milk income by $1.65/cow ($P = 0.17$), resulting in a greater daily net profit of $2.73/cow ($P = 0.15$). The daily net profit was significantly greater in second lactation cows ($5.99/cow; $P = 0.05$). Although there were several potential confounding factors that could not be controlled on the commercial dairy, our results support the original hypothesis that higher dosages of XP during the peripartal period may further increase profit.

Key words: cost analysis, dairy, yeast culture

M39 The effect of feeding pasteurized or non-pasteurized waste milk on fecal populations and prevalence of *Salmonella* in dairy calves. J. A. Garcia*[1], T. S. Edrington[2], G. R. Hagevoort[1], R. F. Farrow[2], T. R. Callaway[2], N. A. Krueger[2], R. C. Anderson[2], and D. J. Nisbet[2], *[1]NMSU Ag Science Center, Clovis, NM, [2]Food and Feed Safety Research Unit, Southern Plains Agricultural Research Center, USDA-ARS, College Station, TX.*

Waste milk is often used as a feed source for young calves. To reduce the potential transmission of pathogens, some producers pasteurize waste milk. To assess the effect of pasteurization on *Salmonella* in dairy calves, 2 groups of calves were randomly allotted to receive either pasteurized (PWM; n = 128 calves) or non-pasteurized waste milk (NPWM; n = 83 calves) and fecal samples collected weekly for the first month of life and at weaning (approximately 2 mo of age). Calves were housed and managed on a single commercial dairy in the southwestern United States; however some calves were born on other dairies and transported at one day of age. A total of 8 collections were made and fecal samples (n = 1118) were quantitatively and qualitatively cultured for *Salmonella*. Fecal concentrations of *Salmonella*, as determined by direct plating, were significantly different at a few collections but similar ($P > 0.10$) when averaged over all collections [3.2 and 3.1 cfu (log10)/g feces for NPWM and PWM, respectively]. The percentage of *Salmonella* positive fecal samples following qualitative culture averaged 68 and 69% for NPWM and PWM, respectively, and ranged from a low of 23 to a high of 88% positive during the experimental period. A treatment effect ($P < 0.05$) was observed only during the fifth collection. Dairy of origin for the calf had a far more significant impact on *Salmonella* prevalence during individual collections, but not when data was combined across collection ($P = 0.12$). Nine different serogroups were identified: C1 (41%), C2 and E1 (approx. 17%), and B (12%). No treatment differences were observed in serogroup prevalence with the exception of the B group which was more common in the PWM treatment (19 versus 6%). Four calves died during the study, 3 in the PWM and 1 in the NPWM treatments. While the results did not find any significant effect of waste milk pasteurization on *Salmonella* prevalence in dairy calves, we do not discourage this practice due to beneficial effects of killing other pathogens such as *Mycobacterium paratuberculosis* possibly present.

Key words: *Salmonella*, waste milk, dairy calf

M40 Effect of paste or wrap oxytetracycline treatment on papillomatous digital dermatitis. J. H. Higginson*[1], J. Walter[1], G. Cramer[1,2], and D. F. Kelton[1], *[1]University of Guelph, Guelph, Ontario, Canada, [2]Cramer Mobile Bovine Veterinary Services, Stratford, Ontario, Canada.*

The objective of this study was to determine if application of oxytetracycline in a topical paste without bandaging would be as effective as an oxytetracycline wrap for the treatment of papillomatous digital dermatitis (PDD). Mature lactating Holstein cows diagnosed with PDD during routine trimming were randomly assigned to one of three treatments, oxytetracycline in a paste, oxytetracycline powder under a wrap, or a negative control. The paste treatment consisted of oxytetracycline 1000 mixed with glycol and vinegar, while the wrap treatment consisted of an equivalent amount of oxytetracycline 1000 powder held against the lesion with a wrap for 3 days. Examination of the affected hooves was carried out at Day 0 (Exam=1), Days 3-7 days post-treatment (Exam=2), and Days 8-12 post-treatment (Exam=3). Data were analyzed using a logistic model with a binary outcome (lesion active or lesion healed). Lesions were considered active if the cow reacted to pressure from an algometer and tissue was still pink and/or inflamed. Sixty-five and 54 cows enrolled in the trial were re-examined at Days 3-7 and 8-12 days post-treatment, respectively. Both Exam and treatment were significant ($P < 0.05$). Cows receiving the paste treatment had 9.5 (1.88, 95.62) times greater odds of recovering from digital dermatitis over the study period than the no treatment cows ($P = 0.01$). Similarly, cows receiving the wrap treatment had 18.6 (3.70, 188.56) times greater odds ($P < 0.0001$) of recovering from digital dermatitis over the study period than cows receiving no treatment. There was no statistically significant difference between the paste and wrap treatments ($P = 0.20$). Oxytetracycline is effective for the treatment of PDD and the use of it in a paste form rather than a powder alone could eliminate the need for bandage application and subsequent removal.

Key words: lameness, dairy cattle, digital dermatitis

M41 Association between virulence factors of *Escherichia coli*, *Fusobacterium necrophorum*, and *Arcanobacterium pyogenes* and uterine diseases of dairy cows. M. Bicalho*, R. Bicalho, and V. Machado, *Cornell University, Ithaca, NY.*

The objective of this study was to evaluate the relationship of bacteria specific virulence factors (VF) present at 3 different stages of lactation (4 ± 2, 12 ± 2, and 35 ± 2 d in milk (DIM)) with the incidence of metritis and clinical endometritis. The following VFs were investigated in this study; for *A. pyogenes* - plo (pyolysin - hemolytic exotoxin, which promotes hemolysis of red blood cells and immune cells), cbpA (collage- binding protein, necessary to collagen rich tissue), and fimA (fimbriae expression, key component in the cell-to-cell or cell-to-surface adherence), for *Escherichia coli*, fimH (type 1 pili), and for *Fusobacterium necrophorum* lktA (leukotoxin). Uterine swab samples were collected from 117 postpartum dairy cows housed on a commercial dairy farm located near Ithaca, New York. Samples were collected from April 2010 through June 2010. Isolation of total DNA was performed using a QIAmp DNA minikit (Qiagen, Santa Clara, CA) according to manufacturer instructions for DNA purification from blood and body fluids. PCR was used for the evaluation of the presence plo, cbpA, fimA, fimH, and lktA. Cows were classified as VF positive when the appropriate amplicon size was observed in the electrophoresis gel and negative when no amplicons were visible in the gel. Data was analyzed by multivariable logistic regression using the logistic procedure of SAS (Cary, NC). The *A. pyogenes* virulence factor cbpA was only detected in 4 samples and was excluded from the association analysis. In summary, *E. coli* (fimH) was significantly associated with metritis and endometritis when detected at 4 ± 2 DIM, *Fusobacterium necrophorum* (lktA) was significantly associated with metritis when detected at 4 and 12 ± 2 DIM and with endometritis when detected at 35 ± 2 DIM, and *Arcanobacterium pyogenes* (fimA and plo) was associated with metritis (fimA) when detected at 4 DIM and endometritis (fimA and plo) when detected at 12 and 35 ± 2 DIM. These findings support the hypothesis that the bacterial etiology of uterine infection is dynamic and multifactorial.

Key words: metritis, *E. coli*, FimH

M42 Repeated oronasal application of lipopolysaccharide lowered the incidence of metabolic diseases in periparturient dairy cows. A. Hosseini*, D. A. Mansmann, Q. Zebeli, S. Iqbal, S. M. Dunn, and B. N. Ametaj, *University of Alberta, Edmonton, Alberta, Canada.*

Metabolic diseases such as udder edema (EU), laminitis, retained placenta (RP), and mastitis are common in dairy cows around parturition, and have major consequences on health and economic sustainability of dairy farming. In this study, we evaluated the hypothesis that repeated oronasal application of lipopolysaccharide (LPS), during the transition period, might influence the incidence of the aforementioned diseases, body condition score (BCS), and manure score (MS) in both primiparous (PP) and multiparous (MP) dairy cows. One hundred Holstein dairy cows (PP and MP with ~BW 620 and 720 kg, respectively) were randomly assigned into control (CTR; PP = 18; MP = 32) and treatment (TRT; PP = 19; MP = 31) groups, and were allowed for ad libitum access to feed and water. Either carrier alone (3 mL of 0.85% saline) or 3 increasing doses (0.01, 0.05, and 0.1 µg/kg BW) of LPS from *E. coli* 0111:B4 were applied oronasally (1 mL nasally and 2 mL orally) twice a week on wk −4, −3, and −2. The UE was evaluated on wk −2, −1, 1 and 2, whereas RP was evaluated during 72 h postpartum. Laminitis was approved in 2 d intervals from −28 to 28 d, while mastitis was evaluated once a wk for 4 wk. The BCS was measured every 2 wk from −4 to 4 wk, whereas MS evaluated on wk −2, 1, 2 and 3. All data were processed statistically by Chi-squared test and the MIXED procedure of SAS. Overall results indicated that TRT lowered the incidence of UE in PP cows ($P = 0.041$), while week, parity and their interaction ($P < 0.001$) on UE was obtained. Data indicated that TRT tended to reduce ($P = 0.074$) the incidence of RP in all cows, while no effect was observed on laminitis and mastitis. In both PP and MP cows BCS decreased ($P < 0.001$) postpartum. The MS decreased by parity ($P = 0.027$), week ($P < 0.001$), and TRT × parity interaction ($P = 0.015$) in PP cows. In conclusion results of this investigation indicated potential involvement of LPS in the etiology of metabolic diseases, and that the oronasal treatment with LPS might be used to lower the incidence of UE and RP in periparturient dairy cows.

Key words: oronasal, lipopolysaccharide, metabolic disease

M43 Peripartal intravaginal application of probiotic bacteria lowered the incidence of uterine infections and improved fertility in dairy cows. S. Sharma*, Q. Zebeli, S. Iqbal, S. M. Dunn, J. F. Odhiambo, M. Gäenzle, and B. N. Ametaj, *University of Alberta, Edmonton, Alberta, Canada.*

Uterine infections affect cow performance and the efficiency of dairy farming. The objective of this study was to investigate the prophylactic effect of intravaginal probiotic bacteria on postpartum uterine infections, uterine involution patterns, and the overall reproductive performance of dairy cows. Eighty-two pregnant primiparous and multiparous Holstein cows, 2 wk before the expected day of calving, were randomly assigned into treatment (TRT; received 1 mL of probiotic bacteria in reconstituted skim milk at 10^{10} to 10^{12}cfu/treatment) and control group (CTR; received 1 mL of carrier only; reconstituted skim milk). Intravaginal infusions were performed once during wk −2, −1, +1, +2, +3, and +4 relative to parturition with probiotic bacteria isolated from the vaginal tracts of healthy cows including a mixture of *Lactobacillus sakei* FUA 3089, *Pediococcus acidilactici* FUA 3140, and *P. acidilactici* FUA 3138. Results showed that probiotic treatment lowered the incidence of metritis (17.1 vs. 51.2%; $P < 0.001$) and tended to lower the incidence of pyometra (12.2 vs. 26.8%; $P = 0.06$) in TRT cows. Treatment also lowered the overall incidence of cases with vaginal purulent discharges between 3 and 5 wk postpartum (10.1 vs. 27.8%; $P < 0.01$). Furthermore, a decrease in the number of cows with abnormal cervical size (28.5 vs. 43.0; $P < 0.0001$), abnormal uterine horn symmetry (40.8 vs. 67.2%; $P < 0.001$), and abnormal uterine fluctuations (18.5 vs. 36.8%; $P < 0.05$) was obtained. Additionally, differences were observed with regard to uterine infections and involution indicators at 3 wk postpartum in treatment group. A tendency to increase the overall pregnancy rates (87.9 vs. 73.5%; $P = 0.08$) was demonstrated in TRT group. The peak concentration of Hp was lower ($P < 0.0001$) in probiotic treated cows than in the CTR group. In summary, intravaginal application of a mixture of lactobacilli in periparturient dairy cows improved the overall postpartum uterine health and performance ands warrants further research into the mechanism(s) involved and potential applications in the future.

Key words: dairy cows, reproduction, probiotic lactobacilli

M44 Partitioning innate immune response variation: How much variation is due to the animal? M. D. Sellers*[1], L. E. Hulbert[1,2], C. J. Cobb[1], and M. A. Ballou[1], *[1]Department of Animal and Food Sciences, Texas Tech University, Lubbock, [2]Department of Animal Sciences, University of California-Davis, Davis.*

The objective was to partition the between-calf variation in ex vivo innate immune responses from Holstein bull calves. Innate immune responses evaluated included total leukocyte and differential counts, neutrophil L-selectin expression, tumor necrosis factor-α (TNFα) secretion from lipopolysaccharide (LPS)-simulated whole blood,

and neutrophil phagocytosis and oxidative burst responses to *E. coli* 0111:H8. Sixty 8 Holstein bull calves were observed for a period of 12 wk. At 21, 24, 28, 45, 49, 63, 66, 70, and 84 ± 2.3 d of age, peripheral blood was collected in heparinized vacutainers for ex vivo immunological analyses. Between-calf variation was partitioned using PROC MIXED in SAS (SAS v9.2). The model included the fixed effect of day. The compound symmetry covariance structure was used for the within-calf variation measurement. The between-calf variation ($V_{between}$) was determined as the variation between subjects after the fixed effect of day was removed. The within-calf variation (V_{within}) was estimated as the mean of the residual variation after the effects of day and $V_{between}$ were removed. Data are reported as ranges on 95% confidence intervals of the proportion of the variation due to $V_{between}$ ([$V_{between}$ / V_{within} + $V_{between}$] x 100). The study was conducted during February–April, 2010. These data suggest that a calf's immune response is highly dependent upon it's interaction with the environment. Identifying and controlling for environmental variation decreases V_{within}, which increases the consistency in immune responses within a calf. This could lead to identifying and managing subpopulations with unique immune responses.

Table 1. Between-calf variation in innate immune parameters in Holstein bull calves

Parameter	Day	$V_{between}$	$V_{between}$MIN	$V_{between}$MAX	$CV_{between}$	CV_{total}
P <	%					
Total leukocyte count	0.001	34.2	21.0	45.3	9.5	27.6
Neutrophil percentage	0.001	22.5	12.1	33.2	8.9	39.4
Whole blood TNF-α secretion	0.001	31.4	19.3	42.0	23.1	73.5
Neutrophil L-selectin expression	0.001	11.3	4.2	18.8	10.3	91.0
Neutrophil phagocytosis	0.001	43.1	29.3	54.0	20.1	46.6
Neutrophil oxidative burst	0.001	33.8	21.0	44.6	9.5	28.1
Cortisol	0.001	14.4	6.2	22.6	11.1	76.8
Glucose	0.001	12.4	4.3	20.7	2.2	17.8

Key words: cattle, immune, variation

M45 Effect of various dosages of *Saccharomyces cerevisiae* fermentation product on health and metabolism of multiparous dairy cows. C. M. Shriver-Munsch*[1], E. M. Ramsing[1], J. R. Males[1], W. K. Sanchez[2], I. Yoon[2], and G. Bobe[1], *[1]Department of Animal Science, Oregon State University, Corvallis, [2]Diamond V, Cedar Rapids, IA.*

Increased nutritional demands and suppressed immune function increase the risk for metabolic and infectious diseases in dairy cows during the transition period. These problems increase with parity number and result in significant losses in milk production and early culling. Supplementation of *Saccharomyces cerevisiae* fermentation product (Diamond V Original XP; XP) may support immune function and greater nutritional demands; thereby, XP may decrease the risk of infectious and metabolic diseases. Doubling feeding rates of XP may provide greater health benefits to dairy cows. The objective of the current study was to evaluate whether feeding a single or double dose of XP during the transition period may decrease the risk of metabolic and infectious diseases in multiparous dairy cows. Multiparous Holstein cows housed in the same pen were given a supplement containing either 0 (control; n = 32), 56 (n = 33); or 112 g (n = 31) of XP daily during morning lock-up as a top dressing to their TMR. The supplement consisted of 0, 56, or 112 g of XP mixed with 84 g of molasses and 168, 112, or 56 g of corn meal, respectively. Serum samples were analyzed for glucose, BUN, NEFA, and BHBA. Feeding XP, regardless of dosage, decreased BHBA concentrations ($P = 0.04$) and increased serum glucose ($P = 0.08$) and BUN concentrations ($P = 0.02$) at the d of calving. Feeding a double dose of XP additionally increased supplement consumption at the d of calving ($P = 0.05$ versus control) and decreased log10 somatic cell scores (SCS) in milk during the supplementation period ($P = 0.10$ versus control). Cows fed a single dose of XP also tended to have lower SCS by wk 4 versus control-fed cows ($P = 0.14$). Our results support the original hypothesis that XP may support immune function and greater nutritional demands in transition dairy cows. Higher XP doses may provide greater health benefits during time periods of increased stress.

Key words: dairy, health, yeast culture

M46 Influence of starch sources in prepartum diet on colostrum quality and blood immunoglobulin concentration of calves. F. Fatahni[1], H. Mirzaei Alamouti*[2], and A. Shahsavar[1], *[1]Department of Animal Science, University of Ilam, Iran, [2]Department of Animal Science, University of Zanjan, Iran.*

The main objective of this study was to evaluate the effect of dietary inclusion of wheat or corn as the main source of starch in prepartum diets on plasma metabolites of cows, colostrum composition, colostrum IgG1 and IgG2 concentrations and calves serum IgG1 and IgG2 concentrations. For this purpose, 30 primiparous and 20 multiparous Holstein cows were used in a randomized complete block design and cows were blocked by parity and expected calving dates and assigned to treatments at 22 ± 7 d before calving. Dietary treatments were either a corn-based diet or a diet containing wheat at 18.5% of diet dry matter. The cows blood were sampled at −21, −14, −7, and −1 d relative to expected calving dates. Calves blood samples were drawn before the first colostrum feeding (0 h) at birth and 24 h of life. The results indicated that Prepartum diets did not affect plasma concentrations of glucose, nonesterified fatty acids and triglyceride of cows, however, plasma total concentrations of proteins in cows fed the wheat-based diet was higher compared with those fed the corn-based diet. Lactose, fat and IgG2 concentrations in colostrums did not respond to dietary treatment, but protein, total solids, IgG1 and total IgG concentrations in colostrums were significantly higher for cows fed wheat containing diet. At 24 h of age, calves fed colostrums from cows fed wheat containing prepartum diet had significantly higher serum IgG1 and total IgG concentrations. But serum IgG2 concentrations were similar between treatments. Prepartum starch source did not affect apparent efficiency of IgG1, IgG2 and total IgG absorption. Results suggested that feeding wheat-based diet in prepartum increased colostrum quality and serum IgG1 concentrations of calves and may have a profound effect on the survival, health and growth of newborn calves.

Key words: prepartum diet, colostrums, calf

M47 Development of a lab-on-a-chip immunoassay system for diagnosis of Johne's disease. A. Wadhwa*[1], K. Yang[1], X. Liu[1], J. Bannantine[2], S. Eda[1], and J. Wu[1], *[1]University of Tennessee Knoxville, Knoxville, [2]United States Department of Agriculture, Ames, IA.*

Johne's disease (JD) is caused by infection of mostly ruminants (including dairy cattle) with *Mycobacterium avium* ssp. *paratuberculosis* and is responsible for a significant economic loss to the US dairy industry. Diagnosis of JD is currently conducted in diagnostic laboratories, creating dairy farmers costly expenses for veterinary service, sample handling, and shipping. An automated on-site diagnostic device for JD would reduce the diagnosis-related costs. Lab-on-a-chip (LOC) technology has been used in various analytical processes and is offering opportunities for the development of on-site diagnostic devices. In this report, we developed and tested a LOC immunoassay system based on AC electrothermal (ACET) effect for detection of JD-specific antibodies in bovine serum samples. The LOC used in this study was composed of poly-dimethylsiloxane microchannels sealed over an ACET electrode chip. The surface of the ACET electrode chip was coated with *M. paratuberculosis* antigen and, after blocking uncoated surface, reacted sequentially with bovine serum sample and fluorescently labeled secondary antibody. Liquid flow was electrically controlled by ACET micropumping effect. The level of antibody binding was then measured by using a LED-induced fluorescence with a low cost mini-spectrometer. JD-positive and JD-negative serum samples were tested with this LOC immunoassay system. Antibody binding in JD-positive serum was detected by this ACET-based system after loading the serum and secondary antibody for 3 min each. Without the ACET effect, the antibody binding was not detectable after the 3-min reactions. The level of antibody binding in the JD-positive serum was greater than that of JD-negative serum. Higher antibody binding was observed at the electrode edges and we assumed that ACET caused a swirl of liquid around the electrode and thereby accelerated the antibody-antigen interaction. This assumption was supported by our theoretical prediction and numerical simulation. This ACET-based LOC immunoassay may form a basis for the development of an on-site JD diagnostic method.

Key words: Johne's disease, diagnosis, lab-on-a-chip

M48 Immune activation after immunization of neonatal calves with a commercial heat-killed vaccine. J. R. Stabel*[1], W. R. Waters[1], J. P. Bannantine[1], and K. Lyashchenko[2], *[1]USDA-ARS-National Animal Disease Center, Ames, IA, [2]Chembio Diagnostic Systems, Medford, NY.*

A major drawback of current whole-cell vaccines for *Mycobacterium avium* ssp. *paratuberculosis* (MAP) is the interference with diagnostic tests for bovine tuberculosis and paratuberculosis. The current study was designed to explore cross-reactivity of the current USDA commercial vaccine for MAP with diagnostic tools for bovine TB and to assess host responses to vaccination. Neonatal dairy calves were assigned to treatment groups consisting of: 1) Control – no vaccine (n = 5); and 2) Vaccinate – Mycopar vaccine (n = 5). Peripheral blood mononuclear cells were isolated before and after vaccination and stimulated in vitro for measurement of interferon-(IFN)-γ, interleukin (IL)-4, IL-10, and IL-12, and to assess differences in lymphocyte populations by flow cytometry. Results from this study demonstrated a rapid initiation of MAP-specific IFN-γ in Vaccinate calves by 7 d, with robust responses continuing throughout the study. Vaccinate calves also had IFN-γ responses to BoPPD, with moderate reactivity to ESAT-6/CFP-10, an *M. bovis* recombinant fusion protein. Interestingly, IL-4 and IL-10 were markedly decreased in Vaccinate calves only on d 7 and 14 of the study and thereafter were similar to Controls. Vaccinate calves began to seroconvert at 4 mo with all calves having detectable MAP antibody by 6 mo. Only one Vaccinate calf had a positive (suspect) skin test response to *M. bovis* PPD and none of these calves reacted in *M. bovis* serologic tests. These results suggest that vaccination with Mycopar will interfere with diagnostic tools for the detection of paratuberculosis but have low interference with *M. bovis* diagnostics.

Key words: *Mycobacterium avium* ssp. *paratuberculosis*, cattle, bovine tuberculosis

M49 Phenotype array analysis of *Mycobacterium avium* ssp. *paratuberculosis* K10 phoP mutant and wild-type. J.-W. Chang, J. Scaria, and Y.-F. Chang*, *Cornell University, Ithaca, NY.*

Mycobacterium avium ssp. *paratuberculosis* (MAP) is recognized as a broad host range mycobacterial pathogen with the ability to initiate and maintain systemic infection and chronic inflammation of the intestine of a range of histopathological types in many animal species. Even though MAP can survive in a variety of environments, it is extremely slow growing and fastidious. A better understanding of the complete physiology of MAP can lead to novel preventive strategies and identification new vaccine candidates in MAP genome. Therefore we have compared the complete metabolic parameters of MAP phoP mutant and its wild-type. A phoP mutant was constructed using allelic exchange method in MAP strain K10. Biolog phenotype MicroArray (PM) is a respiration-based assay system that can test up to 2,000 phenotypic traits simultaneously. The complete metabolic profile of the MAP mutant and wild-type was obtained by screening against Biolog phenotype microarray (PM) panels 1 through 8. For each PM panel, 30% increase in signal intensity over negative control was considered positive. The PM analysis revealed that deletion of phoP had a global impact on MAP metabolism. The greatest impact of phoP deletion was on utilization of nitrogen, sulfur and phosphate sources. Likewise phoP deletion severely impaired the ability of MAP to utilize nutritional supplements, such as hematin, thymine, deferoxamine and N-Acetyl-D-Glucosamine. Alteration of utilization of carbon sources such as L-Arabinose, Acetoacetic acid, D-Psicose and Pyruvic acid was also observed. In several bacteria it has been established that PhoPR 2-component system is the master regulator and in *Mycobacterium* tuberculosis PhoPR 2-component system is essential for virulence. Our results in the present study are consistent with these observations and a detailed study of metabolism related genes identified in this analysis can be good candidates for drug intervention or vaccine development.

Key words: *Mycobacterium avium* ssp. *paratuberculosis*, phenotype microarray, phop mutant

M50 Characterization of monoclonal antibodies specific for molecules uniquely expressed on bovine dendritic cells. G. S. Abdellrazeq*[1], S. Tomida[2], and W. C. Davis[2], *[1]Alexandria University, Edfina, Behara Province, Egypt, [2]Washington State University, Pullman.*

Progress in elucidating the function of dendritic cells (DC) in cattle has been limited by the availability of monoclonal antibodies (mAbs) that

identify lineage restricted molecules expressed on DC. In this report, we describe the development and characterization of a set of mAbs (LND25A, LND41A, DC5A, and DC77A, all IgG1 isotype) that react with molecules expressed on DC. Initial analysis using flow cytometry show the mAbs label a population of CD14-MHCII+CD11c+ cells that comprise less than 1% of peripheral blood mononuclear cells. Cross comparison of specificity of the mAbs using Zenon IgG1 s step reagents conjugated with different fluorochromes showed the mAbs recognize 2 different molecules, one recognized by LND25A and LND41A the other recognized by DC5A and DC77A. In vitro studies with cultures of adherent cells derived from peripheral blood mononuclear cells revealed LND41A labeled a population of loosely adherent cells with the phenotypic features of DC5. The cells possessed numerous dendrites similar to those seen on DC. Preliminary use of LND41A to identify DC present in the ileum of cows at the clinical stage of Johne's disease showed that the mAb recognizes a population that is distinct from macrophages. Further studies are in progress to show the mAbs recognize molecules expressed on all DC.

Key words: dendritic cells, monoclonal antibodies, Johne's disease

M51 Identification of *Mycobacterium avium* ssp. *paratuberculosis* genotypes on Alberta dairy farms with high-resolution melt analysis of multiallelic short sequence repeats. J. David, R. Mortier, H. Barkema, and J. De Buck*, *Dept. of Production Animal Health, Fac. Veterinary Medicine, Calgary, Alberta, Canada.*

Disease prevention through epidemiology-based management practices might be the best option for Johne's disease (JD) control at the moment. This strategy depends partly on a thorough understanding of the genotypic diversity of MAP in Canadian herds as natural strain variants may possess unique pathogenicities that may require tailored management practices. Strain discrimination is also important for epidemiological investigations to understand origins of infection and identify risk factors that influence transmission. Molecular epidemiology might also allow visualization of how specific genotypes are more successful in spreading. In this study we aimed to develop an accurate and rapid genotyping technique based on known short sequence repeat (SSR) variants and to identify the genetic variability of MAP within Alberta. Methods: Serum, milk and fecals were collected from 1917 individual animals over 3 years of age on 24 dairy herds in Southern Alberta. Fecals were cultured using the liquid culture ParaJem system. Positive cultures were subcultured on solid media to obtain single colonies. Genomic DNA from these pure isolates was prepared for genotyping. Apart from sequencing of 3 SSR loci (G1, G2, GGT), high resolution melt (HRM) assays were developed to identify the allelic diversity. Results: Thirty-five isolates were obtained from 10 of the herds. Respectively 3, 3 and 2 alleles were discovered for the 3 SSR loci, resulting in several different genotypes. HRM proved more reliable than sequencing due to problems to resolve the exact number of guanine repeats in G1 and G2 by the classical approach. Farms with multiple genotypes were discovered. The same herds are currently being resampled. Genotyping of the new isolates will allow us to determine the true genotypic diversity on those farms more accurately. Genotyping using SSR HRM analysis is a useful tool to elucidate the distribution of MAP genotypes in a geographic area.

Key words: paratuberculosis, genotyping, transmission

M52 Complete genome sequence of a *Mycobacterium avium* subspecies *paratuberculosis* Isolate from a patient with Crohn's disease. L. Li*[1], J. P. Bannantine[2], S. Sreevatsan[3], and V. Kapur[1], *[1]Penn State University, University Park, [2]National Animal Disease Center USDA-ARS, Ames, IA, [3]University of Minnesota, St. Paul.*

Mycobacterium avium subspecies *paratuberculosis* (MAP) has been identified in some human patients with Crohn's disease. To identify genetic differences between MAP isolates recovered from humans and those associated with bovine Johne's disease, we characterized the complete genome sequence of strain MAP4 recovered from the breast milk of a Crohn's disease patient. Massively parallel sequencing approaches were used to generate a total of 88.5 million base pairs from a randomly sheared MAP4 genomic DNA library, which were assembled into contiguous sequence fragments with an estimated 60 large (~2kb) and 350 small (<0.5kb) gaps physical or sequence gaps. A primer walking approach with Sanger based sequencing was applied to close all remaining gaps in a iterative manner and areas with low quality sequence re-sequenced to obtain an assembled single high quality genome sequence. Compared with the described previously bovine MAP K10 genome, the size of MAP4 genome is about 3.0kb smaller as a result of several sequence deletions, including in one copy of the insertion sequence element, IS900. Importantly, the analysis revealed no large genome scale rearrangements in MAP4 as compared with strain K10, and ~3kb of deletions and ~300 bp of insertions were distributed across the genome. The results also confirmed the presence of 59 additional SNPs, which together with the 174 SNPs identified in our preliminary studies account for a total of 233 SNPs between these 2 isolates. Interestingly, more than half of the newly identified SNPs were located in 2 genes (MAP1432 and MAP2495), both of which contain repetitive sequences and are orthologs of *Mycobacterium tuberculosis* Rv1173 that encodes a cell wall protein. Taken together, our analysis of the MAP4 and K10 genome sequences confirmed the high similarity between strains from these 2 different mammalian hosts, and suggest a relative paucity of genetic variation among strains recovered from humans and cows.

Key words: *Mycobacterium avium* subspecies *paratuberculosis*, genome sequence, Crohn's disease

M53 *Salmonella* delivery system to develop an efficient vaccine against *Mycobacterium avium* ssp. *paratuberculosis*. S. Chandra, J.-W. Chen, S. M. Faisal, S. P. McDonough, M. A. S. Moreira, C.-F. Chang, and Y.-F. Chang*, *College of Veterinary Medicine, Cornell University, Ithaca, NY.*

Salmonella antigen delivery system is an efficient tool to develop an effective and low-cost vaccine. Since *Salmonella* has the ability to enter inside macrophage cells which are very versatile antigen presenting cell, and can deliver the antigen into cytosol using its type III secretion system. Hence, type III secretion system of *Salmonella* presents an efficient antigen delivery to elicit protective immunity especially cytotoxic T lymphocyte (CTL) response. As *Mycobacterium avium* subspecies *paratuberculosis* (MAP) is an intracellular pathogen, type III secretion system of attenuated *Salmonella* could be a efficient vehicle to deliver MAP's immunogenic antigens into cytosol to induce CTL response for better protection in cattle against MAP infection. To induce better protection, we constructed fusion of immunogenic fragment of Ag85A, Ag85 B, and SOD, and 74F using an efficient delivery component of *Salmonella* (sopE promoter and sopE104) in pSU39 expression vector and tested the delivery efficiency of *Salmonella* expressing pSU39-constructs to deliver MAP antigens(Ag85A Ag85 B, SOD, and 74F) into culture medium via type III secretion system. After that we carried out vaccination experiment

in moue model using C57BL/6 mice. Our results show that *Salmonella* Typhimurium (Δ aroA ; Δ yej) a genetically attenuated strain can deliver MAP antigen via type III secretion system. Further, the animal experiment data proved that *Salmonella* expressing MAP antigen can elicit CTL response to induce protective immunity against MAP infection. Immunological and histopathological analysis show that protective immunity mounted by *Salmonella* delivery system against MAP is equivalent to positive controls. Hence, our data indicate that *Salmonella* antigen delivery system could be proven a better tool to develop an effective vaccine to management of Johne's disease in cattle.

Key words: *Mycobacterium avium* ssp. *paratuberculosis*, delivery system, vaccine

M54 Exploring *M. paratuberculosis* pathogenesis using an in vitro cell culture passage model. J. L. Everman*[1] and L. E. Bermudez[2], [1]*Department of Microbiology, College of Science, Oregon State University, Corvallis,* [2]*Department of Biomedical Science, College of Veterinary Medicine, Oregon State University, Corvallis.*

Mycobacterium avium ssp. *paratuberculosis* (MAP) is the etiological agent of Johne′s disease, a chronic intestinal inflammatory disease that affects ruminants worldwide. Once infected, cattle remain in the subclinical stage of infection for many years before the disease progresses to clinical symptoms. The transition from the subclinical to the clinical stage of the disease has been described as a shift from a T_H1 type response to an antibody-dominated type response; however, the cause for the shift and the onset of the infectious process remains to be determined. We describe an in vitro cell culture passage model in an attempt to gain a further understanding of the changes that occur during the host immune response as well as the bacterial changes that occur during the progression of the disease. By passing MAP through MDBK epithelial cells, RAW 264.7 macrophages, and MDBK epithelial cells sequentially, and utilizing real-time PCR to determine transcript levels of immune signals we have observed that cytokine and chemokine levels do not change after 3 passages through RAW 264.7 macrophages. However, a lower passage number results in a higher level of immune signal transcripts of IL-6 and IL-8. These data, as well as previous findings that demonstrate an increase of an invasive phenotype of MAP after intracellular growth in macrophages, suggest that the serial passage of MAP between macrophage populations may select for a population of bacteria that optimizes infection. A more invasive bacterial population allows for increased survival, while the population also appears to be less inflammatory, resulting in less host damage. To fully understand the mechanisms behind these observations, MAP phenotypes have been obtained and RNA will be extracted for DNA microarray analysis at 1 d and 3 d after infection. This hypothesis could potentially explain why the subclinical phase of the disease persists for so many years and our work begins to decipher the dynamics of antigen expression and host response that occur during the progression of Johne′s disease.

Key words: Johne's disease, paratuberculosis, immune response

M55 Effects of *Saccharomyces cerevisiae* fermentation product on ruminal VFA production when supplemented to various beef feedlot diets. I. Yoon*, C. Belknap, J. Butler, J. Lin, A. Brainard, and T. Werner, *Diamond V, Cedar Rapids, IA.*

Feedlot rations vary greatly in both ingredient and nutrient composition depending on the type of animal being fed, stage of production, feeding objective, feed manufacturing capabilities and availability of feedstuffs. An in vitro study was performed to determine the effects of *Saccharomyces cerevisiae* fermentation product (Diamond V Original XPC, XPC) on ruminal VFA production when supplemented to beef feedlot diets obtained from major beef cattle production areas in the US Feedlot diets collected and tested include: finishing diets from feedyards in Illinois (IL), Nebraska (NE1 and NE2), and Texas (TX1), and a backgrounding diet from a feedyard in Texas (TX2). Rations represented a cross-section of ingredients commonly used within the industry. Rumen inocula were obtained from 2 cannulated cows and pooled on an equal volume basis. Forty milliliters of a 1:20 ruminal fluid-to-buffer solution were introduced into 100 mL fermentor bottles containing 0.25 g of diet supplemented with 0.15 g (DM basis) of either XPC or control grain used in production of XPC and incubated for 12 and 24 h at 39°C (n = 10 per treatment). After the 12 h fermentation, XPC increased ($P < 0.05$) propionate and total VFA across all diets compared with the Control. Acetate production was higher ($P < 0.05$) with XPC in the IL, NE1 and TX2 diets. After the 24 h fermentation, XPC increased ($P < 0.05$) propionate across all diets. Total VFA was increased ($P < 0.05$) in the NE1 and NE2 diets. Diamond V Original XPC improves rumen fermentation across a wide variety of feedyard diets, resulting in consistently higher propionate concentrations.

Table 1. Effect of Original XPC on percent increase in VFA production versus Control[1]

	IL	NE1	NE2	TX1	TX2
12 h fermentation					
Acetate	**6.8**	**7.9**	3.2	**4.9**	**8.5**
Propionate	**28.4**	**29.3**	**18.3**	**22.8**	**20.5**
Total VFA	**14.1**	**15.1**	**9.5**	**11.6**	**13.4**
24 h fermentation					
Acetate	4.3	**7.9**	3.2	−0.2	1.9
Propionate	**8.7**	**13.2**	**8.0**	**5.4**	**7.5**
Total VFA	5.4	**9.2**	**5.6**	1.9	4.0

[1]Bold values represent significant percent difference versus Control at $P < 0.05$.

Key words: feedlot diets, yeast culture, in vitro fermentation

M56 Body components on finishing crossbred beef heifers of different residual feed intake groups. S. F. Reis*[1], P. V. R. Paulino[1], S. R. Medeiros[2], G. L. D. Feijó[2], R. A. A. Torres Júnior[2], D. A. Fausto[3], M. A. Rezende[2], and S. C. Valadares Filho[1], *[1]Universidade Federal de Viçosa, Viçosa, Minas Gerais, Brazil, [2]Embrapa Gado de Corte, Campo Grande, Mato Grosso do Sul, Brazil, [3]Universidade de São Paulo, Piracicaba, São Paulo, Brazil.*

Studies have suggested that 37% of the total variation in the residual feed intake (RFI) would be related to energetic expenditure with metabolism of the tissues (mainly liver and gastrointestinal tract). This trial aimed to evaluate the weight of body components (non-carcass) of 31 3-cross beef heifers finished in feedlot, fed with same diet, during 84 d. 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. The actual dry matter intake was obtained daily during 84 d of feedlot and the predicted feed intake according to the equation: $-3.82593 + 0.15438 \times MBW + 1.09531 \times ADG$. At the end of 84 d all animals were slaughtered using conventional humane procedures. The blood was weighed and the body was separated into individual components, which were separately weighed. Included were internal organs (liver, heart, lungs, trachea, kidneys, reproductive tract, and spleen), cleaned digestive tract (rumen, reticulum, omasum, abomasum, and small and large intestines), tongue, tail, hide, head, feet, and carcass. The trial was conducted in a completely randomized design and data were analyzed using the PROC GLM of SAS ($\alpha = 0.05$). The classes of RFI were different for DMI kg/d ($P < 0.05$), the means were: 12.61(high RFI); 11.72 (medium RFI) and 11.00 (low RFI). No differences were found among classes of RFI for the body components evaluated in percentage of empty body weight (EBW) or in kg/d ($P > 0.05$). The overall averages were: 20.32% EBW (organs and viscera); 6.85% EBW (visceral fat); 289 kg (initial EBW), 415.33 kg (final EBW), and 1.22 kg/d (EBW gain). Viscera and internal organs are largely responsible for energy expenditure in ruminants suggesting a role in feed efficiency determination. No difference in the liver weight ($P > 0.05$) among RFI classes was found. The means measured for high and low RFI were respectively 1.41% EBW and 1.36% EBW. Body components (non carcass) do not differ among finishing crossbred beef heifers of different RFI classes, other factors associated with metabolism may have greater influence on feed efficiency.

Key words: beef cattle, net feed intake, internal organs

M57 Finishing steers and bulls with high-vitamin E diets: Effect on circulating immune cells and creatine kinase at time of slaughter. C. Reyes, C. Fuentes, and R. E. Larraín*, *Pontificia Universidad Catolica de Chile, Santiago, Chile.*

Release of glucocorticoids to the blood stream after stress may change the number of immune cells circulating in blood within minutes. A stressful event may also increased creatine kinase (CK) in blood if muscle tissue is damaged or mobilized. Vitamin E reduced activation of the hypothalamic-hypophysis-adrenocortical axis in farm animals, so the objective of this study was to test if finishing bovines with a high vitamin E diet modulate changes in immune-cells counts and CK at time of slaughter. Thirty-eight steers and bulls were blocked by sex, then grouped in 16 pens of 2 or 3 animals of similar weight, and randomly assign to 1 of 2 treatments: a control diet design to provide 60 IU vitamin E•animal^{-1}•day^{-1} and the control diet supplemented with 2000 IU vitamin E•animal^{-1}•day^{-1}. Each pen was considered an experimental unit (n = 8). Feed was offered once daily to each pen to provide ad libitum access to feed. A blood sample was taken by jugular venipuncture at d 0 to be used as baseline for CK. After 123 d on feed, animals were transported for about 1.5 h to a local slaughterhouse and killed approximately 8 h after arrival. A sample of trunk blood was taken at the time of slaughter. Factors in the model were sex and treatment, and initial weight was included as covariate. Differences were considered significant when ANOVA had $P < 0.05$. We observed no changes in any of the variables analyzed, concluding that feeding 2000

IU vitamin E•animal^{-1}•day^{-1} produced no changes in immune cells counts and CK at time of slaughter.

Table 1. Immune cells (cells/μL) and creatine kinase (CK, U/L) after slaughter in bovines fed vitamin E

Item	Control	Vitamin E	*P*-value
Leucocytes	9,329 ± 591	9,298 ± 586	0.98
Bacilliforms	30.3 ± 13.2	53.9 ± 13.0	0.19
Neutrophils	4,840 ± 331	4,823 ± 328	0.97
Lymphocytes	4,149 ± 351	4,305 ± 348	0.74
Monocytes	65.7 ± 24.9	45.6 ± 24.7	0.55
Eosinophils	124 ± 55.2	124 ± 54.7	0.99
Basophiles	29.5 ± 13.0	24.2 ± 12.9	0.76
Change in CK from d0	751 ± 239	735 ± 237	0.96

Vitamin E: 2000 IU•animal^{-1}•day^{-1}.

Key words: vitamin E, immune cells, creatine kinase

M58 Vitamin D_3 effect on metabolite levels in plasma and longissimus musle of steers fed zilpaterol hydrochloride. K. T. Korn*, M. C. Claeys, R. P. Lemenager, and J. P. Schoonmaker, *Purdue University, West Lafayette, IN.*

Two hundred and ten Angus × Simmental steers (init. BW 314 ± 11 kg) were allotted by BW to a 3 × 2 factorial arrangement of 6 treatments (5 pens per treatment; 3 heavy, 2 light blocks) to determine the effect of supplemental vitamin D_3 (0 IU [none], 250,000 IU for 165 d [long-term D], or 5×10^6 IU for 10 d [short-term D]) on plasma total calcium and tissue vitamin D and total calcium levels in steers fed 0 or 8.38 mg/kg zilpaterol hydrochloride (Zilmax) daily for 21 d. Steers were implanted with Revalor XS and fed a growing phase diet (30% corn silage, 20% distillers grains, 1150 IU/kg vitamin D) for 54 d. Finishing phase diets (15% corn silage, 20% distillers grains, 750 IU/kg vitamin D) were fed for 111 d. Zilmax or placebo was added to the diet 24 d and short-term D was added 13 d before slaughter. Treatments were removed from all diets 3 d before slaughter. Plasma was collected at the start of the experiment (0 d), the introduction of Zilmax to the diet (141 d), the start of short-term D (152 d), the withdrawal of treatments (162 d), and the day before harvest (165 d). Longissimus muscles were collected and ground for total calcium and vitamin D analysis. Kidney and liver were collected for vitamin D_3, 25-hydroxyvitamin D_3, and 1,25 dihydroxyvitamin D_3 determination. Short-term D increased ($P < 0.01$) total calcium in plasma at the 162 and 165 d time points compared with none or long-term D. Zilmax increased plasma total calcium at 162 d in steers fed short-term D but not in steers fed long-term D or not fed D (interaction, $P < 0.01$). At 165 d, Zilmax did not increase plasma total calcium in steers fed long or short-term D, but tended ($P = 0.06$) to increase total calcium when steers were not fed supplemental vitamin D (interaction, $P < 0.01$). In conclusion, Zilmax affects plasma total calcium levels depending on dietary concentrations of vitamin D. However, total plasma calcium concentrations do not explain changes in tenderness after 21 d of aging seen previously for Zilmax and long-term D feeding.

Key words: beef, vitamin D, zilpaterol hydrochloride

M59 Early metabolic imprinting events increase marbling scores in fed cattle. M. A. McCann*[1], J. M. Scheffler[1], S. P. Greiner[1], M. D. Hanigan[2], G. A. Bridges[3], S. L. Lake[4], J. M. Stevenson[1], H. Jiang[1], T. L. Scheffler[1], and D. E. Gerrard[1], *[1]Dept. of Animal and Poultry Sciences, Virginia Polytechnic Institute and State University, Blacksburg, [2]Dept. of Dairy Science, Virginia Polytechnic Institute and State University, Blacksburg, [3]University of Minnesota, North Central ROC, Grand Rapids, [4]Dept. of Animal Sciences, University of Wyoming, Laramie.*

Early weaning of calves to a high concentrate diet results in greater fat deposition and suggests that postnatal metabolic imprinting events that may be exploited as a management tool to improve cattle value. The objective of this study was to determine the ability of a short, high energy dietary intervention for subsequently increasing intramuscular fat deposition in finishing cattle. Twenty 4, fall-born Angus-sired steer calves from primiparous cows were stratified by sire and randomly assigned to normal weaned (NW) or metabolic imprinted (MI) treatments. NW calves remained on their dam until 251 ± 6 d of age, whereas MI calves were weaned at 105 ± 6d (135kg) and were transitioned to a diet containing 20% CP and 1.26 Mcal/kg NEg. MI calves were offered 1.0 kg/d of grass hay and were hand-fed twice daily to approximate ad libitum intake. CP levels of the diet were transitioned from the initial level of 20% to 14.5% through the course of the feeding period. Seven days post-weaning of the NW both treatment groups were combined and grazed on a mixed summer pasture from mid-May until early Oct. Post-grazing, steers were adapted to a corn silage-based feedlot diet and performance monitored on a 28-d interval. Ultrasound fat was determined after 75d on feed to stage harvest groups with an estimated 1.0–1.2 cm of backfat. Cattle were harvested and carcass measurements were recorded 24h postmortem. MI calves were heavier ($P < 0.05$) than NW calves (341 vs. 265 kg) at normal weaning age. During the grazing phase NW steers gained more weight than ($P < 0.05$) MI steers (0.69 vs. 0.35 kg/d). Feedlot performance, BF and USDA yield grade were similar between treatments. However, MI steers produced heavier ($P < 0.05$) carcasses (564 vs. 524 kg) with a higher ($P < 0.001$) marbling scores (645 vs. 517; 400 = Sm^0, 500 = Md^0 and 600 = Mt^0). Calves consuming a high concentrate diet for a short period of time early postnatal yielded a higher quality carcass and suggest that metabolic imprinting mechanisms exist in growing beef cattle and may be used for economic gain by cattle producers and feedlot managers.

Key words: calf, weaning age, pasture

Breeding and Genetics: Dairy Cattle Breeding

M60 Differences in the production and reproduction traits of embryo transfer full siblings living under different and identical conditions. J. Bezdicek*[1] and J. Riha[2], *[1]Agriresearch Rapotin Ltd., Rapotin, Czech Republic, [2]Research Institute for Cattle Breeding, Ltd., Rapotin, Czech Republic.*

Embryo transfer plays an important role in terms of using valuable maternal genotypes. The offspring of such embryo transfers are found not only on donors' farms but also on other farms. The aim of this study was to evaluate differences in milk production and reproduction traits in full siblings living on different farms. Evaluation was made in first lactation for 110 sibling pairs (experimental group). For the evaluation, differences full siblings under different conditions comparison was made for milk production differences in full siblings (n = 620) living on identical farms (control group). For production traits we observed milk production in first lactation (in kg), fat production (in % and kg) and protein production (in % and kg). For reproduction we observed age at first calving. The data were analyzed with Statistica 8 (2008, StatSoft Inc., Tulsa, OK) using descriptive statistics and t-tests. Analyzed were Holstein cows (H100) born in the Czech Republic in the years 2000–2005. Observed differences between full sibling pairs under different and under identical conditions (farms) were the following (in parentheses standard deviation): milk production in kg 1149.9 vs. 998.9$^{n.s.}$ (1122.8 vs. 798.1 kg); fat content in percent 0.42 vs. 0.38$^{n.s.}$(0.31 vs. 0.30%); fat production in kg 48.95 vs. 39.86* (40.81 vs. 31.29 kg); protein content in per cent 0.21 vs. 0.17* (0,16 vs. 0,14%); protein content in kg 38.9 vs. 31.6* (33,63 vs. 25,44 kg). For age at first calving the differences between experimental and control group were as follows: 76.6 vs. 65.4* (56.26 vs. 54.9 d). Significant differences is marked * ($P \leq 0.05$); n.s. (nonsignificant). Even though in full sibling pairs, living under different conditions, was found for milk production greater differences (1149.9 kg milk) these differences were not statistically significantly greater than full sibling pairs living under identical conditions. For milk composition and age at first calving the differences were statistically significant. Of the 2 groups there was greater variability in siblings living under different conditions.

Key words: milk production, full siblings

M61 Female fertility in a Guzerat dairy herd: Heterogeneity of variance components for calving intervals. J. C. C. Panetto*[1,2], J. E. Val[3], C. R. Marcondes[4], M. G. C. D. Peixoto[2], R. S. Verneque[2], J. B. S. Ferraz[5], and B. L. Golden[6], *[1]Curso de Veterinária, Universidade de Uberaba, Uberaba, MG, Brazil, [2]Embrapa Gado de Leite, Juiz de Fora, MG, Brazil, [3]Faculdade de Medicina de Ribeirão Preto - USP, Ribeirão Preto, SP, Brazil, [4]Embrapa Pecuária Sudeste, São Carlos, SP, Brazil, [5]Faculdade de Zootecnia e Engenharia de Alimentos - USP, Pirassununga, SP, Brazil, [6]Dairy Science Department, California Polytechnic State University, San Luis Obispo.*

Our objectives were to determine if variance components of calving intervals varied with age and if considering calving intervals as a longitudinal trait would be a superior approach for fertility analysis of zebu dairy herds. Calving records from females born from 1940 to 2006 in a Guzerat dairy subpopulation in Brazil were analyzed in the present study. Contemporary groups, formed by year and farm at birth or at calving, ages at calving, equivalent inbreeding coefficients and day of the year were included as fixed effects in the models. Calving interval (CI) was first analyzed by fitting a random regression model with Legendre polynomials of order 3 for the fixed effect of age at calving, and random effects of animal and permanent environment. In a second approach, a multivariate analysis was conducted, including age at first calving (AFC), first calving interval (CI1), calving interval for young females (CIY) and calving interval for mature females (CIM). Finally, a bivariate analysis was performed for AFC and CI where calving intervals were considered as a single trait in a repeatability model. Additionally, ranking of sires were compared among approaches. Calving intervals decreased with age until females were about 80 mo old, remaining nearly constant after that age. A quasi-linear increase of 11.5 d on the calving intervals was observed for each 10% increase in the female's equivalent inbreeding coefficient. Heritability of AFC was 0.37 from both analyses. In the case of CI, the genetic variance ratios ranged from 0.064 to 0.141, depending on the approach and on the ages at calving. Differences among genetic variance components for calving intervals observed along the animal′s lifetime confirmed the longitudinal aspect of this trait, indicating the importance of such consideration when accessing fertility of zebu dairy females in situations where the available information relies on their calving intervals. Changes observed in the ranking of sires suggested that the genetic progress of the population can be affected by the approach chosen for the analysis of calving intervals.

Key words: calving intervals, female fertility, heterogeneous variances

M62 Detection of early pregnancy and embryonic loss in dairy cows using BioPRYN and a NEW PSPB-based ELISA. J. R. Branen*[1], J. O. Giordano[2], C. Passavant[1], J. M. Howard[1], P. M. Fricke[2], and R. G. Sasser[1], *[1]BioTracking LLC, Moscow, ID, [2]University of Wisconsin, Madison.*

BioPRYN, a blood-based pregnancy test is used in reproductive management of cattle and utilizes antibodies developed against pregnancy-specific protein B (PSPB). There were 2 objectives of this study: 1) measure the number of days since insemination in dairy cows for a change in pregnancy classification using BioPRYN and a new PSPB-specific ELISA (NEW), 2) measure the number of days since induced embryonic loss (in a subset of cows from 1) for a change in pregnancy classification using BioPRYN and NEW. The NEW assay was developed using a PSPB obtained after Butler et al. (1982. Biol. Reprod 26:925–933). Serial blood samples, collected 3 times a week until 29d after timed AI (TAI) from 60 lactating crossbred (75% Holstein, 25% Jersey) cows, were analyzed and categorized for time of changing from an Open status or, changing, after embryonic death, from a Pregnant status (to recheck or open) using the BioPRYN and NEW assays. Sampling continued until 39d for 30 cows found pregnant at 29d using transrectal ultrasound (TUS) while open cows were not analyzed further. At 39d pregnancy was reconfirmed by TUS and 7 cows were treated with PGF2α (PGF; 25 mg, i.m.; n = 4) or an infusion of 120 mL hypertonic saline (INF; 25%, v/v; n = 3) into the uterine horn containing the embryo. Blood samples were then collected every 12h for 6.5d and daily from 6.5d to 10d. Death of the embryo was confirmed by TUS by cessation of an embryonic heartbeat. BioPRYN categorized the 30 pregnant cows as positive at 25d (n = 20), 27d (n = 7) and 29d (n = 3). NEW was compared with BioPRYN for 11 of those cows and provided positive result of all at 25d while BioPRYN classified 5 at 25d, 4 at 27d and 2 at 29d. Following embryonic death in 7 cows, NEW changed the classification at 0, 1, 1, 2, 2, 2, 3, and 4d

earlier than BioPRYN. The NEW can add to the value of BioPRYN in testing for early pregnancy and when there is early embryonic loss.

Key words: PSPB, pregnancy loss, blood-based pregnancy detection

M63 Comparison of BioPRYN and a new pregnancy-specific protein B (PSPB) enzyme-linked immunosorbent assay (ELISA) for determination of early pregnancy status in dairy cattle. J. R. Branen*[1], C. Passavant[1], A. Phatak[2], D. Snider[3], J. Azevedo[4], J. M. Howard[1], D. Pals[1], and R. G. Sasser[1], *[1]BioTracking LLC, Moscow, ID, [2]Consulting Veterinarian, Waterford, CA, [3]Strategy Lab & Dairy Consulting, Visalia, CA, [4]Alta California, Hilmer, CA.*

Pregnancy specific protein B (PSPB) is a protein fraction derived from ruminant placenta that can be used to develop immuno-assays to detect placental proteins in the maternal circulation. Since 2002 a PSPB-based ELISA, BioPRYN, has been commercially used for detection of pregnancy in cattle at least 30 d since last heat (DSLH) and after 89 d in milk (DIM). The objective of this study was to compare the accuracy of BioPRYN and a new PSPB-based ELISA (NEW) for pregnancy status at 28 ± 2 DSLH. NEW was developed using a PSPB protein fraction isolated as described in 1982 (Biol. Reprod. 26:925–933). Lactating Holstein (n = 385) and Jersey (n = 67) cows 70 or more DIM from 10 commercial dairies in California were used in the study. Blood samples were collected at 28 ± 2 DSLH (T1). These and subsequent samples were assayed for pregnancy status using BioPRYN and NEW. A second blood sample was collected at 33–42 DSLH (T2) concurrently with rectal palpation (RP) or trans-rectal ultrasonography (TUS) by trained professionals. A matching result of T2 ELISAs with RP or TUS was considered the true value for pregnancy status. A mismatch at T2 was rectified by ELISA and RP or TUS at 3–10 d following T2 (T3). Animals not available for T3 analysis were removed from the study (n = 82), leaving a total of 370 cows used for analysis. BioPRYN showed 100% sensitivity (100 X pregnant or recheck at T1 or T2/ true pregnant at T2 or T3) at 28 DSLH or later (Truly pregnant, n = 137). NEW showed 100% sensitivity at 28 DSLH or later (Truly pregnant, n = 137) and >98% (95% CI: 95–99%) with the inclusion of 27 DSLH animals (Truly Pregnant, n = 196). Ten true open animals at T2 and positive by BioPRYN at T1 (between 70 and 88 DIM) were categorized open at T1 by NEW. NEW shows promise for earlier testing after insemination and earlier testing in the postpartum period.

Key words: PSPB, blood-based pregnancy detection

M64 Survey of genetic selection practices on pasture-based dairy farms in the United States. K. D. Gay*, T. D. Nennich, and M. M. Schutz, *Purdue University, West Lafayette, IN.*

A survey was mailed to dairy graziers across the country to ascertain their genetic selection practices, but included background information on feeding, production, and health. The overall aim was to collect data to allow eventual development of a genetic selection index. Mailing addresses were obtained from extension cooperators, NRCS advisors, and commercial companies. Producers were able to respond to the survey by mail or internet. Respondents to the survey included 77 farmers in 22 states. Producers were asked questions about the grazing history of their herd and average milk and component production. They were also asked questions about breeding practices to determine number utilizing seasonal grazing and to gain an understanding of breeds present in their herds. Producers were asked to rank genetic traits by the amount of selection pressure they felt should be applied to those commonly available. Traits were ranked from negative 5 to positive 5 with negative being selection against a trait and positive being selection for a trait. Respondents averaged 15.95 ± 9.12 years of grazing history, 129.1 ± 128.52 milking head, and grazed 224.5 ± 60.47 d a year. Production was 20.9 ± 4.89 kg of milk per cow per day, 4.0 ± 0.42% milk fat, and 3.6 ± 0.23% milk protein. Also, 46.7% of producers participated in seasonal calving, defined as 75% of cattle calving in any 3 mo window. Further, 70% utilized crossbreeding to the extent that at least 10% of the herd was crossbred. Percentage of herds that included at least some genetics from major breeds were: 70% Jersey, 65% Holstein, 26.7% Ayrshire, 21.7% Swedish or Norwegian Red, and 20% Milking Shorthorn. The average rank of genetic traits were: productive life 3.87, udder composite 3.57, somatic cell count –3.15, feet and legs 3.08, daughter pregnancy rate 3.05, fat percentage 2.97, calving ability 2.95, protein percentage 2.83, body size –2.73, fat yield 2.69, protein yield 2.56, and milk yield 2.27. It appears that pasture-based dairy producers place more emphasis on traits relating to longevity and fertility and less on production traits than the most widely used US selection indexes.

Key words: grazing, genetics, management

M65 Estimating field conception rates for Holstein sires in US herds (ACE index) and conception rate correlation from the same sires used for AI after natural estrus and timed AI breedings. A. H. Souza*[1,2], H. Rivera[2], P. Crump[1], and V. Cabrera[1], *[1]Department of Dairy Science, University of Wisconsin, Madison, [2]Accelerated Genetics, Baraboo, WI.*

The aim of this retrospective study was to validate a fertility index of Holstein sires from one AI stud in the United States (accelerated conception evaluation – ACE index), using for comparison the sire conception rate index (SCR, AIPL-USDA) as the industry official standard. A second objective was to compare conception rate (CR) rankings from same sires used for AI after natural estrus (EAI) and timed-AI (TAI) breedings. Confirmed CR records from 3 national data centers (AGSource, ATA, DRMS) and farm backups from non-testing herds were merged and used as basis for this data analysis. Criteria edits in the data set were: breedings from last 4 years with confirmed conception results; sires with 300 breedings minimum; herd's CR within 20 and 60%; 30 breedings per herd minimum; sires used in a minimum of 10 herds with no more than 40% breedings in one herd; 1 to 5 breedings occurring within 45 to 375 DIM; and cows within 1 to 5 lactations. After editing 1,142,859 breeding records were available for analysis. A subset of the data (n = 801,636) was used to classify breeding codes into either AI to estrus or timed-AI based on weekly insemination profile in each herd. The procedure Glimmix of SAS took into account effects of state, farm, cow id, breeding month, year, parity, DIM at breeding, and service sire. Then, sire fertility classification was based on standard deviations from the population mean. The Spearman-correlation between ACE and SCR was 0.79 ($P < 0.01$). The same model was used independently for the 2 differing breeding codes and fertility classification within breeding code was done for sires with >700 (94 sires) and again for >1,000 (n = 56 sires) breedings in both EAI and TAI. Spearman-correlation of the rankings produced with EAI and TAI were 0.81 ($P < 0.01$; for >700 breedings) and 0.84 ($P < 0.01$; for >1,000 breedings). Thus, these results indicate a significantly good correlation between ACE and the industry gold standard index-SCR. In addition, conception rankings of the same sires used for EAI and TAI were highly correlated.

Key words: sire fertility, conception rate, dairy cow

M66 Effects of dam's dry period length on heifer development. H. D. Norman and J. L. Hutchison*, *Animal Improvement Programs Laboratory, USDA-ARS, Beltsville, MD.*

Effect of dam's days dry (DD) on calving ease (CE) score (1–5), stillbirth (SB) rate, heifer age at first breeding (AFB), and heifer survival to first calving (SURV1) was investigated with US Holstein records from 1997 through 2010: 774,821 for CE, 347,462 for SB, 27,932 for AFB, and 300,725 for SURV1. The small number of records for AFB was because breeding records for heifers were not stored until 2003 and reporting is minimal. Heifer SURV1 was a binary trait (0 = no, 1 = yes) and included only female calves. Dam calving date was required to be within 10 d of expected calving date (previous calving date + previous days open + 280) to ensure producers knew calving date and dry period length. Dam DD were grouped into 12 categories: 0–30, 31–35, 36–40, ..., 66–70, 71–80, 81–90, 91–120 d. The linear fixed-effects model for analysis of CE and SB included dam calving herd-year and year-state-month, parity, calf sex, and DD category; the AFB model included heifer breeding herd-year and year-state-month as well as DD category. The SURV1 model included dam calving herd-year and year-state-month, dam parity, and heifer parent average for daughter pregnancy rate. For AFB and SURV1 analyses, heifer birth dates were required to be before January 2008 to allow time for completion of a first lactation. Calving difficulty increased linearly as dam DD increased until about 70 d and then leveled off: 1.29 for 0–30 DD, 1.36 for 56–60 DD, and 1.42 for 91–120 DD; corresponding SB were 4.15, 2.36, and 3.33%. Differences between DD categories were all significant ($P < 0.0001$) for CE and SB. For corresponding dam DD, heifer AFB were 463, 458, and 458 d; corresponding heifer SURV1 were 64.6, 70.1, and 68.8%. Heifer AFB and SURV1 differences were significant ($P < 0.05$) between 0 and 30 and 56–60 DD but nonsignificant between 56 and 60 and 91–120 DD.

Key words: days dry, calving ease, heifer survival

M67 Changes in the use of young bulls. K. M. Olson*[1], J. L. Hutchison[2], P. M. VanRaden[2], and H. D. Norman[2], *[1]National Association of Animal Breeders, Columbia, MO, [2]Animal Improvement Programs Laboratory, ARS, USDA, Beltsville, MD.*

Availability of genomic information since 2008 has increased accuracy of genetic evaluations for young bulls in Holstein (HO), Jersey (JE), and Brown Swiss (BS). As a result, AI organizations have been aggressively promoting young bulls and producers have been using young bulls more extensively. Number of inseminations by breeding year and service sire (SSR) age at the time of insemination was investigated using US breeding records from 2007 through 2010. There were a total of 65,686 BS, 14,319,994 HO, and 771,766 JE inseminations. Age of SSR was categorized into 3 groups: young bulls (0.8 to 3.9 yr), first crop sires (4.0 to 7.9 yr), and older sires (≥8.0 yr). There was an increased use of young bulls between 2007 and 2010 for HO and JE (Table 1); increase in inseminations by young bulls was 14 percentage units for HO and 7 percentage units for JE. This was not surprising, because HO gain more in accuracy from genomics than the other breeds. First crop sire usage decreased for HO (14 percentage units) and JE (3 percentage units). Older sire usage remained constant at 15 to 18% for HO, 16 to 23% for JE, and 33 to 36% for BS. Economic ($) rankings have been converted to percentile rankings since 1980 with the average of proven bulls being 50%; as a comparison, the 294 young HO bulls currently being marketed averaged +459 Net Merit and a 83 percentile ranking. When young bulls have reliabilities >60%, simulations indicate that the optimum usage of young bulls may increase to > 90% of the market share. Current average genomic reliabilities for Net Merit are 73, 60, and 48% for HO, JE, and BS, respectively. The shift to increased inseminations to young bulls is likely to continue.

Table 1. Percentages of inseminations by breeding year, service sire (SSR) age, and breed

Breeding year	Service-sire age (yr)	Brown Swiss	Holstein	Jersey
2007	0.8 - 3.9	35	29	25
	4.0 - 7.9	29	56	55
	≥ 8.0	36	15	19
2008	0.8 - 3.9	32	30	27
	4.0 - 7.9	33	52	50
	≥ 8.0	35	18	23
2009	0.8 - 3.9	33	39	31
	4.0 - 7.9	33	44	50
	≥ 8.0	34	17	19
2010	0.8 - 3.9	33	43	32
	4.0 - 7.9	34	42	52
	≥ 8.0	33	15	16

Key words: breeding, insemination, service-sire age

M68 Body condition score comparisons of crossbred Normande-sired cows with herd mates sired by Ayrshire, Holstein, and Jersey. D. E. Brown* and C. D. Dechow, *The Pennsylvania State University, University Park.*

The objective of this study was to investigate the body condition score (BCS) of Normande sired crossbred cows with their herd mates sired by Ayrshire, Holstein, and Jersey. Eight farms in the Northeastern states of Massachusetts, New York, Pennsylvania, and Vermont were visited once during the months of January or February to BCS. The farms varied from year round confinement with large amounts of concentrate supplementation to herds with little confinement and minimal concentrate or silage supplementation. Data included observations for 46 Normande sired crossbreds, 52 Ayrshire sired, 263 Holstein sired, and 55 Jersey sired cows. 42 of the Ayrshire sired cows, 254 Holstein sired cows, and 42 Jersey sired cows were purebred. The Mixed procedure of SAS 9.1.3 was used to analyze the data. Significant fixed effects included days in milk ($P < 0.05$) and sire breed ($P < 0.0001$). Random effects included dam breed and farm. The Normande sired crossbreds had a significantly higher least-square-means for BCS (3.64) than cows from other breeds. Ayrshire cattle had the second highest least-squares-means estimate (2.76), followed by Holstein (2.61) and Jersey (2.35). The Ayrshire sired cow's estimated BCS was significantly higher than Jersey, but not significantly higher than Holstein. Holstein and Jersey sired cows were not significantly different from each other. These results suggest that crossbreeding with Normande may result in substantially higher levels of BCS in a range of herd environments.

Key words: Normande, crossbreed, Ayrshire

M69 Use of cow culling to help meet compliance for somatic cell standards. H. D. Norman and J. R. Wright*, *Animal Improvement Programs Laboratory, USDA-ARS, Beltsville, MD.*

Stricter SCC standards are expected in the United States. The relationship between a single high herd test-day SCC and SCC noncompliance was examined for US DHI herds, and the use of cow culling for maintaining herd compliance was investigated. Data were SCS from 14,346 herds with 15 to 26 tests from January 2009 through October 2010 and ≥10 cows for all tests. Cow SCC were derived from cow SCS by SCC = $2^{(SCS - 3)}$(100,000). Herd test-day SCC was a proxy for bulk tank SCC and was determined by weighting individual cow SCC by test-day milk yields. Herd test-day SCC was used to determine whether a herd would be SCC noncompliant under current or proposed US standards because 3 of 5 consecutive SCC tests exceeded 750,000, 600,000, 500,000, or 400,000 cells/mL. Percentage of herds that were SCC noncompliant 4 mo later for each SCC limit was determined for starting dates of October 2009, February 2010, and June 2010. Effectiveness of 3 different culling approaches was examined: culling cows with a high (above limit) current SCC, culling cows with a high index of previous and current SCC, and culling all cows above a designated parity. The culling objective was to eliminate cows that were likely to have a high SCC for each of their next 4 tests. Culling was simulated by deleting various percentages (1 to 5) of cows with high SCC from the herd when a herd test-day SCC exceeded one of the alternative limits. Herd-test-day SCC were recalculated without the high-SCC cows so that herd compliance for the next 4 tests could be compared with compliance without simulated culling. For herds with a starting test-day SCC of >400,000 cells/mL and no subsequent culling for SCC, percentage of noncompliant herds 4 mo later was 55% for October 2009, 62% for February 2010, and 66% for June 2010. Culling 5% of high-SCC cows lowered herd noncompliance to 46, 50, and 55% for the same starting months; culling cows with parity >4 reduced herd noncompliance to 48, 53, and 56%, respectively.

Key words: culling, somatic cell count, milk quality

M70 The association of high and low parent average with performance for yield, somatic cell score, and productive life in individual herds. C. D. Dechow*[1], H. D. Norman[2], R. C. Goodling[1], and J. R. Wright[2], *[1]Pennsylvania State University, University Park, [2]Animal Improvement Programs Laboratory, ARS, USDA, Beltsville, MD.*

There have been efforts to demonstrate to dairy producers the value of genetic selection by evaluating response to selection within their own herds. The objective of this study was to evaluate how frequently results conform to expectations for various traits and for herds of varying sizes. Parent averages (PA) and standardized records of milk yield, fat yield, protein yield, somatic cell score (SCS), and productive life (PL) were obtained from the Animal Improvement Programs Laboratory at USDA for 1,042,361 sire-identified Holstein cows that calved from 2005 through 2009 in 3334 Pennsylvania herds. Parent averages were obtained from evaluations occurring before a cow's first calving date to prevent part-whole bias. The top 25% (Q1) and bottom 25% (Q4) of cows for PA were identified within each herd and year of calving for each trait. The mean milk, fat and protein yield, SCS, and PL in Q1 and Q4 was determined for all herd-years. Results conformed to expectations when the average for Q1 exceeded the average for Q4. Most herd-years had higher values for Q1 cows than Q4 cows regardless of the number of sire-identified daughters present in the herd, with results ranging from 60% for PL to 78% for fat yield. The mean difference in PA from Q1 to Q4 for fat yield was 34 kg, which was close to the phenotypic difference in fat yield (36 kg). For productive life, the mean difference in average PA from Q1 to Q4 (4.8 mo) was greater than the phenotypic difference (1.5 mo). Greater than 89% of herd-years met expectations for yield traits when the number of cows exceeded 10 per quartile, compared with 74% of herd-years for SCS and 67% of herd-years for PL. All herds with 125 or more cows per quartile met expectations for yield traits compared with 98% for SCS and 68% for PL. Within-herd comparison of top and bottom cows for PA demonstrated a favorable response to selection for yield traits even in herds with relatively few sire-identified daughters. Results were less predictable for lower heritability traits, but the majority of herd-years still conformed to expectations.

Key words: parent average, genetic selection

M71 Genetic differences between New Zealand and North American dairy cows alter milk production and gluconeogenic enzyme expression. H. M. White*[1], S. S. Donkin[1], M. C. Lucy[2], T. M. Grala[3], and J. R. Roche[3], *[1]Purdue University, West Lafayette, IN, [2]University of Missouri, Columbia, [3]DairyNZ Ltd., Hamilton, New Zealand.*

Continuous selection of dairy cows for production traits may alter the regulation of metabolic pathways. High-producing North American (NA) cows produce more milk and have a larger degree of somatotropic axis uncoupling than less intensively selected New Zealand (NZ) cows. The objective of this study was to determine if production-based selection priorities (i.e., NA cows) have altered the regulation of the gluconeogenic pathway differently than selection priorities based on production and longevity traits (i.e., NZ cows). In this study, NZ (n = 27) and NA cows (n = 27) were monitored from 1 wk before calving to 12 wk post calving. Cows were pasture-fed and supplemented with 0, 3, or 6 kg DM of concentrate/d. Liver biopsy samples were collected at −7, +7, and +28 d relative to calving (DRTC) for mRNA analysis. Milk production of NA cows was greater ($P < 0.05$) during wk 5 to 11 postpartum and concentrate supplementation increased ($P < 0.05$) milk production for both NA and NZ cows. There was no genotype (NA vs. NZ) by diet interaction on blood glucose, NEFA, or insulin. Expression of pyruvate carboxylase (PC) mRNA was increased ($P < 0.001$) at +7 and +28 DRTC relative to −7 DRTC (3.04 and 2.42 vs. 1.25 ± 0.13 arbitrary units) and expression of cytosolic phosphoenolpyruvate carboxykinase (PEPCK-C) mRNA was increased at +28 compared with −7 and +7 DRTC (4.78 vs. 2.18 and 2.48 ± 1.41 arbitrary units). Expression of PC mRNA tended to be greater ($P = 0.12$) in NZ cows and declined with concentrate supplementation ($P < 0.05$) in both NZ and NA cows. Gluconeogenic enzyme expression in liver increased postpartum in both NZ and NA cows, with the 2 strains tending to differ for PC expression (greater in NZ cows). Grain supplementation reduced PC mRNA expression regardless of genetic strain. This project was supported in part by DairyNZ, Ltd. and in part by Grant no. 2009-35900-05970 from the USDA National Institute of Food and Agriculture.

Key words: pyruvate carboxylase, genetic selection, concentrate supplementation

M72 Verification of factors to estimate daily milk yield from one milking of cows milked twice 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 verify factors to predict daily milk yield when milk is sampled once per day for cows milked twice (2x) per day. Milk weights for both milkings were recorded automatically by 30 herds and collected by Dairy Herd Improvement supervisors. Data was split into 2 subsets for developing (FACT) and testing

(TEST) factors. Following edits, 179,064 daily milk weight records of 2941 first lactation (L1) cows and 298,905 records of 4757 later lactation (L2) cows remained in FACT and 177,299 records 2120 L1 cows and 335,692 records of 3319 L2 cows remained in TEST. 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) for FACT and applied to TEST. Regression equations (n = 168) were also developed within parity-MINT-DIM classes (2x7x12) [Method 3] to jointly account for MINT and DIM. Separate factors were derived for milking 1, and 2, for 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 in L1 and L2 for FACT. When applied to TEST, Method 1 resulted in rMSE of 2.07 (Milking 1, L1), 2.12 (Milking 2, L1), 2.64 (Milking 1, L2), and 2.85 kg (Milking 2, L2); compared with rMSE of 2.13, 2.26, 2.68 and 2.83 kg, respectively, from current factors for the same milkings for L1 and L2. Methods 1 and 3 provide more accurate prediction of daily milk weight from a single milking for herds milking 2x daily than factors currently in use.

Key words: milking interval, adjustment factor, milking frequency

M73 Estimation of daily yield of major fatty acids from single milking. V. Arnould[1,2], E. Froidmont[4], H. N. Nguyen[5], F. Dehareng[5], P. Dardenne[5], A. Gillon[2,6], N. Gengler[2,3], and H. Soyeurt*[2,3], *[1]CONVIS, Herdbuch Service Élevage et génétique, Ettelbruck, Luxembourg, [2]University of Liège, Gembloux Agro Bio-Tech, Animal Science Unit, Gembloux, Namur, Belgium, [3]National Fund for Scientific Research, Brussels, Brussels, Belgium, [4]Production and Sectors Department, Walloon Agricultural Research Centre, Gembloux, Namur, Belgium, [5]Quality of Agricultural Products Department, Walloon Agricultural Research Centre, Gembloux, Namur, Belgium, [6]Walloon Breeding Association, Ciney, Namur, Belgium.*

There are cost savings when the frequency of milk recording is reduced. Milk recording organizations have implemented alternative schemes that rely on milking interval (MI), but MI can be unreliable. Moreover, nothing is available for milk fatty acids (FA). The aim of this study was to build a model for estimating accurately the daily yields of major FA from single milking without using the MI. The hypothesis was that MI can be reflected by the changes of milk yield and composition. Five Holstein cows were followed generally every day at each milking between March 2008 and December 2010. FA were measured by mid-infrared. The database contained 1,440 records. Eight models were tested to estimate daily yields from morning or evening milking. Different effects were included progressively. The first ones were related to the characterization of the milk production (i.e., days in milk, month of calving, month of test, milk yield, and lactation number). The other effects were related to the milk composition (i.e., fat and protein contents). Models were compared from the coefficient of determination and the mean square errors between estimated and observed daily yields. Results showed that R^2 were higher when the milk composition effects are introduced in the model. For the different studied FA traits, R^2 ranged between 0.87 and 0.88, when daily yields were estimated from morning milking and between 0.75 and 0.86 when daily yield were estimated from evening milking. By comparison, the model approved by ICAR and proposed by Liu et al. in 2000 gave R^2 ranged from 0.81 to 0.84 from morning milking; and from 0.74 to 0.85 from evening milking. Therefore, the introduction of these milk composition effects permit to replace the MI. It was also observed that daily yields estimated from evening data are less accurate than those estimated from morning data. After a larger validation, the best accurate model could be used to evaluate the fatty acid data collected in alternate milking recording and used for breeding purposes.

Key words: milk, fatty acid, daily prediction

M74 Comparison of lactation performance in a panel of genetically diverse inbred mouse strains. D. L. Hadsell*[1], W. Olea[1], J. Wei[2], L. A. Hadsell[1], and P. Williamson[2], *[1]Baylor College of Medicine, Houston, TX, [2]The University of Sydney, Sydney, NSW, Australia.*

Inbred mouse lines have been a powerful tool in the mapping and identification of genes underlying a variety of different qualitative and quantitative traits. Their use in mapping lactation-related traits has been limited. Recently, the application of mapping panels based on existing inbred mouse strains has had some success in identifying quantitative trait loci. The current study compared quantitative indices of lactation performance among a panel of inbred mouse strains with the ultimate goal of apply this data with association mapping strategies to identify potential genes determining variation in milk production. Females from each of 32 inbred strains (n = 8 mice/strain) were studied during the first 8 d of their second lactation. Weight gain (LWG) of cross-foster litters (10 pups/litter) served as the primary indicator of milk production (19.9 ± 8.9 g, mean ± S.D.) and varied ($P < 0.0001$) among strains (range 5.3 – 32.1 g). The number of pups born per litter (7 ± 3) also varied ($P < 0.0001$) among strains (range 4 – 13) and was significantly correlated to crossfoster litter gain ($r = 0.47$, $P < 0.0001$). Maternal body weight and maternal food intake also had significantly positive correlations to crossfoster litter gain ($P < 0.0001$). Initial haplotype association analysis using the 132 k SNP database publically available from the Broad Institute identified suggestive ($P < 10^{-5}$) associations to LWG on chromosomes 4, 11, and 13. These data indicate that significant phenotypic variation exists among genetically inbred mouse strains for traits indicative of milk production. Such variation should be useful to map QTL genes for lactation. Supported by NICHD grant #1R21HD059746–01A1.

Key words: milk production, variation, mouse

M75 Statistical comparison of persistency among calving seasons of Iranian Holsteins. R. Izadkhah*, H. Farhangfar, M. H. Fathi Nasri, and H. Naeemipour, *Birjand University, Birjand, Iran.*

In this study, Wilmink exponential function ($y = a+bt+ce(-0.05*t)$) was utilized to evaluate the effect of calving season on persistency. The function was fit on 130,668 monthly test-day milk yields belonging to 15,183 first lactation Iranian Holstein cows calving between 2000 and 2009. Persistency was calculated based upon predicted milk yield by the function [(milk305/peak yield*305)*100]. Effect of calving season on persistency was analyzed by a linear mixed model. In the model, fixed effect of geographical location, herd, year, season, sire's sperm origin, as well as linear covariables of calving age, peak yield, peak time, days to first milk recording, and sire random effect were included. The model was fit by Mixed Procedure of SAS software. The results indicated that all factors had significant ($P < 0.001$) affect on persistency. Least squares means of persistency were 84.68, 85.45,

85.77 and 84.75% for spring, summer, autumn and winter calvers, respectively. There were no significant differences between spring and winter seasons and between summer and autumn seasons. With respect to positive correlation between persistency and total lactation milk yield, providing constant peak yield, cows calving in autumn and summer are expected to have higher milk yield as compared with spring and winter calvers.

Key words: Wilmink function, persistency, Iranian Holstein

M76 Genetic parameters estimates to Colombian buffalo milk yield under random regression models. N. Hurtado-Lugo*[1,2], S. Sousa Júnior[1], M. Cerón[2], R. Aspilcuelta[1], E. Acevedo[1], S. Gutierrez[2], L. Albuquerque[1], G. de Camargo[1], D. Santos[1], and H. Tonhati[1], *[1]UNESP Faculty of Agriculture and Veterinary Sciences, State University of São Paulo, Jaboticabal, SP, Brazil, [2]Genetics and Animal Improvement Group, Faculty of Agriculture Sciences, University of Antioquia, Medellín, Colombia.*

The random regression model (RRM) has been proposed as an alternative approach to analyze longitudinal data, for instance milk yield records that are collected repeatedly over a lactation, because it considers such data as repeated measures. Buffalo production is part of the agribusiness in developing countries such as Colombia, and there is still little research using RRM. This study has the aim to estimate the genetic parameters using RRM for test-day milk yield in dairy buffalo in Colombian northern coast. First lactations from 10,929 buffalo were recorded monthly from 1998 to 2008. The archive was composed of 11,148 animals, 10,929 female buffaloes and 219 bulls. The fixed effects were contemporary group that was composed of month and year of control, and milking days (the fixed regression to the population mean). The age at calving was used as covariate (linear and quadratic regression) and the random effects were the direct genetic and the permanent environment. The most appropriate model was the one using a Legendre′s polynomial function of 3rd order for the genetic effect and 6th order for the permanent environmental effect. The residual variances were heterogeneous, modeled by a step function, containing 2 classes of variances. The variance components were estimated using the statistical package WOMBAT. Models were compared by Akaike Information and Schwarz Bayesian′s criteria. The heritability varied from 0.33 to 0.17; the highest values were observed at the beginning of the lactation, and the lowest at the end. The genetic and phenotypic correlations were high and positive; it indicates the necessity to model the residual with a heterogeneous structure. Financial support: FAPESP, Foundation for Research Support of São, SP, Brazil.

Key words: Legendre′s polynomial, regression, buffaloes

M77 Mathematical modeling of the lactation curve of domestic donkey (*Equus asinus*). A. M. Guastella*[1], A. Criscione[1], S. Bordonaro[1], D. Marletta[1], R. Steri[2], and N. P. P. Macciotta[1], *[1]Università di Catania, Catania, Italy, [2]Università di Sassari, Sassari, Italy.*

Donkey farming for milk production is getting an increasing interest in Italy mainly for pharmaceutical and cosmetic purposes but also for human nutrition. Actually donkey milk is suitable for people intolerant to cow milk protein and is able to fulfill nutritional requirements of babies. The knowledge of the lactation curve may be of interest for a first definition of production attitudes and nutrition requirements of this species. Data were 453 test day records for milk yield, fat and protein percentage and somatic cell count (SCS) of 62 donkeys farmed in 2 commercial herds located in Sicily. Animals were grouped according to age classes (<5, 5, 6, 7–10 and >10 years respectively). Average lactation curves for age class were estimated with a mixed linear model that included fixed effects of herd, calving season, age class, days in milk interval (9 intervals of 30 d each) and the random effect of the animal. Repeatability was 0.55, 0.14, 0.10 and 0.07 for milk yield, fat and protein percentage and scc logarithm, respectively. Almost all factors included in the model significantly affect milk yield and protein percentage. Youngest donkeys had curves with lower peak and higher persistency compared with older animals. Average curves for fat percentage showed an opposite trend compared with milk yield, even though with a high variability between classes of age. Protein content was characterized by a continuous decreasing trend along the lactation. Somatic cell count was constant throughout the lactation, below 20,000 cell/mL, with a slight increase only at the end. The fitting of individual patterns for milk yield with the incomplete gamma function of Wood resulted in a frequency of 0.43 of curves without a lactation peak. This result is mainly due to the scarce availability of data in early lactation, being the milk of the first month suckled by the foal. Standard curves had an overall mean of 68 d for time at peak occurrence and a peak yield of 2.28 kg/d. Younger animals have later peak occurrence (160 d) than older animals (between 45 and 76 d) and lower peak productions (1.6 kg/d vs. 2.3 kg/d) respectively.

Key words: donkey, lactation curve, mathematical modeling

M78 Genetics of immunocompetence traits in Aseel native chicken of India. S. Choudhary*[1], S. Kumar[2], and B. Nautiyal[1], *[1]MJP Rohilkhand University, Bareilly, U.P. India, [2]Central Avian Research Institute, Bareilly, U.P. India.*

Breeding chickens for higher immunocompetence and disease resistance provides a valuable approach for commercial poultry production. Several immunocompetence traits that can be considered for improving genetic resistance to diseases in poultry are greater antibody response to sheep RBC, lysozyme activity and high titer of immunoglobulin G (IgG) in the serum. Antibody titers against sheep RBC and serum IgG level are the indicators of humoral immune response, whereas bacteriolytic activity of serum lysozyme is the indicator of non-specific immune response. In the present study Aseel (n = 301), an Indian breed of chicken, was studied for high and low immune response by assessing their immunocompetence traits using 3 different tests - hemagglutination (HA) test, lysozyme plate assay and serum IgG level estimation. The data generated on immunological traits were analyzed by least squares ANOVA. The average (expressed as mean+ standard error) HA titer, serum lysozyme activity and IgG level was 8.14 ± 0.35, 4.85 ± 0.20, 10.82 ± 0.64 in males and 8.15 ± 0.31, 4.48 ± 0.22, 12.64 ± 0.75 in females, respectively. Sex of the birds had no effect ($P > 0.05$) on HA titer, lysozyme level and serum IgG level. However, male birds revealed higher IgG level ($P < 0.07$) than the female. We concluded that Aseel has high immune competence status in comparison to broiler and desi fowl chicken reported earlier in the literature.

Key words: Aseel, Immunocompetence traits

M79 Study on the diversity of Yunnan original chicken meat using NIR spectroscopy based on principal component analysis and cluster analysis. J.-L. Wu[1], X. Gao*[1], Y.-Z. Li[3], Y.-F. Yin[1], and Y. Li[2], *[1]Yunnan Animal Science and Veterinary Institute, Kunming, Yunnan, China, [2]Sweden Perten Instruments Representative Office in China, Beijing, China, [3]University of Minnesota, Morris.*

The aim of this study was to investigate the feasibility of using near-infrared (NIR) spectroscopy to identify genetic characteristics of meat quality of Yunnan original chicken breeds. A total of 1310 breast muscle samples collected from 25 original breeds of chicken in 28 counties located in 14 regions of Yunnan Province were analyzed using PERTEN DA7200 NIR spectrophotometer. Data were analyzed by using principal component analysis (PCA) of the Unscrambler (CAMO) software and cluster analysis (CA) of the SPSS software. The results show that the NIR of the 25 breeds of Yunnan original chicken are basically identical. Spectra transformed by SNV, 9 point smoothing, and the first derivative, indicate that absorption band of each breed was significantly different in the range of 1000 to 1050nm, 1130 to 1150nm and 1370 to 1400nm. The greatest difference was observed between the Nixi and the Xichou chicken breeds. Principal component analysis indicated that the NIR spectra of each breed was different, particularly in 5 breeds of the Xichou, Zhenyuan-Piao, Nixi, Luxi Ae, and Huaping-Wu chicken. After pretreatment with Euclidean distance spectrum of the CA, a certain Euclidean distance can be divided into distinctive breeds. The Xichou and Nixi chicken had the most remarkable specificity, with the Euclidean distance of 1 between the 2 breeds. Xichou chicken distribute the southeast of Yunnan and Nixi chicken distribute chicken distribute the northwest of Yunnan, the 2 breeds did not show any genetic connections, probably due to the longest geographical distance of their origin. These results suggest that the 5 breeds are best represent genetic resources of the original chicken, with the greatest conservation value. Meanwhile, this study indicates that NIR can be used to accurately and quickly analyze genetic characteristics of meat quality in chicken breeds and identify genetic resources of special chicken breeds.

Key words: original chicken breed, meat, near-infrared

M80 Breed and egg size effects on weight loss during incubation of Broiler eggs. O. T. F. Abanikannda*, A. O. Leigh, and A. O. Giwa, *Lagos State University, Ojo-Lagos, Nigeria.*

Physiological processes that take place during incubation of eggs often resulted in changes in egg weight during the period. This study investigates the effect of breed and egg sizes on weight loss at 3 points between incubation and hatching viz: pre-incubation, 18th day of incubation, chick weight at hatching. A total of 1002 hatchable eggs from 3 strains; Anak (n = 361), Marshall (n = 359) and Ross (n = 282) of Broiler breeders were weighed and measured using digital weighing scale and digital caliper. Weight, length and width were taken before incubation, while shape index was also computed. Weight losses from incubation to 18 d (WtLoss1), 18th day to hatching (WtLoss2) and incubation to hatch (WtLoss3)] were computed. The Minitab statistical software was used for basic descriptives, regression analyses and statistical modeling of the data. The model used for the regression analysis is described by $Y_{ijklm} = \mu + \alpha_i + \beta_j + \theta_k + \rho_l + \varepsilon_{ijklm}$ describing each of the 3 response variables. Egg weight was between 44.60g and 81.70g, while egg length ranged between 49.99mm and 69.98mm, and egg width was between 38.54mm and 56.75mm, while shape index was between 61.44% and 99.02% across the 3 strains studied. The largest source of variation was breed effect, which was highly significant ($P < 0.001$) on all 4 variables. Similarly, breed significantly ($P < 0.001$) impacted on WtLoss1 and Wt Loss3 but was not a significant ($P > 0.05$) source of variation on WtLoss2. All the predictor variables were significantly ($P < 0.05$) correlated to the response variables except shape index, which had negative and non-significant ($P > 0.05$) correlation with the weight losses. The very low negative and non-significant correlation between egg weight and egg weight loss up to the 18th day of incubation indicated that weight loss was slower in bigger eggs compared with relatively smaller eggs. The study revealed that breed was a significant source of variation on weight loss at the 18th day of incubation (WtLoss1) and throughout the entire period of incubation and hatching (WtLoss3) but was not significant on weight loss after the 18th day (WtLoss2).

Table 1. Egg weight loss at different stages of incubation and hatching by breed

Breed	N	WtLoss 1 (%)	WtLoss 2 (%)	WtLoss 3 (%)
Anak	361	13.75±0.19[a]	19.12±0.47	32.87±0.44[a]
Marshall	359	12.86±0.15[b]	18.37±0.42	31.22±0.42[b]
Ross	282	11.69±0.25[c]	19.41±0.40	31.10±0.36[b]
Combined	1002	12.85±0.11	18.93±0.25	31.78±0.24

[a–c]Means with different superscripts within the same column differs significantly ($P < 0.05$).

Key words: broiler, incubation, weight loss

M81 Estimation of genetic parameters for body weight traits in Mazandaran indigenous chicken. S. Niknafs*, A. Nejati Javaremi, H. Mehrabani Yeganeh, and A. Fatemi, *Agricultural Faculty, University of Tehran, Karaj, Alborz, Iran.*

A breeding station for Mazandaran native chicken was established in 1988 with 2 main objectives: extension and genetic improvement of the local breed. For 18 generations, selection was done for 8-wk BW (BW8), egg number, age at first egg and average egg weight as selection criteria. Besides these traits, some other traits were recorded. As the aim of the current study we estimated genetic parameters for body weight traits including body weight at hatch (BW1), at 8 (BW8), at 12 weeks of age (BW12) and at sexual maturity (WSM). Univariate (for estimating variance components) and bivariate (for estimating covariance components) animal models were fitted using ASREML procedure. The highest and lowest magnitude of heritability estimates belonged to WSM and BW8, respectively. BW8 has been included in selection criteria, so relatively lower heritability may be due to decreased genetic variance during selection process. Genetic correlation between BW8 and BW12 was close to unity. Also, high genetic correlation between BW12 and WSM was observed. Other genetic relationships were moderate generally. No remarkable environmental correlations were obtained among these traits except for moderate environmental relationship between BW8 and BW12.

Table 1. Statistical description of data set, heritabilities (diagonal in bold), genetic (above diagonal) and environmental (below diagonal) correlations of investigated traits (±SE)

Trait	BW1	BW8	BW12	WSM
No of Animal in Data File	35287	43067	38297	31147
Mean	35.53	563.7	953.9	1694
Coefficient of Variance	8.15	17.09	14.49	11.90
BW1	0.46±0.01	0.37±0.02	0.36±0.02	0.41±0.02
BW8	–0.03±0.00	0.24±0.00	0.91±0.00	0.57±0.02
BW12	–0.04±0.01	0.47±0.00	0.29±0.01	0.69±0.01
WSM	–0.09±0.01	0.16±0.01	0.19±0.01	0.47±0.01

Key words: body weight, chicken, genetic parameters

M82 Genetic and phenotypic trends for body weight and egg production in Mazandaran indigenous chicken. S. Niknafs*, A. Nejati Javaremi, H. Mehrabani Yeganeh, and A. Fatemi, *Agricultural Faculty, University of Tehran, Karaj, Alborz, Iran.*

The study of genetic trends is a way for monitoring the selection process. Phenotypic information collected during 1988 to 2009 (18 successive generations of selection) in breeding station of Mazandaran native chicken were analyzed to estimate genetic and phenotypic trends. This population has been selected for traits body weight at 8 weeks, egg number, sexual maturity age and egg weight. Univariate animal model in ASREML software was applied to estimate breeding values. Trends for breeding values and phenotypic performance were obtained by regression of average breeding values and phenotypic least squares means, respectively, on generation number. The table below shows regression coefficients of genetic and phenotypic trends. Results showed that selection can lead to genetic progress in whole recorded traits, except for traits EW28 and EW12. Significant changes in phenotypic level were observed just for BW1, BW8 and WSM, which could be caused by negative environmental trends. Also, inbreeding coefficient on average has increased with the rate of 0.0058 ($P < 0.0001$) per generation of selection.

Table 1. Regression coefficients of average breeding values and phenotypic LSM on generation with *P*-values

Trait	Genetic Trend	*P* <	Phenotypic Trend	*P* <
BW1	−0.035	0.0001	−0.36	0.0164
BW8	2.98	0.0001	9.32	0.0181
BW12	4.74	0.0002	2.3	0.8240
WSM	−4.16	0.0023	21.4	0.0043
ASM	−1.35	0.0001	0.042	0.9497
EN	0.95	0.0001	−0.31	0.2652
EW1	−0.185	0.0001	−0.045	0.6110
EW28	−0.002	0.8684	−0.034	0.8769
EW30	−0.046	0.0184	−0.017	0.9336
EW32	−0.065	0.0040	−0.013	0.9453
EW12	0.01	0.4695	0.061	0.5408
EM	43.8	0.0001	−12.5	0.3665
EINT	1.46	0.0001	−0.103	0.7482

Key words: genetic trends, body weight, egg production

M83 Heritability and genetic correlation estimates for egg production related traits in Mazandaran indigenous chicken. S. Niknafs*, A. Nejati Javaremi, H. Mehrabani Yeganeh, and A. Fatemi, *Agricultural Faculty, University of Tehran, Karaj, Alborz, Iran.*

The best way to improve the productivity of indigenous chickens, without altering any of the morphological characteristics, is to select for production traits within a given population. Such strategy needs accurate estimates of genetic parameters. To achieve this purpose phenotypic information for 18 successive generations which was collected during 1988–2009 in the breeding station of Mazandaran native chicken (north of Iran) were analyzed. Univariate and bivariate animal models in ASREML procedure were used to estimate (co) variance components for traits of age at sexual maturity (ASM) (31349 records), egg number (EN) (31349), average egg weight at 28 (EW28) (17225), 30 (EW30) (19031), 32 (EW32) (18955) weeks of age and average egg weight for first 12 weeks of production (EW12) (18847). Heritabilities, genetic and environmental correlations are shown in the table below. Heritability estimates of egg production traits varied from 0.17 ± 0.01 to 0.43 ± 0.01. Among these traits egg number seemed to be less heritable than others. Genetic correlations among egg weight traits (EW28, EW30, EW32 and EW12) were close to unity. Also, rather moderate environmental correlations among these traits were found. Low negative genetic correlations were obtained between egg number and egg weight traits. Sexual maturity age is moderately negatively genetically correlated with egg number, whereas it has low positive genetic correlations with egg weight traits.

Table 1. Heritabilities (diagonal), genetic (above diagonal) and environmental (below diagonal) correlations (±SE)

Trait	ASM	EN	EW28	EW30	EW32	EW12
ASM	0.36±0.01	–0.41±0.03	0.24±0.03	0.20±0.03	0.21±0.03	0.46±0.03
EN	−0.09±0.01	0.17±0.01	–0.29±0.05	–0.24±0.04	–0.26±0.04	–0.24±0.05
EW28	0.02±0.01	0.02±0.01	0.32±0.01	0.99±0.00	0.98±0.00	0.98±0.00
EW30	0.01±0.01	–0.01±0.01	0.35±0.01	0.41±0.02	0.99±0.00	0.98±0.00
EW32	0.02±0.01	–0.00±0.01	0.30±0.01	0.36±0.01	0.43±0.01	0.97±0.00
EW12	0.19±0.01	0.02±0.01	0.40±0.01	0.38±0.01	0.37±0.01	0.37±0.02

Key words: genetic parameter, egg production, chicken

M84 Effects of salts on foaming properties of milk protein concentrate at neutral pH. J. Han* and B. Vardhanabhuti, *University of Missouri, Columbia.*

Milk protein concentrate (MPC) is one of the major ingredients in foods due to its nutritional and functional properties including solubility, water binding, foaming, and emulsification. The foaming ability of milk proteins could potentially allow them to replace egg white protein; however, there is a lack of research on foaming properties of MPC. The goal of this study was to investigate the effects of salts on foaming properties of MPC. Calcium chloride, sodium citrate, and sodium chloride were mixed with MPC solutions and pH was adjusted such that the final solutions contained 5% w/w protein, 0–20 m*M* $CaCl_2$ and 0–40 m*M* citrate, or 0–100 m*M* NaCl at pH 7.0. Foam was generated by whipping MPC solutions in a KitchenAid mixer. Foaming properties were determined by measuring overrun and drainage ½ life. Physical properties of pre-foam solutions, including solubility, turbidity, and particle size were measured. Interfacial shear rheology was determined using a controlled- strain and rate rheometer with a bicone geometry. Addition of 20 m*M* $CaCl_2$ caused a reduction in overrun ($P < 0.05$) but no significant effect on foam stability. Either with or without of $CaCl_2$, increasing citrate concentration significantly increased overrun ($P < 0.05$) and drainage ½ life of MPC foam. However, samples having higher citrate concentration (40 m*M*) only showed improvement in overrun but a decrease in drainage ½ life. Sodium chloride significantly improved overrun ($P < 0.05$) but had no effect on drainage ½ life. Enhanced overrun corresponded to a reduction in particle size and turbidity and an increase in solubility of pre-foam solutions. Interestingly, interfacial rheology revealed that pre-foam solutions with $CaCl_2$ exhibited higher interfacial viscosity and interfacial elastic modulus, while the presence of citrate reduced interfacial viscosity and interfacial elastic modulus. These results indicated that appropriate concentrations and combination of salts are needed to optimize foaming properties of MPC.

Key words: milk protein concentrate, foaming properties, salts

M85 Microencapsulation of probiotic cultures using polymerized whey proteins as wall material. Z. Zheng[1], Y. Jiang[1], X. Chen[2], J. Wang[2], J. Cheng[1], H. Zhang[2], and M. Guo*[1], *[1]University of Vermont, Burlington, [2]Inner Mongolia Agricultural University, Hohhot, Inner Mongolia, China.*

Commonly used probiotics are sensitive to the environment and processing conditions. The objective of this study was to develop a microencapsulation technique using polymerized whey proteins (PWP) as a wall material for protecting probiotic cultures. PWP was prepared by heating whey protein isolate solution (12%, w/v, pH 8.0) at 85°C for 40 min. The solution was then adjusted to pH 7.0 after cooling. The ratio of the PWP solution to the probiotic culture *Lactobacillus acidophilus* NCFM (8.31×10^8 cfu/mL) was 7:3. The mix was extruded using a 50-mL syringe through a needle (0.6 mm) to the cross linker $CaCl_2$ solution (16.7%) containing Tween-20 (0.4%, v/v) at 40°C while stirring. After being kept in the $CaCl_2$ solution for 20 min and rinsed twice with 0.9% NaCl solution, the beads were freeze-dried after mixing with protecting agents including non-fat dry milk (20%), peptone (1%), and ascorbic acid (0.4%). Microencapsulation using sodium alginate (SA) was prepared as a control. The microencapsulated cultures by PWP and/or SA, and free culture were subject to artificial digestions (gastric juice for 3 h and intestinal juice for 6 h) to determine the survival rate. The diameters of PWP based and SA based beads were 2.70 ± 0.22 mm and 1.28 ± 0.09 mm, respectively. The entrapment yield for the PWP method (89.3 ± 4.8%) was significantly higher ($P < 0.01$) than the control method (73.18 ± 1.4%). Viable counts of the culture after digestion processes were $3.63 \pm 1.48 \times 10^4$, $1.83 \pm 1.10 \times 10^4$ and $1.35 \pm 0.72 \times 10^2$ cfu/mL for the PWP beads, SA ones and free culture, respectively. Results showed that the PWP based microencapsulation seems more effective in protection of probiotics than SA method in the model system. Survivability of PWP encapsulated probiotic cultures in fermented milk products will be further investigated.

Key words: microencapsulation, polymerized whey protein, probiotic

M86 Proteolysis in UHT milk produced with CO_2 added raw milk. P. C. B. Vianna[1], E. H. M. Walter[2], M. E. F. Dias*[3], J. A. Faria[3], F. M. Netto[3], and M. L. Gigante[3], *[1]Universidade Norte do Paraná, Londrina, SP, Brazil, [2]Universidade Federal do Pampa, Bagé, SP, Brazil, [3]Universidade Estadual de Campinas, Campinas, SP, Brazil.*

The goal of this work was to evaluate the effect of CO_2 addition to raw milk on proteolysis of UHT milk during storage. Control milk (without CO_2 addition) and treated milk (added with CO_2 until pH 6.2) were stored in bulk tanks at 4°C during 6 d. After storage, milks were processed using indirect heating (140°C/5s). Samples were aseptically packed in low density polyethylene pouches and stored in the dark at room temperature. Raw milk was evaluated at reception and after 6 d-storage to standard plate and psychrotrophic bacteria count. UHT milk samples were analyzed for proteolysis twice a month until 120 d-storage. Increased in non casein nitrogen as a percentage of total nitrogen was used as index of proteolysis. Analysis of peptides of non casein nitrogen filtrates by RP-HPLC was performed after 1 and 120 d of storage. Split-plot design was used and the complete experiment was replicated 3 times. The results were evaluated by ANOVA and Tukey's test ($P \leq 0.05$). Raw milk presented standard plate and psychrotrophic bacteria counts of 2.8×10^3cfu/mL and 5.2×10^2 cfu/mL, respectively. After 6 d-storage, these counts increased 3 and 4 log cycles for milk without CO_2 addition, respectively, while in the CO_2 added milk the counts remained constant, resulting in a better microbiological quality of raw milk to UHT processing. The proteolysis increased significantly during 120 d of storage to both treatments, but the increase was 1.4 times faster for UHT control milk (UHT_C) than UHT produced from raw milk with CO_2 addition (UHT_{CO2}). One day after processing, the chromatograms showed similar peaks for both milks, corresponding to hydrolysis by plasmin and heat resistant psychrotrophic proteases. However, after 120 d the amount of peptides in UHT_{CO2} milk was almost constant, while peptides produced by plasmin and proteases of psychrotrophic increased in UHT_C, indicating higher proteolysis in this sample. The better microbiological quality of CO_2 added raw milk resulted in less proteolysis and possibly less susceptibility of age gelation in UHT milk, the main problem that limits its shelf life.

Key words: UHT milk proteolysis, carbon dioxide, psychrotrophic

M87 The effect of commercial sterilization regimes on micellar casein concentrates (MCC). C. M. Beliciu, A. Sauer*, and C. I. Moraru, *Cornell University, Ithaca, NY.*

The increasing interest of using micellar casein concentrates (MCC) obtained by membrane separation in the manufacture of shelf-stable,

high protein beverages creates a need to understand the effect of processing conditions, particularly sterilization, on the stability of this ingredient. In this work, MCCs of 5% - 10% casein concentration were subjected to both continuous-flow UHT treatment and in-container retorting, at the same cumulative value of the lethality factor (F_0 = 9.9). The effects of sterilization on the stability and physical properties of MCCs were investigated by determining their rheological properties, zeta potential, particle size and mineral distribution. The study was performed in triplicate. Significant differences among samples were determined at $P \leq 0.05$. Sterilization led to significant changes in zeta potential, from −37mV to −24mV for the controls (non-heat-treated MCCs), to −30 mV to −17mV in retorted MCCs and −34 mV to −20mV in the UHT treated MCCs. This was attributed to the re-distribution of minerals, specifically a loss in solubility of calcium phosphate at the micelle level; soluble Ca content decreased by an average of 30% as a result of the UHT treatment and by 21% as a result of retorting, as compared to untreated samples. Average particle diameter increased as a result of heat treatment: 240nm in retorted samples vs. 180nm in the untreated MCCs (control). UHT treatment led to formation of aggregates visible with the naked eye. Retorting of MCCs led to a 50% decrease in apparent viscosity as compared to the untreated samples, while the UHT treated MCCs had higher apparent viscosity than the controls. For the UHT treated samples, dynamic rheological testing revealed a solid-like behavior at a casein concentration >5%, which was indicative of structure formation. An evaluation of sterilization behavior of MCCs obtained by reconstitution of spray dried powders showed that drying enhanced the instabilities that occurred during sterilization. The results of this study are particularly relevant for using MCCs obtained by membrane separation for the manufacture of shelf stable milk protein beverages.

Key words: micellar casein, zeta potential, retorting

M88 The crystallization of large lactose crystals in skim milk concentrate. B. Toledo* and F. X. Milani, *University of Wisconsin-Madison, Madison.*

The presence of lactose crystals greater than 10 μm in concentrated skim milk is normally considered a quality defect. These large crystals can be avoided by manipulating process parameters such as cooling rate, seed concentration and agitation speed. The objective of the present study is to investigate the formation, characterization and performance of large α- lactose monohydrate crystals in concentrated skim milk at 40% total solids. A 2-level, fractional factorial design with 4 factors was used for the study. The factors tested were holding temperature (5 and 10°C), lactose seed concentration (0.005% and 0.010%), lactose seed size (200 and 40 mesh), and agitation speed (50 and 100 RPM). Lactose crystallization in concentrated skim milk was done by reconstituting skim milk powder to 40% total solids and allowed to hydrate for 24 h at 5°C. After reconstitution, the concentrate was pasteurized, cooled, and seeded with α- lactose monohydrate crystals. Lactose crystallized during 24 and 48 h in a 150 mL stirred reactor. Crystallization started at the selected temperatures and continued with a cooling rate of 0.02 to 0.04°C per hour. Photomicrographs were taken and analyzed with ImageJ 1.44i software. The formed crystals had mean sizes of 71 ± 35 μm and 93 ± 45 μm at 24 and 48 h, respectively. Analysis of the present model concluded that a 24 h crystallization period is significantly influence by the lactose seed size and holding temperature. As the lactose seed size increased, the mean value of crystals increased by 12 μm. When the holding temperature increased, the mean value of the crystals decreased 5 μm. Analysis for 48 h crystallization did not reveal significant influence from any of the tested factors. This is associated with shattering of large crystals, which diminished the influence of initial experimental design factors. The results from the present study are intended to be used as preliminary information in the design of skim milk processes and products that utilize large lactose crystals as a value added feature.

Key words: crystallization, lactose, skim milk

M89 Investigation of twin-screw extrusion puffing of non-fat dry milk powder and starch to produce puffs and crisps for snack and ingredient uses. A. J. Tremaine* and T. C. Schoenfuss, *University of Minnesota, Department of Food Science and Nutrition, St. Paul.*

The use of twin-screw extrusion to produce puffs and crisps for cereals and snacks is widely used in the food industry. Soy protein is the leading protein used in extrusion puffing, but caseinates and whey protein concentrates and isolates have also been researched extensively. Less research has focused on non-fat dry milk (NDM). NDM has the advantage of an abundant and inexpensive supply, has the full amount of calcium found in milk, and has a cleaner flavor than whey protein concentrates. One disadvantage of NDM is the difficulty in creating protein-protein interactions in the extruder to obtain a stable puff. The objective of this study was to evaluate the effect of acid addition and varying moisture levels on the attributes of expanded puffs containing high levels of NDM. Varying concentrations of low-heat NDM were combined with modified cornstarch and processed on a Buhler 44mm twin-screw extruder. Extruded product was collected in ropes, cut into 2 inch lengths, and dried on a fluidized bed dryer. The experimental parameters included three NDM concentrations (45, 65, 85%), three lactic acid levels (0, 33, 50% of the moisture) and two moisture levels (6.5, 7.3 kg/h). Process (die temperature, die pressure, motor torque and specific mechanical energy) and product responses (color, solubility, expansion ratio and bulk density) were statistically analyzed to assess the effects of NDM, acid and moisture levels, and response surface plots were generated. The results obtained indicate that NDM concentration, moisture and acid level all affected process and product responses. These results will be useful in product development in the food industry when incorporating NDM into extruded products.

Key words: extrusion, non-fat dry milk, response surface plots

M90 Browning and pH of UHT whole milk as influenced by time and temperature of storage. M. E. F. Dias*[1], P. C. B. Vianna[2], and M. L. Gigante[1], *[1]Universidade Estadual de Campinas, Campinas, SP/Brazil, [2]Universidade Norte do Paraná, Londrina, PR/Brazil.*

The CO_2 addition has been used in maintaining the quality of refrigerated storage of raw milk. The objective of this work was to evaluate the effect of time and temperature of storage on pH and browning of UHT whole milk produced from refrigerated raw milk with or without CO_2 added. Raw milk (250 L) with and without CO_2 addition was stored in bulk tanks at 4°C during 6 d before UHT treatment. The milk was sterilized by direct steam injection (143°C/4 s, homogenization pressure 220 bar), cooled to 25°C and packaged in Tetra Brik (125 mL). The samples were stored at 25, 35 and 45°C for 180 d. During storage, samples were taken at random after 1, 30, 60, 90, 120, 150 and 180 d and evaluated for pH and browning. The color was assessed with a colorimeter Hunterlab ColorQuest II, with D65 illuminant according to conditions provided by the manufacturer. The increase in Hunter b* value (measures blue [-] to yellow [+]) was used for determination of browning. The pH was measured in milk samples at 20°C using a combined pH glass electrode fitted to a pH meter (Digimed Model DM 22).

The split-split-plot design with 3 replications was used. The results were evaluated by ANOVA (ANOVA) and Tukey′s test ($P \leq 0.05$). The CO_2 addition to raw milk significantly affected the pH of UHT milk and it was 6.66 and 6.70 for samples with or without CO_2 added, respectively. The rate of browning for UHT samples obtained from raw milk without CO_2 was higher than the rate obtained for samples from raw milk added of CO_2. During storage the pH of all samples decreased, while browning, as indicated by b* values, increased. The lower pH and increase of browning was greater at 45°C, followed by samples at 35°C and 25°C. After 6 mo storage period, UHT milk stored at 45°C showed pH value of 6.24 while this value was 6.74 at 25°C. At the same time, b* values were 18.93 and 7.03 for UHT milk stored at 45°C and 25°C, respectively. Changes in pH and browning are related to Maillard reactions.

Key words: browning, UHT milk, CO_2

M91 Evaluation of vacuum packaging on physical properties and solubility of dry dairy ingredients. H. Eshpari* and P. Tong, *California Polytechnic State University, San Luis Obispo.*

Dry dairy ingredients can have a longer 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, bulk, and tapped) densities, flowability, compressibility, color, and solubility of 6 types of dry dairy ingredients. Commercial samples of nonfat dry milk powder, whole milk powder, buttermilk powder, milk protein isolate whey protein concentrate 80, and sweet whey powder 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, 6, and 12 mo at 25°C and 60% relative humidity. Each powder was sampled and analyzed in duplicate for all the quality attributes mentioned above upon receiving and after 3, 6, and 12 mo storage. At $\alpha = 0.01$: particle size, (particle bulk and tapped) densities, and flowability of the powders increased (P-values = 0.001), while the compressibility decreased ($P = 0.004$) due to the significant effect of storage time. Powders packaged under vacuum showed a higher mean of L- color value ($P = 0.003$), but significantly lower means of (a- and b-) color values, (p-values = 0.005, and 0.001 respectively) due to the significant effect of vacuum pressure. This change in color values was more dramatic in high fat containing powders such as whole milk powder. No significant change was observed in solubility of the powders. The results suggest that the proposed vacuum packaging method may be beneficial to maintain the quality of the powders studied.

Key words: vacuum packaging, dairy powders, solubility

M92 Hydrophobic aroma encapsulation in whey protein nanoparticles. H. J. Giroux and M. Britten*, *Food Research and Development Centre, Agriculture and Agri-Food Canada, St-Hyacinthe, (QC), Canada.*

The development of foods with health benefits prompts the manufacturers to review products formulation and processing conditions. The modification of food components or processing can impact directly on flavor release and perception. Moreover, aroma compounds are volatile, sensitive and might be degraded during manufacturing, storage or digestion. Encapsulation technologies have been proposed to entrap, protect and deliver sensitive or bioactive components and improve the sensory properties of functional foods. Because the interest in reducing capsule size to further reduce the impact of encapsulated ingredients on food texture, protein nanoparticles present a good potential to serve as carriers and delivery systems. The objective of this study was to encapsulate hydrophobic aroma in whey protein nanoparticles. Aroma-loaded nanoparticles ($d < 300$ nm) were prepared by cross-linking denatured whey protein through pH-cycling. The effect of nanoparticulation conditions (aggregation pH, calcium addition) and aroma concentration on the physicochemical characteristics of nanoparticles and the dynamic release profile of aroma was studied. The release behavior of aroma encapsulated in nanoparticles was compared with those of aroma added to native or denatured whey protein. Better retention of aroma was observed for nanoparticles produced at pH 5.0 and 5.5 without calcium addition. These nanoparticles are characterized by a less compact and more porous internal structure allowing a higher loading of aroma. Increasing aroma concentration increased the diameter and the voluminosity of the aroma-loaded nanoparticles. The percentage of aroma retention showed an increase from 7 to 24% over the tested concentration range while the value averaged 2% for native or denatured whey protein. Encapsulation of ethyl hexanoate in whey protein nanoparticles reduced the mass transfer of aroma at the surface of the matrix and improved its retention.

Key words: encapsulation, whey protein, aroma

M93 Formation of β-lactoglobulin/alginate nanoemulsion containing coenzyme Q10. H. N. Choi*, M. R. Lee, and W. J. Lee, *Division of Applied and Life Science (Institute of Agriculture & Life Science), Jinju-si, South Korea.*

The bioavailability of poorly water soluble nutrients, such as coenzyme Q10 (Co Q10), can be enhanced by the use of nanoemulsion system. It is hypothesized that exposed hydrophobic residues of β-lactoglobulin (β-lg) from heat treatment and additional protection from the complex formation of β-lg/alginate may affect physicochemical properties of nanoemulsion as a Co Q10 delivery system. The objectives of this study were to produce oil-in-water β-lactoglobulin/alginate nanoemulsion loaded with Co Q10 (β-lg/AL NE) and to investigate how processing variables, such as heating temperature and alginate concentration, affect the physicochemical properties and encapsulation efficiency of β-lg/AL NE. β-lg/AL NE was prepared at different heating temperatures from 60 to 70°C. Alginate concentration was varied from 0 to 0.05%. Morphologies of β-lg/AL NE were observed using a transmission electron microscopy. Size and zeta-potential values of β-lg/AL NE were measured by electrophoretic light scattering spectrophotometer. High performance liquid chromatography was used to assay encapsulation efficiency of Co Q10. The spherical shapes of β-lg/AL NE with the size of 150 to 250 nm were successfully formed. There was an increase in size from 160 to 240 nm and encapsulation efficiency from 70 to 80% with increasing heating temperature from 60 to 70°C. A significant ($P < 0.05$) increase in zeta-potential value from −5 to −13 mV was observed with increasing heating temperature from 60 to 70°C. Increasing alginate concentration from 0 to 0.05% resulted in a significant ($P < 0.01$) increase in encapsulation efficiency from 70 to 80%. In Split plot design, both heating temperature and alginate concentration had a significant ($P < 0.05$) effect on encapsulation efficiency of Co Q10. In conclusion, heating temperatures and alginate concentrations, which were β-lg/AL NE manufacturing variables,

were the key-processing factors to affect size, zeta-potential value, and encapsulation efficiency of β-lg/AL NE.

Key words: β-lactoglobulin, nanoemulsion, coenzyme Q10

M94 Homogenization and lipase addition influence methyl ketone generation. M. Cao*, E. L. Anderson, and S. A. Rankin, *University of Wisconsin-Madison, Madison.*

Specific methyl ketones contribute to the characteristic flavor of blue cheese. Various metabolic and enzymatic pathways contribute to the generation of these methyl ketones including the β-oxidation of fatty acids by the mold *Penicillium roqueforti*. Little recent research has explored means by which methyl ketone production can be altered or controlled. Earlier work and current industry practices have implicated milk or cream homogenization and exogenous lipase addition as means to alter methyl ketone production. Thus, the objective of this work was to determine the effects of milk homogenization and lipase addition on methyl ketone production in milks inoculated with *P. roqueforti*. Milks were homogenized pressures (e.g., 3.5 MP/3.5 MP, 10.5 MP/3.5MP). Homogenized milks were randomly treated with one of 3 lipases (porcine pancreatic, *P. roqueforti* and calf), inoculated with *P. roqueforti* spores and allowed to incubate (24 h, 20°C). Changes in milkfat size and milkfat globule surface areas were determined by laser scattering. Fatty acid and methyl ketone concentrations were determined using GC/MS. In general, average milkfat globule size decreased from 3.5 to 0.37 μm and surface areas increased from 1.8 to 25 m2/g. Concentrations of FFAs varied dramatically as a function of lipase treatment. Even-chain fatty acids from C4 to C10 increased as a function of homogenization treatment with approximately 10- and 2-fold increases in fatty acid concentrations for the calf and *P. roqueforti* lipase treatments, respectively. FFA levels from the porcine lipase treatment were not consistently affected by homogenization, yet had high levels of FFA. There was an interaction between pressure and lipase treatment that affected the concentrations of specific methyl ketones. In general, the *P. roqueforti* lipase treatment resulted in the highest levels of methyl ketone generation. Ketone concentration did not correlate well to particle size, milkfat globule surface area or initial level of free fatty acid. This study demonstrates that lipase treatment and homogenization alter accumulation of methyl ketones as affected by the metabolic activity of *P. roqueforti*.

Key words: blue cheese, methyl ketone, lipase

M95 Use of fluorescence spectroscopy for monitoring vitamin D fortification of skim milk. J. K. Amamcharla* and L. E. Metzger, *Midwest Dairy Foods Research Center, Dairy Science Department, South Dakota State University, Brookings.*

It is well recognized that a sufficient level of vitamin (vit.) D is necessary in the human diet. Most animals and plants have the ability to synthesize vit. D when exposed to sunlight. However, various factors can reduce the cutaneous synthesis of vit. D and products can be fortified with vit. D. In this regard, retail milks in the United States are fortified with 400 IU/quart of vit. D. In a recent release of the Dietary Guidelines for Americans 2010, USDA and Department of Health and Human Services recommended 600 IU/day of vit. D for children and most adults. As per the regulations of the FDA, milk fortified with vit. D is required to be at least equal to the declared value on the label with no regulations on the upper limit. In a recent study, 51% of 120 retail milk samples contained either below 400 IU/quart or above 501 IU/quart of vit. D. The lack of control of vit. D fortification of milk may be due to the fact that the current methods for vit. D analysis are laborious and precision of the method is dependent on the experience of the analyst. The objective of the present work was to develop a rapid method for measurement of vit. D in skim milk using front face fluorescence spectroscopy. For this purpose, comingled raw whole milk was fat separated, pasteurized and stored under refrigerated conditions. Sixty-six skim milk samples with various concentrations of vit. D (0, 200, 400, 600, 800, and 1000 IU/quart) were prepared using water dispersible vit. D and A mixture. Fluorescence spectra of vit. D (excitation: 360nm; emission: 400 to 600nm) were collected on each sample at 37°C using a front-face accessory. The spectra were normalized, mean-centered, and partial least square regression (PLSR) and neural network (NN) models were developed. Coefficient of determination (r^2), root mean square error of cross validation (RMSECV, IU/quart), and relative standard error of prediction (RSEP, %) were 0.98, 41.8, and 0.9, respectively, for PLSR and 0.97, 54.0, and 1.2, respectively, for NN model. The results indicate that the proposed method can be used as an effective tool to monitor vit. D fortification of skim milk.

Key words: vitamin D, skim milk fortification, fluorescence spectroscopy

M96 Milk composition evaluation as screening criteria to investigate fraudulent addition of cheese whey to milk. M. M. Falcão, F. A. P. Paula, M. O. Leite*, C. F. A. M. Penna, L. M. Fonseca, M. M. O. P. Cerqueira, and M. R. Souza, *Universidade Federal de Minas Gerais.*

Fraudulent addition of cheese whey to milk is a detected practice in several countries around the world. Low cheese whey costs and high costs for fraud detection, together with other aspects are factors that result in this problem for the dairy sector. The method worldwide accepted for detection of cheese whey addition to the milk is the caseinomacropeptide (CMP) index determination by HPLC. However, it is a high cost method for routine screening. To evaluate the milk composition as a principal components analysis for screening of fraudulent addition of cheese whey to milk, 30 individual raw milk samples were pooled to 6 samples containing milk from 5 animals. Each of the 6 samples was split and cheese whey was added to a final concentration of 0%, 5%, 10%, 20%, and 40% (vol/vol) of whey in the milk. Milk composition was evaluated by infrared (Bentley CombiSystem 2300), and obtained data evaluated by ANOVA with average composition by Student Newman Keuls (SNK) test. Average composition for the normal samples was 4.04 g/100g, 4.11g/100g, 4.38g/100g, and 13.56g/100g for, respectively, fat, protein, lactose and total solids. For the samples added with 40% (vol./vol.) cheese whey average composition was 2.48 g/100g, 2.36 g/100g, 4.73 g/100g, and 10.74 g/100g for, respectively, fat, protein, lactose and total solids. The results were statistically different among different treatments, and in practice this method can be used as screening tool with a logistic regression treatment of data in the results database.

Key words: cheese whey, milk quality, milk fraud

M97 Measuring milk treatments and storage temperature effects on fat globules aggregation. N. Fucà[1], G. Impoco[1], M. Caccamo*[1], and G. Licitra[1,2], *[1]CoRFiLaC, Regione Siciliana, Ragusa, Italy, [2]DISPA, Catania University, Catania, Italy.*

Milk treatments and storage temperatures cause changes to the microstructure of the lipidic phase. This study aims to demonstrate that confocal microscopy (CLSM) and quantitative analysis of resulting

images can give useful clues to estimate fat globules' aggregation. Two experiments were carried out. First, 5 types of milk subject to different treatments (homogenization-UHT, homogenization-high pasteurization, homogenization-pasteurization, pasteurization, microfiltration) and one sample of raw milk (used as control) were compared, to evaluate the effects of treatments on the lipidic phase. Then, the same milk types were analyzed at 2 different storage temperatures (4 and 16°C). Milk samples were stained with Nile Red to visualize lipids. Images were acquired using 60x objective lens and 1.5 zoom factor of a confocal laser scanning microscope. Image analysis was used to quantify fat globules aggregation in CLSM micrographs. Aggregation favors non-homogeneity both of distribution and volume of fat clusters. These 2 effects can be measured more reliably than aggregation itself. Eleven measures were computed on each image to capture variation in size and distribution of fat globules. After pairwise correlation assessment, 6 out of these 11 measures were chosen for their statistical independence and significance, and for their realistic description of the geometry of the lipidic phase. As expected, treatments did affect distribution and size of clusters. High significant difference ($P < 0.0001$) was found among the measurements related to the 5 types of milk. Statistical analysis revealed that storage temperature significantly affected distribution and size ($P < 0.0001$) as well, promoting aggregation. Quantitative analysis of CLSM micrographs turned out to be capable of capturing fundamental effects of fat globules' aggregation due to milk treatments and storage temperature.

Key words: milk, microstructure, quantitative analysis

M98 Effects of residual lactose and galactose on cheese moisture determination. H. Lee*, F. X. Milani, and S. A. Rankin, *University of Wisconsin-Madison, Madison.*

Accurate measurement of moisture in cheese is important to maximize yield and ensure economic parity. Official methods determine moisture based on the mass lost due to the thermal volatilization of available water. Because cheese is a chemically complex and variable medium, there is a potential that additional volatile compounds may be created during analytical moisture determination. Maillard browning and other various thermally catalyzed reactions may alter the final mass after drying. Based on their reactivity, the residual sugars lactose and galactose are 2 components in cheese that may be natively present at varying levels and that may participate in reactions capable of artificially elevating moisture determination. The objective of this study was to examine the effects of residual lactose and galactose on cheese moisture determination. In this study, 4 medium cheddar and 4 mozzarella cheese samples were analyzed for moisture content in triplicate using a microwave system (CEM Corporations, Matthews, NC). Cheese samples were manufactured with 5% added α-lactose monohydrate or galactose as the reducing sugar treatments. For reasons of control and comparison, an untreated sample and treatments containing 5% added sucrose or natrium carboxylmethyl cellulose (non-reducing carbohydrates) were included. There was an effect ($\alpha < 0.05$) for the main treatments of cheese type and sugar type. In general, the lactose and galactose samples had higher moisture levels than the non-reducing treatments. Compared with the untreated controls, the reducing treatments overestimated the moisture content by approximately 1.4% for the cheddar samples and 2.4% for the mozzarella samples. The samples with reducing sugars also displayed substantial dark brown color after the drying process as compared with minimal color change for other samples. There was no difference between the lactose and galactose treatments. This study demonstrates that the presence of residual reducing sugars may result an overestimation of cheese moisture concentration and that these effects may be different for cheeses of varying composition.

Key words: cheese, moisture, sugar

M99 Quantification of textural properties of composite milk gels using laser-scanning fluorescence confocal microscopy and image texture analysis. R. Hennessy*[1], L. Laiho[1], A. Laubscher[2], and R. Jimenez-Flores[2], *[1]Cal Poly Biomedical Engineering, San Luis Obispo, [2]Cal Poly, DPTC, San Luis Obispo.*

Current techniques of food texture analysis require destruction of the sample, ignore the spatial relationship between principal constituents, or require subjective data that depends on the skill of human subjects. A 2-dimensional, non-destructive, objective measurement technique is needed to quantify the spatial relationship between the principal constituents of dairy products. Our purpose was to investigate whether textural properties can be measured using laser-scanning fluorescence confocal microscopy (LSFCM) by quantifying the spatial relationship between the principal constituents of dairy products. In this study, 2 different types of composite milk gels were created, and stabilized by either freeze drying or baking. The milk gels were stained with the fluorescent markers; Nile red, for lipids, and fast green FCF, for protein. LSFCM was used to image the stained composite milk gels. For each sample, a stack of 30 images, each 5μm apart, were captured to create a 3-dimension set of data. Maximum intensity projection (MIP) was then performed on the stack of images to create a single image where the entire field of view contains pixels that are in focus. Using the MIP image, the following parameters were calculated: 1) fat/protein ratio (FP), 2) fat and protein overlap (OL), and 3) the image texture (T). All three parameters were calculated using an algorithm written in MATLAB. FP was calculated by counting the number of pixels labeled as fat and divides that number by the number of pixels labeled as protein, OL was calculated by counting the number of pixels labeled as both fat and protein and dividing that number by the total number of pixels in the image, and T was calculated using the gray level co-occurrence matrix of the image. OL was found to be the best parameter for distinguishing between baked and freeze dried gels, with $OL = 0.67 \pm 0.12$ for baked gels, and $OL = 0.23 \pm 0.09$ for freeze dried gels. A high OL was found to indicate a chewy texture, while a low OL was found to indicate a more brittle texture that commonly occurs from freeze drying.

Key words: texture, confocal microscopy, composite gels

M100 Evaluation of two kits based on microbial inhibition for detection of antimicrobial residues in milk. A. D. Lage, L. P. Freire, N. M. A. Silva, M. M. P. Araújo, R. D. P. Santos, G. M. Resende, A. F. Cunha, M. R. Souza, C. F. A. M. Penna, L. M. Fonseca, M. O. Leite, and M. M. O. P. Cerqueira*, *Universidade Federal de Minas Gerais, Belo Horizonte, Minas Gerais, Brazil.*

Two kits based on microbial inhibition (Charm Cow Side II Test and Charm Blue Yellow II Test) were evaluated for detection of antimicrobial residues in milk in different concentrations. The ability of both kits to detect the tetracycline group in a lower concentration of that considered by the Brazilian law was also tested. Milk samples were inoculated with standard solutions of 23 different antimicrobial agents and metabolites of ceftiofur in 2 different concentrations: the lower limit of detection stated by the manufacturer (level 1) and the maximum residue limit (MRL) (level 2) established by the Brazilian legislation. The results were submitted to the McNemar test at 95% of confidence.

Both kits were effective in detecting most of antimicrobials tested in 2 concentrations. It is necessary to review information from the manufacturer of the kit Charm Cow Side II Test for the detection of residues of oxacillin, penicillin G, spiramycin, and sulfonamides and Charm Blue Yellow II Test for the detection of erythromycin, cloxacillin, sulfadiazine, tylosin, and penicillin G in milk. Both kits detected residues of tetracyclines given the MRLs required by the Brazilian law and can be safely used for monitoring these drugs in milk. Ceftiofur and their metabolites were detected by the 2 kits and can be safely monitored by the methods tested.

Key words: milk, antimicrobials, residues

M101 Validation of CombiScope FTIR for milk urea evaluation in raw milk. M. C. P. P. Oliveira*, N. M. A. Silva, L. P. F. Bastos, R. S. Conrrado, L. M. Fonseca, M. M. O. P. Cerqueira, R. Rodrigues, and M. O. Leite, *Veterinary School/Universidade Federal de Minas Gerais, Belo Horizonte, Minas Gerais, Brazil*.

The measurement of milk urea nitrogen (MUN) concentration in raw milk is a useful tool for herd nutritional evaluation. The aim of this study was to validate the CombiScope FTIR (Advanced/Delta Instruments) for analysis of urea content in raw milk samples, based on non protein nitrogen calculated urea (NPN-CU). A total of 513 samples of bulk tank raw milk were screened in the Laboratory for Milk Quality Analysis (Veterinary School, Universidade Federal de Minas Gerais) for this study. Calculated urea results generated by Fourier Transform Infrared in the CombiScope FTIR were compared with urea concentration obtained from analysis of the same samples by enzymatic automated method (Chemspec 150 Analyzer; Bentley Instruments). The repeatability of CombiScope was tested using 20 pools of raw milk samples preserved with bronopol. Each pool was distributed in 10 vials and each vial was placed in a rack, to complete 10 racks containing 20 samples each. There was no significant difference ($P > 0.05$) between the results generated by both methods. The FTIR showed an average of 9.93 mg/dL of urea, while the average for the automated enzymatic method was 9.49 mg/dL of urea. The standard deviation and coefficient of variation were, respectively, 3.31 mg/dL and 33% for FTIR and 4.22 mg/dL and 44% for enzymatic methods. The result of repeatability of the FTIR analysis of urea showed an average of 10.22 mg/dL, standard deviation of 0.87 mg/dL, coefficient of variation of 8.42% and repeatability limit of 2.43 mg/dL. Therefore, FTIR is a reliable method to be used for urea analysis in raw milk, with the advantage of being a rapid, efficient, versatile and low cost method. Acknowledgments: FAPEMIG, CNPq, CAPES, Laboratório de Análise da Qualidade do Leite/EV-UFMG/FUNDEP.

Key words: milk, FTIR, urea

M102 Identification of starch in cheese using laser scanning confocal microscopy. W. R. McManus, E. N. Oberg, R. Wadhwani, K. M. Brown, and D. J. McMahon*, *Western Dairy Center, Utah State University, Logan.*

Polysaccharides such as starches and gums have been used to modify texture in dairy products. However, there has been little published on the microstructure of these additions to foods unless they are large microparticles because of the difficulty in identifying them in a complex matrix. Laser scanning confocal microscopy (LSCM), is able to optically dissect thin layers through a food sample and identify multiple components when they have an attached fluorophore. For example, in cheese, fat can be labeled with Nile red, a hydrophobic fluorophore, excited by light with wavelength of 488 nm, and protein can be labeled with several fluorophores, including Rhodamine B (RHODB) excited at 568. There has not been a method for readily attaching fluorophores to polysaccharides. To do so, we have developed a method for chemically modifying starch in a food gel (after fixing protein and fat), so that it can bind a fluorophore. Milk gels, Cheddar and Mozzarella cheese containing starches were fixed with osmium tetroxide, as vapor or as a 1.0% (aq) solution, then oxidized using 0.5%(aq) periodic acid, stained with 1% (aq) Acriflavin HCl (ACRFL), and 0.01% (aq) RHODB. The fluorophores were excited and their fluorescence collected separately (using filters of 512 to 532 nm and above 585 nm, respectively) to generate images in which there was strong imaging of the locations of both polysaccharide by ACRFL and protein by RHODB. Control images of samples containing no polysaccharides demonstrated there was no cross reactivity of ACRFL with the fixed protein. Fixation in LSCM is not commonly used, however, using periodic acid to produce reactive dialdehyde groups on starch that can bind ACRFL mandates fixation, so that the proteins are not degraded. This also physically traps the polysaccharides within the protein gel, assuring that in an LSCM image of a milk gel or cheese, the relationship of the polysaccharides to fats and proteins has not changed from their original position.

Key words: cheese, starch, microstructure

Extension Education

M103 Assessing a comprehensive udder health and mastitis control program for practicing dairy veterinarians. G. M. Schuenemann*, P. Rajala-Schultz, E. Gordon, S. Bas, and J. D. Workman, *Department of Veterinary Preventive Medicine, 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, information to dairy veterinarians. A comprehensive udder health and mastitis control program 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 program (~2.5 d and ~20 h of learning). Mammary gland and host defenses; epidemiology, treatment and preventive strategies for clinical and subclinical mastitis (i.e., chronic mastitic cows); dry cow therapy; environmental interactions (physical and biological); record-keeping (new infections, SCC, cure rate, and monitoring dry cow therapy); training to dairy personnel; facilities (bedding and ventilation); assessment of milking routines; and milking machine analysis (on-farm evaluation of equipment) were discussed. Educational materials were delivered through in-class lectures followed by case-based learning, group discussions, and an out-of-class assignment. Attendees were assessed using pre- and post-tests of knowledge to determine the level of knowledge gained in the program. Participants evaluated the program and provided feedback at the conclusion of the module. Veterinarians reported that the overall program, presentations and discussions were useful. Attendees found the presented information relevant for their work and of great immediate use to them. The presented materials and the implemented educational delivery methods substantially increased the knowledge level of the attendees (17.9% points increase from pre-test to post-test scores; $P < 0.05$). Interpreting culture and bulk tank results; milking machine assessment; treatment principles; dry cow management and selective dry cow therapy; managing new infections; and cleanliness of dry cow facilities were listed as learned concepts that participants can apply in their practices. Results suggested that the udder health module was relevant and effective; offering management practices with immediate field application.

Key words: education, mastitis, veterinary

M104 The relationships between weight, age, and average daily gain of Georgia 4-H & FFA commercial dairy heifers. M. L. London, J. K. Bernard, M. A. Froetschel, J. K. Bertrand, and W. M. Graves*, *University of Georgia, Athens.*

Studies were conducted to evaluate growth of dairy heifers involved in Georgia Extension youth programs where heifers are shown by weight. In the first study, 1,744 heifers were evaluated to determine effects of growth from Georgia 4-H & FFA Commercial Dairy Shows from 2007 to 2010. Birth weights were determined using breed averages (with crossbreeds being the average of the 2 parent breeds). Average daily gains (ADG) were calculated and ranked for age, weight and placing. Data were analyzed using the Spearman correlation calculations in SAS. Age and ADG were inversely correlated ($r = -0.89$, $P < 0.0001$). Mean ADG for all heifers was determined to be 0.65 kg, below NRC recommendations of 0.7–0.8 kg. No strong relationship ($r = -0.07005$, $P = 0.0034$) was observed between ADG and placing. Heavier heifers, within a class, showed a small positive ($r = 0.10399$, $P < 0.0001$) relationship with placing. In Study 2, a total of 238 Holstein heifers shown at the 2010 Georgia Junior National Livestock Show were evaluated for ADG, body weight, age, wither height, hip height, hip width, jaw width, placing and switch clearance from the ground. Height at withers had a moderate relationship ($r = 0.42$, $P < 0.0001$) with placing, followed by hip height ($r = 0.32$, $P < 0.0001$). A positive relationship ($r = 0.65$, $P < 0.0001$) was observed between wither and hip height. The correlation between weight and placing was determined ($r = 0.11$, $P = 0.10$). Age and ADG had a strong inverse relationship ($r = -0.87$, $P < 0.0001$). Switch clearance from ground positively ($r = 0.17$, $P < 0.01$) correlated with placing. Study 3 evaluated 1,489 Holstein heifers shown from 2007 to 2010. Data were analyzed using the Penn State Growth Spreadsheet. A total of 63.75% did not meet recommendations for body weight gain and indicates these heifers are under-fed. These animals will likely require more time before they enter the milking herd. The Commercial Dairy Heifer Program is vital for youth development in Georgia. However, management practices must be improved, growth monitored and weight requirements increased.

Key words: average daily gain, heifer growth, weight and size, Georgia Commercial Dairy Heifer Program

M105 Advising and technical support for the formulation and evaluation of diets for dairy cows and goats: The extension experience of Antonio Narro Agricultural University in north Mexico. P. A. Robles-Trillo*[1], F. G. Veliz-Deras[1], R. Rodriguez-Martinez[1], M. A. De Santiago-Miramontes[1], and C. A. Meza-Herrera[2], *[1]Universidad Autonoma Agraria Antonio Narro, Torreón, Coahuila, México, [2]Universidad Autónoma Chapingo, Unidad Regional Universitaria de Zonas Áridas, Bermejillo, Durango, Mexico.*

Production of food of animal origin for human consumption requires adequate animal feeding strategies. The aim of this extension project was to establish a link between the University and the productive sector by providing advice and technical support in the design and evaluation of rations for dairy cows and goats in local farms, while offering technical training to students involved as practitioners and social service providers. The technical support and training was completed by visiting these local farms and performing the following activities: a) formulation and evaluation of rations, b) management of feed and water intake, c) chemical analysis of ration ingredients d) storage and care of ration ingredients, e) evaluation of the physical, reproductive, and productive state of livestock, and f) determination of milk chemical characteristics. The project covered approximately 9,000 animals that produce approximately 250,000 L of milk daily, distributed in 9 dairy farms in the states of Coahuila and Durango (i.e., Comarca Lagunera). Fifteen students participated as social service providers, while 120 students performed as animal nutrition practitioners, generating a total of 200 technical visits. Regarding technical information generated from this project, 2 technical papers were published in a regional journal (Agropecuaria Laguna). The Comarca Lagunera is one of the most important dairy producing areas in Mexico. Therefore, linking both technical and academic activities through projects like this should help to increase the productive efficiency of dairy goats and cows in this region, thus increasing the economic profit of producers while rising milk availability for human consumption.

Key words: extension, feeding, ruminant

M106 An extension tool to assess forage production and utilization on dairy farms. M.-C. Coulombe*[1], D. Pellerin[1], R. Roy[2], G. Allard[1], P. Savoie[3], D. Parent[1], and E. Charbonneau[1], *[1]Université Laval, Quebec, Quebec, Canada, [2]Valacta, Dairy production centre of expertise, Ste-Anne-de-Bellevue, Quebec, Canada, [3]Agriculture and Agri-Food Canada, Soils and Crops Research and Development Centre, Quebec, Quebec, Canada.*

The optimal utilization of forages on dairy farms is an important factor for their profitability. However, tools to diagnose forage use on farms are rare. The present study aims to develop an evaluation tool to assess the production and utilization of forages on dairy farms. Parameters concerning the optimal usage of forages on dairy farms were identified as forage production (quality and yield), production cost, harvest efficiency and utilization by the herd. Evaluation criteria and methods were defined to measure these parameters and to develop the evaluation tool. This tool was tested on 21 Quebec dairy farms with different forage management. Forage quality was evaluated using a quality index that includes ingestibility, total digestible nutrients and digestible protein. A reference forage (53.8% NDF, 1.14 NEL, 16.3% CP) was given an index of 100. All forage samples (n = 147) had an index of 131 ± 16.7 (mean ± SD). Average annual forage yield per farm was 6.1 ± 1.8 TDM/ha (n = 18). When corrected for nutrient contents, yield was enhanced to 6.5 ± 1.9 eqTDM/ha. Production cost of forages is highly correlated (r = 0.85) to total machinery cost. Thus, to simplify on-farm data collection, forage production cost was estimated as a multiple of machinery cost. The estimated forage production cost was 210 ± 87 $/TDM (n = 17). To evaluate harvest efficiency, the daily capacity of machinery available was compared with the farm′s annual forage needs and the number of days available for harvesting during the optimal cutting periods. Most farm machinery sets (18/25 sets observed on 21 farms) were considered efficient, i.e., able to harvest required forage within the available time. Milk from forage (MF) averaged 2785 ± 1024 kg/cow per year (n = 17) while mean potential MF was 6939 ± 1692 kg/cow per year. Within a herd, efficient forage utilization would be reflected by a small difference between potential and observed MF. The diagnosis included an assessment of actual vs. predicted DM intake, and milk urea N and protein:fat ratio. Using our evaluation tool, producers can identify strengths and weaknesses, and correctly assess actions to improve performance.

Key words: dairy cow, forage, on-farm tool

M107 Fiber production and fiber characteristics of alpacas farmed in United States. T. Wuliji*, *Lincoln University, Jefferson City, MO.*

The alpaca is the most important fiber producing member of the South American camelids. This paper presents the recent analysis of both huacaya (n = 714) and suri (n = 502) alpacas sampled at 18 alpaca ranches located within the west, central and eastern regions in US There are 2 types of alpacas introduced into the United States, namely, huacaya and suri; however, most alpacas are that of the huacaya breed. Currently, there are 171,316 alpacas registered to the Alpaca Registry Inc. (ARI) from 1986 to 2010 in the US Alpacas can be found in every state of the United States and are farmed in various geographical environments ranging from hot desert to high mountain ranges. Alpacas were shorn at 10 to 18 mo of fiber growth intervals and produced 2 kg per head fleece per year. Coat color is widely varied in the alpacas, ranging from white to black and various shade combinations in 22 different natural color categories. Body weight, average fiber diameter, fiber diameter variation and fiber bulk characteristics were significantly ($P < 0.05$) different between huacaya and suri alpacas (Table). There was no difference in mean staple length (74.5 mm vs. 75.5 mm) but comfort factor estimate was significantly ($P < 0.01$) higher for huacayas (81.4%) over suris (77%). Although it appeared that suri alpacas were heavier for body weight and about 1.5 micron coarser than huacaya fleeces tested in this study, there was no evidence for any fiber production or fiber characteristic superiority in the one breed over the other except the preference of a breed specialty trait.

Table 1.

	Huacaya breed		Suri breed		SE
Traits	N	Mean	N	Mean	P-value
BWT kg	104	61.8	382	65.5	3.5*
AFD µ	713	24.9	471	26.5	1.5*
FDcv%	713	19.4	471	20.7	1.2*
Bulk cm3/g	421	20.5	449	16.5	1.0**

BWT: body weight; AFD: average fiber diameter (µ); FDcv%: fiber diameter variation; SE: standard error of mean.

Key words: alpaca, coat color, fiber diameter

M108 Advice from the experts: Processor assessment of planning considerations for an on-farm dairy processing enterprise. E. A. Chaney* and J. M. Bewley, *University of Kentucky, Lexington.*

Across the dairy industry, many producers are considering on-farm processing to add value to the milk produced on their farms. Like any other business venture, proper planning is imperative to establishing a successful business. The primary objective of this research was to survey existing processors to provide a compilation of advice for future on-farm processors. An electronic survey (Key Survey, Braintree, MA) was distributed to 120 on-farm processing businesses across the United States. A total of 31 surveys were completed (26%). Questions focused on cash flow, financing, sources of information used to start a business, and advice given to prospective business owners. The time needed to attain positive cash flow varied tremendously among survey respondents. Cheese (68%), milk (58%), and ice cream (33%) were the most common products manufactured on-farm. Funding needed to start the business was obtained from bank loans (68%), personal savings (58%), family loans or gifts (45%), and grants (35%). Factors influencing the decision to start the business venture included commodity milk prices (61%), desire to work with the public (42%), opportunity to promote the dairy industry (39%), desire to maintain or expand a family business (29%), and desire to differentiate a product (16%). When asked to describe the most difficult part of starting the business, the most frequently cited challenge was dealing with regulations (26%) followed by product marketing (19%), manufacturing technicalities (19%), and securing funding (16%). The most frequently used sources of information used in developing the business were existing processors (87%), books (65%), and the Internet (58%). The majority of respondents indicated they were either extremely satisfied (52%) or satisfied (44%) with their decision to start on-farm processing while 3% of respondents were neutral. When asked for advice to future processors, common themes included market research, business plans, seeking advice from existing processors, and thorough planning. Results of this research may be useful for entrepreneurs considering a value added dairy enterprise.

Key words: on-farm processing, survey, value-added

M109 Using whole farm assessment tools to identify strategies for change to increase dairy farm profitability. R. A. White*, L. A. Holden, A. Ishler, G. A. Varga, and M. B. Douglass, *The Pennsylvania State University, University Park.*

The objectives for this project were to use the Profitability Assessment Dairy Tool (PA Dairy Tool) and the Income Over Feed Cost (IOFC) Tool to 1) identify bottlenecks that limited dairy farm profitability on Pennsylvania dairy farms and 2) to show dairy producers how to make improvements to both overall profitability and IOFC. The PA Dairy Tool calculates key financial ratios, capital efficiency, operational efficiency as well as economic losses in 5 areas of dairy production management that directly impact profitability: milk yield (MY) and components, reproduction, milk quality and udder health, culling, and replacements. Farms were invited to participate in the project by farm advisors and 38 farms completed both tools in year one. The PA Dairy Tool data utilized year-end numbers for 2009. Herd size averaged 184 with a range 31 to 1,582 cows; average milk production was 29 kg per cow per day (15–41); return on assets averaged −0.7% with a range of −10.2 to 8.7%. The PA Dairy Tool showed the greatest economic losses were due to milk yield ($296 per cow per year) but the majority of farms had economic losses with replacements (age at first calving; 31 of 38 farms), udder health (somatic cell linear score >4.0; 29 of 38 farms), and reproduction (pregnancy rate; 25 of 38 farms). From January through October 2010, IOFC ranged from $3.08 to $10.61 per lactating cow per day. Quarterly reports are sent to participants throughout the project that include summarization of data and educational materials. In year 2 of the project, monthly IOFC will be continuously collected and year-end numbers will be collected for the PA Dairy Tool. Follow up work will be completed on farms that have economic losses in production areas that will enable the producer to focus on specific management improvements to decrease these economic losses. Effective use of evaluation assessments like the PA Dairy Tool and IOFC Tool are effective strategies in helping producers to target the most economically beneficial areas for changes to improve their bottom line.

Key words: benchmarking, feed costs, profitability

M110 Evaluation of the use of pasture pork demonstration sites for on-farm educational programming. N. C. Whitley* and M. L. Eley, *North Carolina A&T State University, Greensboro.*

Farms with pasture-based swine production systems were identified and developed as demonstration sites for selected best management practices that are environmentally and animal welfare friendly. The objective of this project was to evaluate the use of those demonstration sites for educational farm tours. Two eastern region farms were toured in Year 1, 3 in Year 2. Topics discussed included nutrient management and animal feeding, riparian buffers, ground cover and soil testing among others. Farmers discussed their farm and production practices. A multiple question survey was developed and provided to participants after each tour. The second year, a follow-up survey was used to determine first year tour impact. There were 19 surveys distributed and 11 returned (58% response rate) for Year 1; 82% raised hogs outdoors. The producers (100%) indicated they would make changes on their farm based on things they learned during the tour. After the tour, 91% agreed they had a better understanding of environmental issues/planning related to raising hogs on pasture; 100% had a better understanding of (and 91% would apply for) USDA/State programs and/or other grant or certification programs. For Year 2, approximately 30 surveys were distributed and 24 were returned (80% response rate), however, at least half of the respondents were NRCS staff and other agricultural professionals attending to learn more so they could, in turn, train farmers. Participants agreed they learned more about: water sources and location (96%), buffers to filter nutrient run-off (96%), crops to remove nutrients (92%), managing woodlots containing hogs (87%), pasture rotating and stocking rates (80%) and soil testing (76%). Only 60% indicated they would make changes on their farm. Of participants responding to the first year follow-up survey, 71.4% had made changes to create a more environmentally– and animal–friendly farm. The types of changes made included planting more forages and rotating animals, adding new pastures and shelters, giving pigs more space and moving pigs away from streams. Due to the success of these tours, more are being planned.

Key words: environment, outdoor pork, pasture based swine

M111 Summary of Texas Panhandle dairy producer forage use. K. J. Lager* and E. R. Jordan, *Texas AgriLife Extension Service, Texas A&M System, College Station.*

To calculate the mix of forages used on Texas Panhandle dairies, dairy producers in the region from Select Milk Producers, a milk marketing cooperative, were sent a one page questionnaire regarding the forages raised and purchased to feed the dairy cows and heifers in their herd. Surveys from 14 milking herds were returned. Two herds had heifer operations associated with them that raised heifers for other individuals. One heifer operation had separate feed inventories. In the second operation, heifers from 6 to 12 mo were fed from the combined feed inventory. Heifer roughage consumption in this operation was estimated and removed from the remaining calculations. Weighted estimates were calculated after these adjustments. The mean (±SD) of animals was 7643 ± 2961 with total owned ha ranging from 0 to 2274 ha and an average (±SD) of 857 ± 632 ha. Herds averaged 86.4% of the cows in milk; comparable to industry standards. No adjustment for the bulls/steers in herds was made since many herds use bulls in various reproductive roles. Total forage dry matter per milking cow was 19.3 kg/d (16.7 kg/d if total cows) and includes the dry land small grains produced and forages from outside the area. Total irrigated ha within Texas averaged 0.37 ha per milking cow or 0.32 ha per cow (milking and dry). Approximately 10% of total ha or roughly 39% of double cropped ha required per cow was irrigated using water captured in retention control structures. Table 1 displays the weighted average number of ha of forages raised by the producer or purchased locally needed to feed either one milking cow or one adult cow with the associated young stock and bulls/steers in Texas Panhandle herds for one year.

Table 1. Hectare per milking cow or per total cows required to raise forages being fed (CS = corn silage; SS = sorghum silage; SGS = small grain silage)

	Mean	SE	Per Milking Cow and Replacement	Per Total Cows and Replacement
Irrigated Raised Forages, ha				
CS	468	105	0.13	0.11
SS	143	40	0.04	0.03
SGS	402	69	0.11	0.09
Alfalfa	145	50	0.04	0.03
Of the Raised Forage Land, ha				
Double Cropped Owned	373	90	0.09	0.08
Double Cropped, RCS Water	158	47	0.04	0.03
Irrigated Purchased Forage from Panhandle, ha				
CS	172	78	0.04	0.03
SS	16	16	0.004	0.003
SGS	28	15	0.01	0.01

Key words: dairy management, forages, land use

M112 An overview of compost bedded pack management in Kentucky. R. A. Black*, J. L. Taraba, G. B. Day, F. A. Damasceno, and J. M. Bewley, *University of Kentucky, Lexington, KY, United States.*

Compost bedded pack (CBP) barn design and pack maintenance procedures vary considerably, making advising and problem-solving challenging. The objectives of this research were to characterize herd performance and management practices employed by CBP managers in Kentucky (45 farms and 54 CBP facilities). Mean (±SD) producer-reported bulk tank SCC and daily milk yield per cow were 238,162.2 ± 81,702.5 cells per mL (n = 37) and 27.3 ± 4.8 kg, respectively (n = 46). The TTEST procedure of SAS (Cary, NC) was used to compare herd performance metrics for the year before and year after transitioning to a CBP for farms using DHIA (n = 9). No significant differences ($P > 0.10$) were observed for changes in SCC (325,222.2 ± 197,188.9 to 274,888.9 ± 135,102.2 cells per mL), rolling herd average milk yield (9,476 ± 601.7 kg to 9,363.1 ± 586.4 kg), heat detection rates (21.6 ± 20.7% to 24.3 ± 23.1%), or culling rates (32.2 ± 8.9% to 28.6 ± 5.7%). Kiln-dried sawdust was used by 25 producers (53.2%) with green sawdust used by 15 producers (31.9%) and 7 using a mix of green and kiln-dried sawdust (14.9%). Mean (±SD) time between additions of new bedding to the pack in summer was 15.3 ± 12.7 d and 11.7 ± 10.4 d in winter. With regard to pack stirring, 38 producers (80.8%) used a field cultivator while 6 used a rototiller (12.8%) and 3 alternated between using a cultivator and rototiller (6.4%). Mean (±SD) daily stirring frequency was 1.6 ± 0.5 d in summer and 1.7 ± 0.5 d in winter. The mean pack area was 9.5 ± 3.8 m^2 per cow. Mean (±SD) herd average locomotion and hygiene scores were 1.51 ± 0.30 (n = 35) and 2.20 ± 0.28 (n = 38), respectively. Most frequently cited benefits of CBP included cow comfort (n = 28), cow cleanliness (n = 15), and improved health and longevity (n = 14). Recommendations to other producers included securing an adequate bedding supply (n = 8), stirring twice daily (n = 8), and using kiln-dried shavings (n = 5). Criteria for adding new bedding included pack moisture (n = 30), compost sticking to cows (n = 12), and cow cleanliness (n = 7).

Key words: compost bedded pack barn, facilities

M113 Weighted cost of capital on dairy farms in Florida. K. Kaniyamattam*[1], A. De Vries[1], and D. T. Galligan[2], *[1]University of Florida, Gainesville, [2]University of Pennsylvania, Kennett Square.*

The objective of this study was to describe the weighted cost of capital (WACC) for dairy farms in Florida. Proper analysis of investment opportunities on dairy farms requires that the expected changes in cash flow need to be discounted by the cost of capital. The preferred discount rate is the WACC which is calculated as rd * (1 - tax rate) * D/(E + D) + DER * E/(E + D) where rd is debt rate, D is debt/cow, E is equity/cow and DER is the desired equity rate. Hence the WACC is farm specific. Financial farm-year records from 2000 to 2008 (n = 80) were obtained from the Florida Georgia Dairy Business Analysis Project database. Equity rates were calculated from the relative differences of farm equity on January 1 of each year. Debt rates were calculated as interest expenses divided by average outstanding loan amounts. Tax rate was set at 33%. Average ± SD for assets/cow, debt/cow, and equity /cow were $5,008 ± 2,226, $1,389 ± 777, $3,620 ± 2,264 respectively. Average debt rate and equity rate were 6.3 ± 3.9% and 6.3 ± 8.6% respectively. The Pearson correlation coefficient between assets/cow and equity/cow was 0.94. The correlations between equity rate, and assets/cow and equity/cow were −0.29 and −0.29 respectively. Other correlations were not significant. At 5% DER, WACC was 4.7 ± 0.6% (range 3.0% to 6.3%) and at 10% DER, WACC was 8.2 ± 1.2% (range 5.3% to 10.7%). At 5% DER, the correlation between WACC and debt rate was 0.82. Other correlations were not significant. At 10% DER the correlation between WACC, and debt rate, assets/cow, debt/cow, equity/cow were 0.45, 0.29, −0.70, and 0.52 respectively. The regression analysis of WACC (5% DER) with year, assets/cow, debt/cow, milk sold/cow, average number of cows showed significant effects of year and average number of cows(R2 = 0. 37). At 10% DER, greater assets/cow and greater milk sold/cow were associated with greater WACC (R2 = 0.72). In conclusion, WACC for dairy farms in Florida for DER varying from 5% and 10% ranged from 3.0% and 10.7% and were on average similar to textbook cost of capital of 5% to 10% per year.

Key words: interest, investment, profit

M114 Current situation and further training needs: A case of Master Goat Producers. U. Karki*[1], N. K. Gurung[1], O. Bolden-Tiller[1], and L. B. Karki[2], *[1]Tuskegee University, Tuskegee, AL, [2]PadmaDal Memorial Foundation, Auburn, AL.*

Master goat producer's certification training program (MGPCTP) is being conducted by Tuskegee University annually to train goat producers, basically from Alabama and neighboring states. Finding out whether trainees have improved their enterprises after the training, and if they still have problems and training needs is important to improve the existing training program and/or organize further training. Objectives of this study were 1) to evaluate the current situation of goat farms belonging to master goat producers, 2) to assess the impact of master goat producer's certification training program, and 3) to identify further training needs of master goat producers. A set of structured questionnaire was developed and all master goat producers were requested to fill it. Also, goat farms of all producers who agreed to participate in this study were inspected. Almost all producers were rais-

ing meat goats, and more than 70 percent producers had Boer goats. The most common marketing was to sell directly to the consumers followed by bringing to stockyards. Average herd size was 24, and average pasture and woodland acreage were around 10 and 11 respectively. Almost all farms were pasture-based and supplementing with hay and concentrate was a common practice when forage production was low. Seventy-three percent of the producers were found to provide mineral mix regularly. Majority of the producers mentioned that they improved different aspects of their farms after attending MGPCTP: 85 percent improved farm structures and pastures, 70 percent improved health care, and 67 percent improved record keeping. More than 70 percent of the producers expressed that parasite was the major problem. Most of the producers stated that they need more training on various aspects of goat enterprises, such as marketing, parasite and disease control, record keeping, and pasture management. Results indicate that 1) majority of the producers are small-scale, pasture-based, meat-goat producers, 2) these producers improved their farm and production practices after attending MGPCTP, and 3) there are still many problems producers are facing, and they need further training to solve these problems.

Key words: Alabama, Boer, meat goats

M115 Judging Pro: A dynamic software program for scoring judging contests. M. L. Eastridge*, B. Cobanov, A. Moffett, L. A. Winkelman, and A. E. Radunz, *The Ohio State University, Columbus.*

Judging contests continue to be valuable educational programs for teaching youth about selection of high merit animals, animal product quality, and life skills, especially in communication and working together as a team. Scoring of these contests can be quite laborious and a limited number of computer programs are available and those available are not very dynamic in presentation of the results. In addition, other computer programs will typically score only one type of contest. Judging Pro was developed for scoring judging contests with dairy cattle, livestock, equine, and poultry. The contest setup allows the user to define placing classes, questions for classes, and classes with reasons. Optional events in the contest setup include written questions, keep/cull, grading, retail cuts, specified stations, team problems, and linear evaluation. After the contest setup is completed, the animal and breed divisions are then defined and the proper placing and assigned cuts entered. Age category and designations of open, FFA, or 4-H are provided for each team and individual entered. Contestant placings and special event scores are entered, along with any specified event team scores. The program calculates placing scores based on the entered official placing and cuts. Reports can be designed by the user to provide the results of interest. Scores can be tallied by age division, youth membership category, and animal division (e.g., breed). Total scores can be summed for individuals and teams. Individuals and scores can be sorted in ascending or descending order. Results can either be printed or copied into a spreadsheet. Additional information about the program and ordering details are available at http://barnyardsoft.com.

Key words: computer software, judging contests, youth education

Forages and Pastures: Antinutritive Compounds in Forages

M116 Fermentation and microbial protein synthesis from anthocyanidin accumulating Lc-alfalfa in rumen liquid. A. Jonker[1,2], M. Y. Gruber[2], Y. Wang[3], D. A. Christensen[1], J. J. McKinnon[1], and P. Yu*[1], *[1]Department of Animal and Poultry Science, University of Saskatchewan, Saskatoon, Saskatchewan, Canada, [2]Saskatoon Research Station, Agriculture and Agri-Food Canada, Saskatoon, Saskatchewan, Canada, [3]Lethbridge Research Station, Agriculture and Agri-Food Canada, Lethbridge, Alberta, Canada.*

It is well documented that mono/polymeric anthocyanidin have the capacity to regulate ruminal fermentation and degradation characteristics of feed. Therefore, alfalfa was modified with a maize leaf color (Lc) gene to synthesize these metabolites. Three of these modified Lc-alfalfa progeny (BeavLc1, RambLc3, RangLc4) that expressed a purple-green phenotype were harvested at a vegetative pre-bud stage to determine fermentation and microbial protein synthesis. Ground freeze-dried samples were compared for their ruminal fermentation characteristics in rumen liquid with 15N as marker for microbial N using an in vitro gas production system. The 3 Lc-progeny had a similar anthocyanidin concentration with an average of 232 μg/g DM. Gas production rate was faster for RamLc3 ($P < 0.001$) than the other 2 Lc-progeny and faster for RangLc4 than BeavLc1. Methane production rate tended to be faster for RambLc3 ($P = 0.07$) compared with the other 2 Lc-progeny but total methane production was similar. Ammonia accumulation was faster ($P = 0.04$) but total ammonia accumulation and branch chain fatty concentration were lower ($P < 0.001$) for BeavLc1 compared with the other 2 Lc-progeny. Total volatile fatty acid accumulation was higher for RangLc4 ($P = 0.001$), propionate was higher and acetate lower for RambLc3 ($P < 0.001$) and butyrate was lower and acetate higher for BeavLc1 ($P < 0.001$). Microbial protein synthesis was higher for BeavLc1 ($P < 0.001$) compared with the other 2 Lc-progeny. In conclusion, all 3 Lc-alfalfa progeny accumulated anthocyanidin and fermentation profiles and end products differed between the 3 progeny.

Key words: anthocyanidin-accumulating alfalfa, in vitro ruminal fermentation and microbial-N, methane and ammonia

M117 How tannin deactivation can affect nutrient digestibility and metabolizable energy contents of sainfoin (*Onobrychis viciifolia*). H. Khalilvandi-Behroozyar*[1,2], M. Dehghan-Banadaky[1], and K. Rezayazdi[1], *[1]Department of Animal Science, University of Tehran, Karaj, Tehran, Iran, [2]Department of Animal Science, University of Urmia, Urmia, West Azerbaijan, Iran.*

Nutritive value of forages for ruminants is inherently variable and depends on many factors such as forage species, climate, degree of maturity, anti nutritional factors, etc. The objective of this study was to examine tannin deactivation effects on energy and nutrient availability from sainfoin. Second cut forage was shade dried and chopped (3 –5 cm length), and then exposed to nothing (Control) or 5% (w/v) solution of polyethylene glycol (PEG 6000 MW) that was sprayed on the forage (v/w ratio of 1:1). Water soaking was applied with tap water (v/w ratio of 4:1). Treatments were carried out at an ambient temperature of 25°C for 20 min with hand shaking for water, and overnight for PEG. Water was added to forage just before feeding in an in vivo trial. The extractable CT content was determined (Butanol–HCl reagent). Ruminally fistulated Holstein cows (3 multiparous, 680±20kg of BW) were used in 3×3 change over design. Each period consisted of 10 days for adaptation and 7 days for total fecal and forage sample collection. Forages were fed as sole diet (0800 and 1600) along with mineral/vitamins to meet 110% of maintenance requirements of dairy cows. Digestibility coefficients determined and ME estimated with ME= 0.0157 × DOMD. MIXED PROC of SAS 9.1 was used for statistical analysis at 0.05 probability level. Water and PEG deactivated 92.06 and 98.57% of CT, respectively. Digestibility coefficients of EE and ADF were not statistically different ($p \leq 0.05$). Differences of means for OM, NDF and CP digestibility and ME among treatments were statistically significant. Digestibility of NDF was 512.5^{b} for control and 610.1^{a} and 613.4^{a} g/kgDM for water and PEG groups respectively. Digestibility coefficients for CP were 649.8 ^{b}, 753.9 ^{a} and 770.4 ^{a} and for OM were 592.3 ^{c}, 731.4 ^{a} and 709.9 ^{b} g/kgDM for control, water and PEG groups respectively. ME content increased from 8.69 ^{c} to 10.72 ^{a} and 10.22 ^{b} for water and PEG treated forages. Tannin deactivation might be responsible for increasing ME.

Key words: sainfoin, polyethylene glycol, metabolizable energy

M118 Effects of sainfoin (*Onobrychis viciifolia*) processing for tannin deactivation on nitrogen content of cell wall and available nitrogen. H. Khalilvandi-Behroozyar*[1,2], K. Rezayazdi[1], and M. Dehghan-Banadaki[1], *[1]Department of Animal Science, University of Tehran, Karaj, Tehran, Iran, [2]Department of Animal Science, University of Urmia, Urmia, West Azerbaijan, Iran.*

The objective of this study was to examine the effectiveness of tannin deactivation on potential nitrogen availability of sainfoin. DM was determined by drying at 105°C overnight. Extractable condensed tannin content of second cut sainfoin was determined using the butanol-HCl reagent. Forages were chopped, and then exposed to nothing (Control) or 5%(w/v) solution of polyethylene glycol (PEG 6000 MW) that was sprayed on the forage (v/w ratio of 1:1). Soaking with water was applied using tap water (v/w ratio of 4:1). Treatments were carried out at an ambient temperature of 25°C for 20 min with hand shaking for water, and overnight for PEG. Treated forages (3 replicates) were then exposed to 40°C temperature in a forced air oven, for 48 h. Neutral detergent fiber and ADF analyzed using Fibertech system. Sodium sulfite not included in NDS solution. Nitrogen content of entire feed and ADF and NDF residues were measured by the Kjeldahl method. Crude protein was calculated as N×6.25 and available nitrogen was considered TN-ADIN. Comparison of means was done using GLM procedure of SAS 9.1(SAS, 2002). CRD and Duncan's multiple range test was conducted to comparison of means between treatments were used ($p \leq 0.05$). Condensed tannin content declined from 21.3^{a} (control) to 1.7 ^{b} and 0.3 ^{c} g/kg DM respectively for water and PEG treated forages. On the other hand total nitrogen content (g/kgDM) was increased for treated forages due to DM losses of 19.4^{c} to 20.7^{a} and 19.9^{b} for water and PEG treatments, respectively. Acid detergent insoluble nitrogen decreased from 6^{a} (unprocessed forage) to 2.1^{b} and 2.2^{b} g/kgDM for water and PEG treatments, respectively. Also, NDIN decreased from 6.3^{a} in untreated forage to 5.7^{b} and 5.1^{c} g/kgDM for water and PEG treatments, respectively and this contributed to increased available nitrogen content (38.8 and 32.1%). Efficient deactivation of tannins can is likely responsible for the results.

Key words: sainfoin, available nitrogen, tannin

M119 Effects of tannin deactivation with different chemicals on protein fractions of sainfoin (*Onobrychis viciifolia* Scop.) in Cor-

nell Net Carbohydrate and Protein System (CNCPS). H. Khalilvandi-Behroozyar*[1,2], M. Dehghan-Banadaky[1], and K. Rezayazdi[1], *[1]Department of Animal Science, University of Tehran, Karaj, Tehran, Iran, [2]Department of Animal Science, University of Urmia, Urmia, West Azerbaijan, Iran.*

Sainfoin (*Onobrychis viciifolia* Scop.) is tanniferous legume forage. Reports about sainfoin crude protein and condensed tannin contents have a wide range from 102 to 285 and 25.2 to 100 (g/kg of DM), respectively. Cornell Net Carbohydrate and Protein System (CNCPS) is a growing feed evaluation and ration balancing system in the world and create data about feed protein fractions is essential for accurate ration balancing for dairy cattle to improve cattle performance and reduction of environmental pollution due to nitrogen excretion from dairy industry. To our knowledge this is the first report on CNCPS protein fractions of sainfoin and effects of tannin deactivation on this measure. Sainfoin hay was treated with different chemicals to deactivate tannin. Treatment procedure and data about phenolic compounds content after treatment were presented in a companion abstract (M124). The CNCPS protein fractions of sainfoin, determined according to standardized procedure where the A fraction (non-protein N including ammonia, peptides and amino acids and considered to be completely soluble) was determined using trichloroacetic acid solution. Neutral detergent insoluble nitrogen and ADIN were determined as N content of residuals after neutral and acid detergent procedures, respectively. The B_2 fraction was calculated by difference, and results are presented as percentage of CP. All chemical analysis and forage treatments were done in triplicate. Data were analyzed by SAS 9.1, using GLM procedure for a completely randomized design ($P \leq 0.05$). Total phenolics, total tannins and condensed tannins content of sainfoin were 39.4 ± 0.6, 38.5 ± 1 and 21.3 ± 0.4 g/kg of DM respectively. Crude protein content was 121.3 ± 1.7g/kg of DM. Results (Table 1) showed that in untreated forage a large portion of crude protein was in the C fraction, which is unavailable the for animal. This can be due to condensed tannin- protein complexes. Tannin deactivation treatments improved nutritional availability of protein by decreasing the C fraction and increasing the A and B3 fractions.

Table 1. Effects of tannin deactivation on CNCPS protein fractions of sainfoin. (CP percentage)

	A	B_1	B_2	B_3	C
Control	16.8 ^{c}	9.7 ^{b}	28.6 ^{c}	13.9 ^{d}	30.9 ^{a}
Water	34.2 ^{ab}	1.3 ^{e}	37.2 ^{b}	17.1 ^{b}	10.2 ^{d}
Urea	17.1 ^{c}	13.4 ^{a}	40.9 ^{d}	7.5 ^{c}	21.1 ^{b}
$KMnO_4$	30.1 ^{b}	9.7 ^{b}	27.7 ^{c}	17.3 ^{b}	15.2 ^{c}
PEG	16.6 ^{c}	6.7 ^{c}	52.4 ^{a}	13.6 ^{d}	10.6 ^{d}
Wood ash	36.4 ^{a}	1.3 ^{e}	34.1 ^{bc}	16.6 ^{b}	11.6 ^{d}
NaoH	11.1 ^{d}	7.5 ^{c}	36.5 ^{b}	24.1 ^{a}	20.9 ^{b}
$NaHCo_3$	35.5 ^{a}	4.4 ^{d}	28.1 ^{c}	16.8 ^{bc}	15.2 ^{c}
S.E.M	1.53	0.45	3.11	0.95	1.05

$^{a–e}$Means within each column with different superscript letters are statistically different ($P \leq 0.05$).

Key words: sainfoin, condensed tannin, CNCPS

M120 Effects of chemical treatments for tannin deactivation on in situ organic matter degradability of sainfoin (*Onobrychis vicifolia*). H. Khalilvandi-Behroozyar*[1,2], K. Rezayazdi[1], and M. Dehghan-Banadaky[1], *[1]Department of Animal Science, University of Tehran, Karaj, Tehran, Iran, [2]Department of Animal Science, University of Urmia, Urmia, West Azerbaijan, Iran.*

Sainfoin is a temperate legume forage, with medium to high concentrations of condensed tannins (CT). The objective of present study was to examine the effectiveness of tannin deactivation on ruminal organic matter (OM) degradability of sainfoin. Forages (second cut) were chopped and treated without (control) or with solutions of NaOH (0.05 *M*) and wood ash (180g/l) with forage to solution ratio of 1:4. Also, 5% solution of PEG (6000 MW) was sprayed on the forages (1:1 w/v). The pH of solutions were determined (12.28 and 12.13 for NaOH and wood ash, respectively). condensed tannin contents were determined using butanol-HCl reagent. Organic matter degradability was determined using three ruminally fistulated Holstein cows, fed balanced rations with forage:concentrate ratio of 60:40. samples were ground to pass 2 mm screen and 5 g was weighed into nylon bags with 50 micron pore size (sample size:surface area was 12.5 mg/cm^2). Duplicates were incubated for 4,8,12,24,48,72 and 96 in the ventral rumen. Effective degradability (ED) was calculated with NEWAY computer package. Complete randomized block design (animals as block), GLM PROC of SAS 9.1 and Duncan's Test were used for data analysis ($P \leq 0.05$). The CT concentration of the control forage was 21.3+0.4 g/kg dry matter. PEG caused a marked increase in the soluble fraction, but not in the "b" fraction. NaoH slightly increased the "a" fraction but wood ash decreased it compared with control. Only wood ash increased the rate of degradation of the "b" fraction, although this was not statistically significant. Effective degradability (K=0.05) were 54.83^{b} + 1.91, 54.33^{b} + 3.40, 50.30^{c} + 0.56 and 62.70^{a} +0.61 for control, NaoH, wood ash and PEG treatments, respectively.

Key words: sainfoin, organic matter, tannin

M121 Chemical compositions and anti-nutritive factors of *Acacia mangium*. T. Clavero* and R. Razz, *Centro de Transferencia de Tecnologia en Pastos y Forrajes, Universidad del Zulia, Maracaibo, Estado Zulia, Venezuela.*

A field experiment was carried out under tropical dry forest conditions in northwest Venezuela to determine the chemical compositions and anti-nutritive factors of *Acacia mangium*. The study included 3 defoliation frequencies (6, 9, 12 weeks). Treatments were replicated 3 times in a randomized block design. Measurements included total nitrogen (TN), in vitro dry matter digestibility (IVDMD), non-structural carbohydrates (TNC), Ca, Mg, P and anti-nutritional compounds (condensed tannins-CT-, saponins-S-, phenols, alkaloids-ALK-, steroids-ST-). Data were subjected to ANOVA, using general linear models procedures of SAS statistical package. Treatments means were contrasted using Tukey test. Several chemical changes of *A. mangium* were noted from 6 to 12 weeks of growth. At each interval TN content declined significantly ($P < 0.05$). The highest value of IVDMD (56.4% ± 2.1) was obtained on 6 weeks of growth and declined on 12.9 digestible units from 6 to 12 weeks. TNC did not differ ($P > 0.05$) among treatments. Concentrations of Ca, Mg, P were affected significantly ($P < 0.05$) by maturity. Mineral concentrations decrease due to translocation from leaves to stems with increasing maturity. The highest concentrations of CT, phenols and ALK (0.48, 2.91 and 0.80%) respectively, were observed at 6 weeks of growth and significantly affected ($P < 0.05$) by the stage of growth. In contrast, S and ST were not affected by stage of growth. Young leaves had higher content of secondary metabolites than older leaves. Because the levels of CT and phenols were under 4% in all treatments, no adverse effects in ruminants would be expected. The chemical compositions and anti-nutri-

tional values of *Acacia mangium* indicate that this specie has potential as feed source in tropical ruminant diets.

Key words: *Acacia mangium*, chemical compositions, anti-nutritional factors

M122 Nutrient composition, polyphenolic compound content, in situ degradation and in vitro rumen fermentation characteristics of leaves from three mulberry species. H. J. Yang* and W. X. Wang, *State Key Laboratory of Animal Nutrition, College of Animal Science and Technology, China Agricultural University, Beijing, China.*

Mulberry leaves of 14 cultivars of *M. atropurpurea* Roxb. (MAR), 7 cultivars of *M. alba* Linn (MAL) and 8 cultivars of *M. multicaulis* Perr (MMP) were harvested in May and June in Guangzhou city of China and assessed for differences in nutritive value and potential for use as an alternative forage by chemical analysis, in situ ruminal degradation and in vitro batch culture. CP (N × 6.25), NDF, ADF and ether extract (EE) in the leaves ranged from 243 to 262, 260–289, 162–177 and 32–42 g/kg DM, respectively. Means and standard errors (s.e) for CP, NDF, ADF and EE in mulberry leaves were 253 ± 4.5, 275 ± 7.1, 169 ± 3.5 and 37 ± 2.5, respectively. No differences were found for CP or NDF. EE content was ranked: MMP > MAL > MAR ($P < 0.05$), with the highest mean (60 g/kg DM) of cultivar Tongxiangqing in MMP. Total phenol, total tannin and condensed tannin contents were lower than those reported for other tree leaves in literature and did not differ among mulberry species. In situ degradation rate (c) of either DM or CP in 3 cannulated lactating dairy cows, fitted to an exponential curve of the type: $Y = a + b \times (1- e^{-c \times time})$, was similar for mulberry species. However, differences were found in the effective degradation of DM (0.48 in MAR, 0.45 in MAL and 0.41 in MMP with a pooled s.e of 0.008; $P < 0.01$), CP (0.40 in MAR, 0.40 in MAL and 0.36 in MMP with a pooled s.e. of 0.012; $P = 0.05$) and in vitro DM disappearance ($P < 0.01$), and all of these parameters consistently were ranked: MAR > MAL > MMP. In vitro cumulative gas production (also fitted to the same exponential curve), ammonia N, volatile fatty acid characteristics showed no differences among mulberry species. Total phenolic and tannin content were positively correlated with the degradation rate of DM and CP ($P < 0.05$). MAR had the lowest total tannin content and was more degradable in the rumen than MAL and MMP. In general, mulberry leaves had a higher protein and lower fiber content. Consequently, mulberry leaves could be an acceptable and highly digestible rumen-by-pass protein feed supplement for use by ruminant animals on the occasions when silkworm production is not always profitable.

Key words: mulberry leaves, in situ degradation, cumulative gas production

M123 Fluoride content of leaves and stems of alfalfa hay at different stages of maturity. C. Arzola*[1], M. R. Murphy[2], J. Salinas[3], R. Copado[1], A. Corral[1], O. Ruiz[1], C. Rodriguez[1], E. Santellano[1], and H. Gaytan[1], *[1]Universidad Autonoma de Chihuahua, Chihuahua, Chihuahua, Mexico, [2]University of Illinois, Urbana-Champaign, [3]Universidad Autonoma de Tamaulipas, Cd. Victoria, Tamaulipas, Mexico.*

Fluoride (F) accumulation by forages can be of great significance for cattle nutritionists because high-contents of this element can cause dental and osseus lesions on cattle. Besides ingestion of fluoride by drinking water, alfalfa which is a very common forage for dairy cattle can be a source of fluoride. Because there is some concern about the F content of water in some areas of the central part of the state of Chihuahua in Mexico, it is believed that crops can accumulate F. To investigate the pattern and amount of fluoride deposition of 2 varieties of alfalfa ('Cuff-101' and 'Excellent multileaf') harvested on 2 seasons (summer and fall), F content was analyzed in leaves and stems of hay harvested 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. The overall mean content of fluoride in the alfalfa hay (94.24 ppm as fed basis) was in general high as compared with typical fluoride concentration reported in tables. When comparing F values in hay samples of the whole plant, no differences ($P > 0.05$) were detected between varieties, season, or stage of maturity. In leaves there was a greater ($P < 0.05$) concentration of F in Cuff-101 variety (104.53 ± 9.97 ppm) than in Excellent multileaf (82.99 ± 10.28). In stems, Cut-101 also had a greater ($P < 0.05$) of F as compared with Excellent multileaf (97.66 ± 9.76 and 86.75 ± 9.60, respectively). A general conclusion was that F content was high regardless of the stage of maturity and harvesting season of hay. A more detailed study should be conducted to determine the levels of F in ingesta to provide information regarding the F status of cattle consuming alfalfa hay.

Key words: fluoride, alfalfa, *Medicago sativa*

M124 Distribution of antiherbivory compounds in *Flourensia cernua*. R. E. Estell*, E. L. Fredrickson, D. K. James, and D. M. Anderson, *USDA-ARS, Jornada Experimental Range, Las Cruces, NM.*

Flourensia cernua is used as a shrub model to study the influence of terpenes on intake by livestock at the Jornada. Two studies (20 plants per study) were conducted using a completely randomized design to examine within plant distribution of volatile compounds to improve sampling protocol. Leaves from 3 positions (outer canopy, subcanopy, and basal) were collected from 4 quadrants (northeast, southeast, northwest, southwest) in Exp. 1. Leaves were removed from 2 leaders of current year's growth for each position in each quadrant. In Exp. 2, 10 leaders of current year's growth were collected from the outer canopy in each quadrant and 3 leaf age categories were formed by separating leaders into thirds and removing leaves. Terpenes were extracted from 5 leaves in duplicate with ethanol and analyzed with gas chromatography/mass spectrometry. Data were log-transformed and analyzed by univariate ANOVA and means separated using Tukey's honestly significant difference. Ninety-three compounds (including 15 unknowns) were present on the leaf surface of *F. cernua*. Only 7 compounds in Exp. 1 and 9 in Exp. 2 differed ($P < 0.05$) among quadrants, and no consistent effect of quadrant was observed in either study. In Exp. 1, 31 compounds differed ($P < 0.05$) among leaf positions, but outer canopy and subcanopy leaves did not differ for any compound. Basal leaves contained greater concentrations than outer canopy and subcanopy leaves for 10 compounds, and less than the other 2 positions for 10 compounds. Thirty-two compounds differed for leaf age in Exp. 2, with immature leaves containing greater concentrations than mature leaves for 30 compounds and greater than the middle age category for 26 compounds ($P < 0.05$). Total concentration (cumulative concentration of all compounds) did not differ among leaf positions but differed for leaf age (greater in immature than mature leaves; $P <$

0.05). Terpenes that differed in Exp. 1 were represented about equally by mono- and sesquiterpenes, whereas compounds affected by leaf age were predominantly sesquiterpenes (3 of 32 were monoterpenes). Both leaf position and age affect terpene concentrations and sampling variability in this shrub.

Key words: terpenes, chemical distribution, leaf age

M125 Degradation kinetics of calcium caseinate incubated in vitro with increasing levels of tannin extract from *Acacia mearnsii* with or without polyethylene glycol addition. D. Zeni*, A. C. Fluck, G. V. Kozloski, A. A. Martins, F. Zanferari, and S. Stefanello, *Universidade Federal de Santa Maria, Santa Maria, RS, Brazil.*

The effects of tannin extract from *Acacia mearnsii* and polyethylene glycol (PEG) on in vitro gas production from calcium caseinate was evaluated in a study with a 3 × 2 factorial treatment arrangement. Approximately 1 g of calcium caseinate was incubated in triplicate for 48 h with 100 mL of buffered-ruminal fluid in 160 mL glass jars. Treatments were 0 (no tannin) or 20, 40 or 60 g tannin extract/kg of calcium caseinate with presence (+PEG) or absence (-PEG) of 2 g of PEG. Inoculum was obtained from a rumen fistulated steer receiving ad libitum fresh ryegrass (*Lolium multiflorum*). Pressure in the jars, which was converted into gas volume, was measured at 2, 3, 4, 5, 6, 9, 12, 18, 24, 36, and 48 h after incubation. Gas production data were fitted to an exponential unicompartmental model to estimate degradation kinetic parameters. ANOVA analysis was performed and when the treatment effect was significant ($P < 0.05$), linear and quadratic effects were tested by regression analysis. Gas volume increased at increased levels of tannin with addition of PEG ($P = 0.040$) and was not affected without PEG addition (Table 1). Degradation) rate linearly decreased at increasing levels of tannin addition without PEG ($P = 0.047$), but remained constant when PEG was added. Lag time was not affected by tannins without addition of PEG whereas it decreased linearly (P= 0.078) when PEG was added to the incubation media. In conclusion, the tannin extract did not negatively affect calcium caseinate fermentation in vitro.

Table 1.

Tannin	Gas volume (mL)		Degradation rate (%/h)		Lag time (h)	
(g/kg DM)	-PEG	+PEG	-PEG	+PEG	-PEG	+PEG
0	80.7*	57.0	2.83	3.71*	10.3	9.80
20	80.7*	63.0	3.87	3.75	6.73	12.5*
40	92.7*	75.3	2.59	3.90*	8.0	8.10
60	95.7*	63.7	2.82	3.12*	5.26	10.2*
SD	9.34	8.30	0.52	0.25	2.61	2.27
P-value[1]	0.040	0.186	0.486	0.047	0.078	0.650

[1]Linear tannin effect. *Effect of PEG by ANOVA ($P \leq 0.05$).

Key words: tannins, PEG, rumen degradable protein

M126 Degradation kinetics of cellulose incubated in vitro with increasing levels of tannin extract from *Acacia mearnsii* with or without polyethylene glycol addition. D. Zeni*, A. C. Fluck, G. V. Kozloski, A. A. Martins, F. Zanferari, and T. R. Longo, *Universidade Federal de Santa Maria, Santa Maria, RS, Brazil.*

The effects of tannin extract from *Acacia mearnsii* and polyethylene glycol (PEG) on in vitro gas production from cellulose was evaluated in a study with a 3 × 2 factorial treatment arrangement. Approximately 1 g of crystalline cellulose (AVICEL) was incubated in triplicate for 48 h with 100 mL of buffered-ruminal fluid in 160 mL glass jars. Treatments were 0 (no tannin) or 20, 40 or 60 g tannin extract/kg of cellulose DM in the presence (+PEG) or absence (-PEG) of 2 g of PEG. Inoculum was obtained from a rumen fistulated steer fed ad libitum fresh ryegrass (*Lolium multiflorum*). Pressure in the jars, which was converted into gas volume, was measured at 2, 3, 4, 5, 6, 9, 12, 18, 24, 36, and 48 h after incubation. Gas production data was fitted to an exponential unicompartmental model to estimate degradation kinetics parameters. ANOVA analysis was performed and when the treatment effect was significant ($P < 0.05$), linear and quadratic effects were tested by regression analysis. Gas volume was not affected by tannin extract with or without PEG addition (Table 1). However, PEG increased gas volume ($P < 0.05$) independently of tannin level. Gas production rate linearly decreased at increased levels of tannin extract, independently of PEG addition ($P < 0.05$). Lag time, in turn, increased linearly with tannin levels without PEG ($P < 0.05$) whereas it was not affected by tannins when PEG was added to the incubation media. Tannin extract negatively affected cellulose fermentation in vitro. However, this effect was not clearly overcome by PEG inclusion. This implies that the contribution of PEG alone to gas production should be accounted for when it is used as a tannin inhibitor in in vitro assays.

Table 1. Degradation kinetics from cellulose incubated in vitro with 20, 40, or 60 g/kg DM of tannin extract with or without PEG

Tannin	Gas volume (mL)		Degradation rate (%/h)		Lag time (h)	
(g/kg DM)	-PEG	+PEG	-PEG	+PEG	-PEG	+ PEG
0	221	229.3*	3.86*	3.54	5.97	5.45
20	225*	205.3	3.74*	3.49	5.43	6.76*
40	219*	210.6	3.32	4.01*	6.16*	5.31
60	222*	212.3	3.71*	3.65	5.2	5.6
SD	7.93	10.3	0.25	0.34	0.54	0.38
P-value[1]	0.821	0.332	0.036	0.024	0.849	0.016

[1]Linear tannin effect. *Effect of PEG by ANOVA ($P \leq 0.05$).

Key words: tannin, PEG, in vitro

M127 Nutrient and tannin contents of purple prairie clover (*Petalostemon purpureum*) harvested at different growth stages. L. Jin*[1,2], Z. Xu[1], A. D. Iwaasa[3], Y. G. Zhang[2], M. P. Schellenberg[3], T. A. McAllister[1], and Y. Wang[1], *[1]Agriculture and Agri-Food Canada, Lethbridge Reserach Centre, Lethbridge, AB, Canada, [2]Department of Animal Science, Northeast Agricultural University, China, [3]SPARC-AAFC, Swift Current, SK, Canada.*

The native legume purple prairie clover (PPC; *Petalostemon purpureum*) is well adapted to the prairie region of Canada and is considered an important palatable component of prairie hay. However, there is no information available on its nutritive value for ruminants. Whole plants of PPC were harvested from 5 regions of native pastures at Swift Current, SK, Canada at vegetative (VEG) and full-flowering/early seeding (FL) stages (4 samples for each maturity stage in each region). Proportions of leaf, stem and flower were determined. Whole plants were analyzed for organic matter (OM), N, neutral detergent fiber (NDF) and acid detergent fiber (ADF). Leaf, stem, flower and whole plant were also analyzed for total phenolics, total tannins and condensed tannin (CT). Plant had higher ($P < 0.001$) proportion of leaf, but lower ($P < 0.001$) proportion of flower at VEG than at FL stage. Contents of OM, NDF, ADF and their associated N were higher ($P < 0.01$), but

N content was lower (21.4 vs. 26.7 g/kg DM; $P < 0.01$) for FL than for VEG stage. Condensed tannin was detected in all tissues (i.e. leaf, stem and flower) of the plant; with flower containing the highest (198-213 g/kg DM) and stem containing the lowest (17-18 g/kg DM) levels. Contents of total phenolics, total tannins and total CT in leaf were all higher ($P < 0.01$) at the VEG than at the FL stage, whereas they were present at similar concentrations in stem and flowers at both growth stages. Whole plant harvested at the VEG contained lower (59 vs. 94 g/kg DM; $P < 0.001$) level of CT than that harvested at the FL stage, due to the increased proportion of flower at the FL stage. Overall, PPC is characterized by its high level of N content and a unique array of bioactive compounds and therefore may have considerable potential as a high-quality forage for beef cattle. Its yield and persistence need to be further evaluated.

Key words: purple prairie clover, nutrient, tannins

M128 Evaluation of tannins in indigenous forage plants of the Brazilian semi-arid. M. L. Chizzotti*[1,2], F. R. B. Oliveira[2], R. T. S. Rodrigues[2], K. C. Busato[2], T. S. Silva[2], J. A. Siqueira[2], and F. H. M. Chizzotti[1], *[1]Universidade Federal de Lavras, Lavras, MG, Brazil, [2]Universidade Federal do Vale do São Francisco, Petrolina, PE, Brazil.*

This experiment was conducted to evaluate the presence of tannins in indigenous plants of the Brazilian semiarid region Caatinga. Samples of seedling and adult leaves of fourteen species were used: *Albizia inundata*, *Amburana cearensis*, *Anadenanthera colubrina*, *Caesalpinia ferrea*, *Erythrina velutina*, *Handroanthus impetiginosus*, *Handroanthus spongiosus*, *Hymenaea martiana*, *Myracrodruon urundeuva*, *Pseudobombax marginatum*, *Spondias tuberose*, *Syagrus coronata*, *Tabebuia aurea* and *Ziziphus joazeiro*. The condensed tannin complexing agent, Polyethylene glycol (PEG), was used to evaluate the presence of tannins by semi- automated in vitro gas production and in vitro digestibility after 96 h. Five replicates were dried at 55° C and ground (1 mm) and 100 mg of samples were incubated with or without 200 mg of PEG. The fermentation kinetic parameters were fitted to the following exponential model: $Y = b \times (1 - e^{(-c \times (t - L))})$, where Y is the accumulated gas, mL/100g of incubated DM; b is the asymptote of gas production, mL/100g of incubated DM; c is the fractional rate of gas production, %/h ; t is the time, h; and L is the lag time, h, for t>L. The 95% confidence interval was used to compare coefficients. There was an effect of PEG ($P < 0.05$) on asymptote of gas production for the leaves of adult plants *A. colubrina*, *H. martiana*, and *M. urundeuva*, indicating the presence of tannins in these species. For the rate of gas production, there was an effect of PEG ($P < 0.05$) for seedling leaves of *A. colubrina*, *H. martiana*, *M. urundeuva*, and *P. marginatum*. The DM digestibility after 96 h of incubation was higher ($P < 0.05$) in the presence of PEG for the adult and seedlings leaves of *A. colubrina* (56.5% vs. 39.4% and 74.2% vs. 61.0%, respectively), for seedling leaves of *M. urundeuva* (72.4% vs. 59.0%), and for adult leaves of *C. ferrea* (51.5% vs. 47.4%) and *H. martiana* (47.7% vs. 29.3%). The leaves of species *Albizia inundata*, *Amburana cearensis*, *Erythrina velutina*, *Handroanthus impetiginosus*, *Handroanthus spongiosus*, *Spondias tuberose*, *Syagrus coronata*, *Tabebuia aurea* and *Ziziphus joazeiro* did not present a significant content of tannins. Funded by FACEPE, CRAD and CNPq.

Key words: anti-nutritional factors, Caatinga, polyethylene glycol

M129 Effect of grazing toxic tall fescue prior to or immediately following insemination on beef cattle reproductive performance. M. G. Burns*[1], J. G. Andrae[1], S. L. Pratt[1], W. C. Bridges[1], and F. N. Schrick[2], *[1]Clemson University, Clemson, SC, [2]University of Tennessee, Knoxville.*

The impact of toxic tall fescue (F) on beef cattle reproductive performance has been sporadically addressed, and few studies examine the effect that exposure timing has on conception rates. The objective of this study was to determine if F affects cattle reproduction differently when cattle are exposed before or immediately following insemination, to assess effects during gamete development or in altered uterine environment, respectively. Two and 3 yr old beef cows (99 hd total) were blocked by breed, BCS and age and allotted to groups (n = 50) grazing F-(>92% wild-type infected) or alternate forages (O; common bermudagrass and annual ryegrass) for 210 d before timed insemination. On d −8 all cows were subjected to a standard 5-d CIDR estrous synchronization program and were artificially inseminated on d0. Immediately following insemination, 25 cows from each group were switched to the alternate grazing treatment for the remainder of the trial, consistent with a 2 × 2 factorial arrangement. This resulted in 4 total forage treatment combinations when grazed pre and post breeding: fescue-fescue (FF n = 25), fescue-other (FO n = 25), other-fescue (OF n = 24), and other-other (OO, n = 25). Cows were visually checked for estrus behavior from d0 to d10 after which bulls were placed with cows for 60d. Blood was collected on d-18 and d-8 for P4 analysis to assess cyclicity. Blood was also collected on d-8 and d10 for prolactin concentrations. Pregnancy was determined using ultrasonography at d 130 and verified with calving records. Data were analyzed using PROC GLM of SAS. Cattle grazing tall fescue on d-8 had lower ($P < 0.05$) serum prolactin levels than cattle grazing O. There was a F x O interaction ($P < 0.05$) for serum prolactin on d10. Prolactin concentrations of FF and OF did not differ and were lower ($P < 0.01$) than both OO and FO groups. Prolactin levels of FO were higher ($P < 0.05$) than OO at d10. Pre AI treatment had no effect ($P > 0.05$) on final pregnancy rate. Cattle grazing F post AI had lower ($P < 0.01$) final pregnancy rates compared with O.

Key words: fescue, beef cattle, reproduction

M130 Endophyte-infected tall fescue seed extract induces constriction of bovine vasculature. A. P. Foote*[1], D. L. Harmon[1], K. R. Brown[2], J. R. Strickland[2], K. R. McLeod[1], L. P. Bush[1], and J. L. Klotz[2], *[1]University of Kentucky, Lexington, [2]USDA-ARS, FAPRU, Lexington, KY.*

Ergovaline (ERV) has been extensively used to study vasoactive effects of endophyte (*Neotyphodium coenophialum*) infected tall fescue (*Lolium arundinaceum*). However preliminary in vitro tests show that an extract of toxic tall fescue seed (E+EXT) is more potent than ERV alone indicating other compounds contribute to vasoconstriction. Thus, experiments were conducted to determine if vasoactivity of an E+EXT is different than a mixture of ergot alkaloids (ALK) of equal concentration and to determine if an endophyte-free extract (E-EXT) is vasoactive. Segments of lateral saphenous vein and right ruminal artery and vein were collected from steers (n = 6) shortly after slaughter. Vessels were cleaned of excess connective tissue and fat and sliced into segments that were suspended in a multi-myograph chamber with 5 mL of continually oxygenated Krebs-Henseleit buffer, equilibrated for 90 min, and exposed to a reference compound, 120 m*M* KCl for ruminal vessels and 0.1 m*M* norepinephrine for saphenous vein. Increasing concentrations of each treatment (E+EXT,

E-EXT, ALK, and ERV) were added to the respective chamber every 15 min following buffer replacement. Data were normalized as a % of maximal contractile response of the reference compound and analyzed as a CRD. For saphenous vein, ALK and E+EXT induced similar responses ($P = 0.19$ for $10^{-6}M$; $P = 0.28$ for $10^{-7}M$) that were greater than $10^{-6}M$ ERV ($P < 0.01$ and $P = 0.09$ respectively) and $10^{-7}M$ ERV ($P < 0.01$ and $P < 0.01$ respectively). The potency of ALK and E+EXT was greater than ERV ($P < 0.01$) in saphenous vein. For ruminal artery, ALK and E+EXT induced similar responses ($P = 0.31$ for 10^{-6}; $P = 0.06$ for 10^{-7}) that were greater than ERV at $10^{-6}M$ ($P < 0.01$ and $P < 0.01$ respectively) and $10^{-7}M$ ($P = 0.04$ and $P < 0.01$ respectively). For ruminal vein, ALK and E+EXT induced similar responses ($P = 0.13$) but E+EXT did not differ from ERV ($P = 0.61$). The E-EXT did not induce a contractile response in any vessel tested ($P > 0.1$). Although low in concentration, non-ergovaline alkaloids in E+EXT contribute to the observed contractile response and should be considered when studying fescue toxicosis.

Key words: tall fescue, vasoconstriction

M131 Contractile response of bovine lateral saphenous vein to ergovaline, serotonin$_{2A}$, α_{2A}-, and α_{2C}-adrenergic receptor agonists relative to time off endophyte-infected tall fescue. J. L. Klotz[1], G. E. Aiken[1], A. P. Foote*[2], L. P. Bush[2], K. R. Brown[1], B. M. Goff[2], and J. R. Strickland[1], *[1]USDA-ARS-FAPRU, Lexington, KY, [2]University of Kentucky, Lexington.*

Previous research has demonstrated differences in contractile responses to ergot alkaloids, serotonin (5HT), and adrenergic agonists by lateral saphenous veins collected from cattle that grazed either endophyte (*Neotyphodium coenophialum*)-infected or endophyte-free tall fescue (*Lolium arundinaceum*), possibly influenced by an altered vascular biogenic amine receptor profile. To aid in understanding of how cattle recover after exposure to toxic tall fescue, lateral saphenous vein biopsies were conducted on 21 predominantly Angus steers (357 ± 3 kg) at 0 (n = 6), 7 (n = 6), 14 (n = 5), and 28 d (n = 4) after removal from grazing KY31 tall fescue pasture (3.0 ha) for 126 d. Off-pasture, animals were housed in a dry lot and fed a corn silage and soybean hull mixed diet. Biopsied segments of vein were sliced into 2–3 mm cross-sections and suspended in myograph chambers 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 (1×10^{-11} to $10^{-4}M$) of ergovaline (ERV), TCB2 ($5HT_{2A}$ agonist), guanfacine HCl (GF; α_{2A}-adrenergic agonist), and (R)-(+)-m-nitrobiphenyline oxalate (NBP; α_{2C}-adrenergic agonist). Data were normalized to a reference addition of $1 \times 10^{-4}M$ norepinephrine and analyzed as a CRD for main effects of days off pasture, agonist concentration, and d off pasture × concentration with steer as experimental unit using mixed models of SAS. Agonist concentration and day (d 7 and 14 were greater than d 0 and 28) were significant ($P < 0.01$), but days off pasture × concentration was not significant ($P > 0.1$) for all 4 compounds tested. Ergovaline and TCB2 had the greatest maximal responses and 2 adrenergic agonists elicited relatively smaller responses. Response to increasing concentrations GF was the least and varied most across days. The α_{2C} agonist NBP, was the more vasoactive adrenergic agonist. The effect of animal recovery during the 28-d off of tall fescue did not affect the relative response through changes in the biogenic amine receptor profile as evaluated pharmacologically in the bovine saphenous vein.

Key words: Bovine, ergovaline, tall fescue

M132 Differences in chemical composition of crown rust resistant and susceptible oat cultivars in Northern Mexico. H. Bernal-Barragán*[1,4], M. A. Cerrillo-Soto[2,4], A. S. Juárez-Reyes[2,4], F. G. Ríos-Rincón[3,4], E. Gutiérrez-Ornelas[1,4], M. Guerrero-Cervantes[2,4], N. C. Vásquez-Aguilar[1], and J. E. Treviño-Ramírez[1], *[1]Facultad de Agronomía UANL, Escobedo, N.L., México, [2]Facultad de Medicina Veterinaria y Zootecnia UJED, Durango, Dgo., México, [3]Facultad de Medicina Veterinaria y Zootecnia UAS, Culiacán, Sin., México, [4]Red Internacional de Nutrición y Alimentación en Rumiantes, México.*

Forage nutritive value of 2 groups of oat (*Avena sativa* L.) cultivars (about 120 days growing season) bred in Mexico were determined and related to their differences in the susceptibility to crown rust disease caused by *Puccinia coronata*. Three crown rust resistant oat cultivars (CRR= code cultivars L112, L124 and L164), released in 2007 from the Agronomy Department at the University of Nuevo Leon (UANL) in Mexico, and two commercial crown rust susceptible oat cultivars (CRS=Guelatao and Chihuahua), were sown in December 2007. No crown rust disease was present in any of the plots during this experiment. Three random whole plant samples were collected from small plots at 101, 110 and 117 days of growth. Samples were oven dried at 55° C, and ground to pass through 1-mm screen. dry matter, ash, CP, fat, NDF, ADF, and ADL, were determined and expressed on a DM basis and contents of cellulose, and hemicellulose were calculated. A 2 × 3 factorial arrangement with two groups of oat cultivars (resistant and susceptible), and three cutting stages (101, 110, and 117 days), was used in a complete randomized design, with three replicates per cultivar. There were no significant interactions between the main factors. Ash content was lower ($P < 0.05$) in CRS (12.1%) than in CRR (13.1%). Differences in CP ($P < 0.05$) were found between 101 (11.1%) and 117 days (8.5%). Fat content was similar ($P > 0.05$) between groups of oat cultivars; however fat content at 117 days (3.5%) was higher than at 101 and 110 days (2.9% in average). Crown rust resistant cultivars had higher ($P < 0.05$) NDF (56.6%) than CRS (54.6%). There were no differences ($P > 0.05$) in ADF (31.0%), hemicellulose (24.6%) and cellulose (26.4%) between CRR and CRS; however cellulose content at 101 days (27.7%) was higher ($P < 0.05$) than at 117 days (24.8%). There were small ($P = 0.051$) differences in lignin content between CRR (4.8%) and CRS (4.3%) oat cultivars, and between cutting at 101 (4.2%) and 117 days (4.9%). In conclusion, differences in ash, NDF and lignin contents were detected between crown rust resistant and susceptible oat varieties cultivated in northeastern Mexico.

Key words: *Avena sativa*, nutritive value, crown rust resistance

M133 Dry matter yield and chemical composition of twenty-eight alfalfa cultivars grown in Brazil. P. R. Meirelles*, C. Costa, M. A. Q. Vieira, M. A. Factori, and E. A. R. Santana, *College of Veterinary Medicine and Animal Science, UNESP, Botucatu, Sao Paulo, Brasil.*

An experiment was conducted at the forage sector of the College of Veterinary Medicine and Animal Science, Botucatu-SP, with the objective of evaluating 28 alfalfa cultivars in terms of dry-matter yield and crude protein (CP), neutral detergent fiber (NDF) and acid detergent fiber (ADF) contents. The cultivars were the Crioula, Monarca, BR 4, Alto Great, MH 4, SW 9210 A, P 5929, BR 1, El Grande, P 5715, MH 15, Valley Plus, BR 2, Rio, SW 8210, Maricopa, ICI 990, P 5888, P 30, Alfa-200, WL 516, SW 8112 A, BR 3, Florida 77, Araucana, Falcon, Semit 921 and Sutter. The soil chemical characteristics in the experimental area were: pH in water 4.3, Al=0.70 meq/100cm^3, Ca=12.0 mmolc.dm^3, Mg=10.0 mmolc.dm^3, K=0.9 mmolc.dm^3, P=4.0 mg/dm^3. Lime was applied at the rate of 6 t/ha, followed by pre- planting fertilization, which consisted of 600 kg superphosphate/ha, and 150 kg potassium chloride/ha. The seeds were planted in rows 30 cm apart at the rate of 15 kg/ha. A randomized block design with three replicates was used. The Monarca cultivar was the most productive and its dry matter yield differed ($P < 0.05$) from that of MH 15, Valley Plus and SW 8112. Crude protein content differed ($P < 0.05$) among cultivars, with the highest value in Valley Plus (22.39%) and the lowest in Semit 921 (18.8). NDF content did not differ ($P < 0.05$), but there were statistical differences for ADF; the highest value (36.01%) occurred in ICI 990 and the lowest (29.44%) in P 30, with no difference ($P < 0.05$) detected among others treatments. The most promising cultivars for the ecological characters of Botucatu-SP are the following: Monarca, because of its higher dry matter yield, followed by Rio, Sutter, Alto and Crioula, due to their low decrease in dry matter yield over three harvest years.

Key words: neutral detergent fiber, *Medicago sativa* L., acid detergent fiber

M134 Tillering pattern and dry matter production of Mombasa grass submitted to nitrogen fertilization during regrowth. A. F. Garcez Neto*[1,3], K. F. Gobbi[2,3], T. M. Dos Santos[1], E. E. B. Baldasso[1], and J. Da Silva[1], *[1]Federal University of Parana, Palotina, Parana, Brazil, [2]Agronomic Institute of Parana, Paranavai, Parana, Brazil, [3]Federal University of Vicosa, Vicosa, Minas Gerais, Brazil.*

Increase in forage growth rate can be related to different factors, such as energy supply for photosynthesis process and tillering potential. This work was carried out with the aim to study how a tropical forage with extensive growth potential (*Panicum maximum* Jacq. 'Mombaça') responds to different levels of nitrogen (N) fertilization during its regrowth, in terms of its tillering capacity and forage yield. The tillering capacity was measured by the number of tillers and tiller weight. Three levels of N were used (N0 = 0 mg/dm^3; N25 = 25 mg/dm^3 and N50 = 50 mg/dm^3) and six regrowth times (1, 2, 4, 8, 16 and 32 days after an initial staging or standardization cut). Nitrogen was provided weekly from 30 days before the standardization cut up to the last regrowth cut. The statistical analyses were performed using a randomized block design with a 3 × 6 factorial treatment arrangement, with 3 replicates. At each harvest the number of tillers per plant were counted and all the aboveground biomass was weighed (g DM/plot). A significant interaction ($P < 0.05$) between levels of N and the regrowth times was found for all variables studied. No effect was found for regrowth time to the number of tillers for N0. A lower number of tillers was found for N25 compared to N50 during all regrowth times (Y=64.8408+0.7771x, R^2=0.795; Y=67.4411+1.5982x, R^2=0.854, respectively for N25 and N50). In N0, the increase in tiller weight (g DM/tiller) occurred linearly during regrowth times, but at very low intensity (Y=0.2+0.175x, R^2=0.979) compared to N25 and N50. The tiller weight responded quadratically to N in N25 and N50 treatments (Y=0.2752+0.259x+0.0006x^2, R^2=0.996; Y=0.2946+0.0093x+0.0014x^2, R^2=0.997, respectively to N25 and N50). The aboveground biomass production also followed the same pattern found for tiller weight during regrowth times between N levels (Y=11.366+0.8546x, R^2=0.986; Y=17.993+1.7056x+0.0789x^2, R^2=0.995; Y=18.4238+1.1575x+0.1674x^2, R^2=0.999, respectively to N0, N25 and N50). The highest N fertilization can be supplied to the grass from 16 days after regrowth.

Key words: grass, partition, tiller

M135 Effects of growing conditions on alfalfa hay quality and production. A. Palmonari*, M. Fustini, G. Canestrari, and A. Formigoni, *Dipartimento Scienze Mediche Veterinarie, Universita degli Studi di Bologna, Bologna, Italy.*

Alfalfa hay is one of the most utilized forages in Italy. Its growth is ensured by environmental and climate conditions, which usually allow farmers to obtain 5 or sometimes more cuts per year. Numerous studies have shown that yield and quality of forages are affected by growth stage, forage species, cultivar, climate (e.g., rainfall, temperature), and growing condition. In alfalfa, growth conditions are probably the main factors responsible for changes in quality, due to the physiological modification of several tissues. This study focused on the quantification of these changes in fibrous and protein fractions and changes in fiber digestibility as a consequence of increased maturity. Within one field, 6 plots were designed and then paired in 3 treatments (A,B,C,A,B,C). Each treatment was harvested at 3 cutting intervals; trt A every 21 d (pre bloom), trt B every 28 d (first bloom) and trt C 35 d (full bloom) for 4 times each during 2008 spring and summer. Rainfall, temperature and yield were recorded for each cut and each pair of treatments during the trial. Fibrous and protein fractions, along with in vitro NDF digestibility at 24h were evaluated. Statistical analysis was performed among treatments using the ANOVA model with repeated measures of the software STATISTICA. CP, along with SolP and NPN, was significantly higher ($P < 0.01$) for trt A (20.8% DM) than trt B or C (17.3% DM and 17.0% DM respectively). Similar results were observed for ADL and in vitro NDF digestibility at 24 h (trt A = 44.0% DM, trt B = 37.8% DM, trt C = 34.1% DM respectively; $P < 0.01$). Increased maturity resulted in increased lignin deposition and loss of protein. This situation is reflected in fiber digestibility, which was compromised as maturity increased. Moreover, treatment A yielded similar amount of dry matter as treatment C (103.8 kg and 116.5 kg respectively), while the lower production was obtained from treatment B (96.2 kg). Together with analytical fractions, production results indicated that quantity of product is not always related to days of growth, which are typically correlated inversely with forage quality.

Key words: alfalfa, maturity, chemical composition

M136 Nutritional value and silage fermentation parameters of elder (*Sambucus nigra*) as a supplement for dairy cattle in the Colombian Tropics. L. Reyes, L. C. Bernal*, and A. Conde, *Universidad de La Salle, Bogotá, Colombia.*

The aim of this study was to determine the nutritional value and fermentation parameters of an ensiled mixture of elder with corn bran and potato by-products. Elder leaves were cut after 90 days of regrowth and 2 years of establishment. Eight treatments and four replicates per treatment were evaluated. The elder leaves were chopped and mixed with either corn bran or potato bran, at inclusion levels of 20, 40, 50 and 60% for the respective brans. These mixtures were stored in a microbag (1 kg capacity) for 42 days. At the end of the fermentation period, samples were taken for analysis of nutritional quality (dry matter DM, crude protein CP and Gross Energy GE) and fermentation parameters (pH, ammonia nitrogen and its relation with total nitrogen). The experimental design was a 2 × 4 factorial, (Factor a. corn bran vs. potato bran; factor b. 20, 40, 50 and 60% inclusion level of corn bran or potato bran). Data were analyzed using the GLM procedure of SAS. Inclusion of corn bran resulted increased ($P < 0.001$) dry matter DM (60.83 vs. 19.38%) and gross energy GE concentrations (4.4 vs. 3.9 Mcal/Kg) as compared to inclusion of potato bran. Inclusion of potato bran resulted in increased ($P < 0.001$) CP (16 vs. 12%) as compared to inclusion of corn bran. The ratio of ammonia nitrogen/total nitrogen was greater for the potato bran treatments (14.4 vs. 6.8%). There was no difference in pH ($P > 0.001$) but the critical value of pH and water activity required for stabilizing a silage were not achieved in the elder leaves with potato bran silage because the DM values were low (DM 19% and pH 4.47). In the elder leaves with corn bran, the DM values were high (DM 60% and pH 4.39) which indicates the silage was stabilized. The DM, CP and GE values increased ($P < 0.05$) with inclusion level of corn bran in the silage whereas those variables decreased ($P < 0.05$) with increasing inclusion level of potato bran. Finally, the results of fermentation and nutritional quality showed that use of elder leaves mixed with corn bran at 50% is a good option and may be a viable alternative as a dietary supplement for dairy cows.

Key words: *Sambucus nigra*, corn bran, silage

M137 Organic fertilization improves growth of *Paulownia* spp. V. M. Llamas-Rodríguez*, R. Luevano-Escobedo, V. Gallardo-Santillan, A. S. Juárez-Reyes, and M. A. Cerrillo-Soto, *Universidad Juárez del Estado de Durango, Durango, México.*

The genus *Paulownia* exhibits rapid juvenile growth with excellent characteristics for timber, fodder, ornamental and medicinal uses. A study was conducted to estimate the effect of applying either organic or inorganic fertilizer to plants of *P. tomentosa* maintained in field conditions. The study area is located in a semiarid region of Northern Mexico at an altitude of 1921 m above sea level and temperature ranging from −18 to 35°C. Five treatments were applied to plants of 15 d of age. Two fertilizers; inorganic (based on N, P, K with doses of 20%, 8% and 4%, respectively in 100 mL of solution) and organic humic acid (n = 11.5%, $P = 9.5\%$, K = 10.0%, Ca = 0.9% and S = 0.8%) and 2 types of application (foliar and radicular) and a control (water) were evaluated. One hundred milliliters of solution was mixed in 1 L of water and applied every 15 d during 13 weeks. Height of the trees and amount of leaves were recorded. Data were analyzed according to a completely randomized design with 20 replications using ANOVA while mean comparison were performed using Tukey's test. Radicular application of inorganic fertilizer resulted in higher heights, while no effects were recorded due to inorganic foliar application. On the contrary, organic fertilization in both ways of application resulted in positive effects. The amount of leaves was positively affected by the inorganic fertilizer applied in soil (radicular), whereas the organic humic acid favored this variable after both radicular and foliar applications ($P < 0.01$). No differences were recorded between the foliar application of inorganic fertilizer and the control (water). Foliar and radicular application of organic fertilizer improved growth of *Paulownia* spp. compared to no treatment. Therefore, use of organic fertilizers might promote growth with less chance of soil contamination.

Table 1. Effect of type of fertilizer on height and number of leaves in *Paulownia tomentosa*

	Treatments					
	Inorganic		Organic		Control	
Concept	Radicular	Foliar	Radicular	Foliar	Radicular	SEM
Height (cm)	21.5[a]	11.9[c]	18.2[b]	16.0[b]	12.6[c]	14.16
Number of leaves	12.5[a]	7.9[b]	11.5[a]	11.2[a]	9.3[b]	3.19

[abc]Means within rows with different superscripts differ ($P < 0.01$); SEM = standard error of the mean.

Key words: *Paulownia*, fertilization, growth

M138 Ruminal degradability of crude protein of Marandu grasses. A. J. D. Pacheco Junior*[1], F. A. P. Santos[1], C. M. M. Bittar[1], L. R. D. Agostinho Neto[1], R. A. M. Vieira[2], L. O. Tedeschi[3], B. C. Matos[1], and G. B. Mourão[1], *[1]University of São Paulo, University of Sao Paulo, USP/ESALQ, Piracicaba, SP, Brazil, [2]State University of North Fluminense Darcy Ribeiro, State University of North Fluminense Darcy Ribeiro, Campos dos Goytacazes, RJ, Brazil, [3]Texas A&M University, Texas A&M University, College Station.*

This study aimed to characterize the degradation rates of degradable fractions of CP (in situ methods) in samples of Marandu grass (Brachiaria brizantha cv. Marandu) managed with high stocking rates and variable intervals of grazing according 95% of light interception (LI) during spring, summer and fall. The study was conducted in University of São Paulo, Piracicaba, São Paulo, Brazil. We used 3 paddocks of 0.26 ha each, which were fertilized with 260 kg N/ha between the months of evaluation. The criterion for entry of animals in the paddocks was when they reached 25 cm in height and the stubble was 15 cm. Samples of Marandu grass to determine the rate of degradation of CP (in situ), represented the mean value from 20 sampling points per paddock. We collected the entire canopy above the height of stubble (15 cm). The samples were incubated in the rumen for 0, 3, 6, 12, 18, 24, 30, 36, 48, 60, 72, 96 and 120 hours. The data analyses were performed using Generalized Compartmental Model of Digestion and PROC MIXED of SAS. Estimation of in situ degradability of CP did not differ ($P < 0.1$) among seasons (Table 1). Crude protein contained approximately 50% of soluble protein (Fraction A) and 40% of potentially degradable fraction of protein (Fraction B), respectivally.The rates of degradation of fraction B were low and effective degradability was approximately 69%.

Table 1. Composition of crude protein fractions (in situ) in samples of Marandu grass along spring, summer and fall

	Season				
Fraction[1] (%)	Spring	Summer	Fall	SE	Pr > |t|
A	54.5	44.2	50.4	4.4	0.3
B	33.3	45.4	38.3	3.5	0.1
C	12.2	10.4	11.3	1.4	0.7
Kd (%/h)*	6.3	7.6	8.0	1.3	0.5
λ (%/h)**	4.4	5.5	5.9	1.1	0.4
Effective degradability (%/h)	63.1	71.3	72.5	4.3	0.2

[1]A = soluble fraction; B = potentially degradable fraction; C = undegradable fraction.

*Degradation rate of fraction B; **asymptotic age-dependent fractional availability rate of the fraction B.

Key words: protein fraction, in situ degradability, tropical grass

M139 Effect of stage of maturity of alfalfa hay upon in vitro dry matter and crude protein digestibility. R. Copado-Garcia*[1], O. Serna[2], C. Arzola[1], O. Ruiz[1], C. Rodriguez[1], A. Corral[1], and H. Gaytan[1], *[1]Universidad Autonoma de Chihuahua, Chihuahua, Chihuahua, Mexico, [2]INIFAP, Chihuahua, Chihuahua, 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 dry matter and protein of alfalfa hay. To evaluate the effect of maturity upon those traits, 2 varieties of alfalfa ('Cuff-101' and 'Excellent multileaf') harvested in 4 seasons (spring, early, late summer and fall), were sampled and dry matter (IVDMD) and protein digestibility (IVCPD) were determined in vitro using an Ankom digester. Eight, 4 square m plots were harvested 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). An exclosure was subdivided into 5 sections at each of 8 locations in Delicias, Chih., Mexico, and sampled within 5 d intervals after an initial cut. Data were analyzed with a subplot design, with variety and period as main effects and day of cutting as sub-plot term. Statistical analysis used the GLM procedure of SAS. Alfalfa maturity, expressed as the number of days of cut after alfalfa had attained stage 2, did not show a significant difference ($P > 0.05$) on IVDMD. However, in late summer and fall the CP tends to increase, but in fall IVCPD decreased noticeably, likely as result of a more rapid maturation of the plant. Also, as the maturity of the plants increased, CP increased, and IVCPD decreased linearly ($P < 0.01$). We concluded that it is useful to take in consideration the stage of maturity to manage the nutritional quality of alfalfa in terms of digestibility of protein.

Key words: alfalfa, IVDMD, IVCPD

M140 Nutrient composition, metabolizable energy, in situ rumen degradation and in vitro fermentation characteristics of linted cottonseed hulls, delinted cottonseed hulls and cottonseed linter waste. H. J. Yang* and Y. K. Bo, *State Key Laboratory of Animal Nutrition, College of Animal Science and Technology, China Agricultural University, Beijing, China.*

Dietary supplementation with conventional linted cottonseed hulls (LCSH) is a common practice in livestock production all over the world. However, supplementation with mechanically delinted cottonseed hulls (DCSH) and cottonseed linter waste (CSLW) has not been well accepted by local farmers in Xinjiang province of China. In this study, representative samples of DCSH, LCSH and CSLW were collected in different areas of Xinjiang and assessed by chemical analysis, in situ and in vitro degradation methods. The CP (N × 6.25) content of CSLW (302 ± 3.2 g/kg DM) was approximately 3 times that of LCSH and 5 times that of DCSH. The ether extract (EE) content was 3 times higher in CSLW (269 ± 3.12 g/kg DM) than that of LCSH and 4 times higher than that of DCSH. NDF (311 ± 2.0) and ADF (243 ± 6.2) contents of CSLW were less than half values of DCSH or LCSH. Metabolizable energy, based on in vitro gas production and chemical analyses, ranked: CSLW (12.58 ± 0.65 kJ/kg DM) > LCSH (6.81 ± 0.61 kJ/kg DM) > DCSH (5.90 ± 0.60 kJ/kg DM) ($P < 0.05$). The in situ degradation of DM and CP were fitted to an exponential equation: $Y = a + b \times (1 - e^{-c \times time})$. CSLW showed the highest effective degradabilities for DM (0.36 ± 0.01) and CP (0.52 ± 0.04) ($P < 0.05$). One step in vitro ruminal DM disappearance and 2 step Tilley and Terry ′s digestibilities of DM, NDF and ADF ranked: CSLW > LCSH > DCSH ($P < 0.05$). The 72-h batch culture experiment also showed the highest production of volatile fatty acids occurred in CSLW ($P < 0.05$), but the maximum gas production did not differ among the 3 cottonseed by-products. Molar proportions of methane in the fermentation gases were 23.5%, 25.0% and 17.5% for DCSH, LCSH and CSLW with a pooled standard error of 2.5, respectively. Dietary inclusion of CSLW could be beneficial to host ruminants by providing more glucogenic precursors (e.g., propionate) than non-glucogenic acids (e.g., acetate and butyrate). In general, CSLW appears to be valuable as a substitute for conventional protein feed for ruminant animals, with less potential for greenhouse gas emission than either LCSH or DCSH.

Key words: cottonseed by-products, in situ degradation, cumulative gas production

M141 Chemical composition and nutritional value of *Prosopis laevigata* harvested at three differents maturation stage. R. Rojo*, E. Castelán, A. Z. M. Salem, J. F. Vázquez, B. Encarnación-Elizalde, M. Palma-González, and J. Cedillo-Monrroy, *Centro Universitario UAEM-Temascaltepec, Universidad Autónoma del Estado de México, Temascaltepec, Estado de México, México.*

A experiment was carried out to evaluate chemical composition and nutritional value of *Prosopis laevigata* pods harvested at three different maturity stages (IMP=immature pods, SMP=semi- mature pods, MAP= mature pods). Chemical analyses were: CP, NDF, ADF and Total condensed tannins (TCT) and nutritional components were: in vitro dry matter degradability (IVDMD), gas production (GP24), fermentation kinetic parameters (b: asymptotic gas production, c: rate of gas production from the slowly fermentable feed fraction b (/h) and lag time), short chain fatty acids (SCFA), metabolizable energy (ME), net energy (NE) and partition factor (PF). The inoculum was obtained from two adult male goats fitted with a ruminal fistula, fed a 40:60 forage:concentrate diet. Data were submitted to variance analysis by the GLM procedure and mean effects were separated by the Tukey test. The content of CP (g/kg DM) was greater ($P < 0.05$) in IMP (28.1%) pods ($P < 0.01$) compared to SMP (11.0%) and MAP (11.4%). The NDF and ADF were greater ($P < 0.05$) in MAP in comparison with IMP and SMP. The TCT (g/kg DM) (TCT) was greater ($P < 0.05$) in MAP (37.08) and SMP (36.77) than IMP (12.63). The gas production at 24 hours and kinetic gas production parameters (b y c) were greater ($P < 0.05$) in SMP and MAP compared with IMP; the oppo-

site occurred with the lag time, with IMP having the lowest value ($P = 0.0001$). The SCFA production was greater in SMP and MAP ($P = 0.0001$) than IMP. However; PF and IVDMD were greater in IMP ($P<0.05$). Measures of energy (i.e, ME and NE) were not affected by the maturity stage. Based on the results we conclude that MAP and SMP of *Prosopis laevigata* are promising nutritional alternative food sources for small ruminants, especially in the dry season.

Key words: chemical composition, nutritive value, *Prosopis laevigata* pods

Graduate Student Competition: ADSA Dairy Foods Poster Competition

M142 The influence of process time and heat treatment on bleaching efficacy of liquid whey and retentate. X. Li* and M. A. Drake, *North Carolina State University, Raleigh.*

The residual annatto colorant in fluid whey is removed by bleaching to provide a desired neutral color in dried whey ingredients. Studies have established that bleaching negatively influences whey ingredient flavor. Optimization of bleaching parameters is necessary to minimize flavor effects on finished ingredients. Studies are needed to determine if the cheesemake procedure or processing factors influence bleaching efficacy. The objective of this study was to evaluate if starter culture, whey pasteurization, fluid whey storage, or spray drying affected the bleaching efficacy of liquid whey and retentate. Cheddar cheese whey with 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 ultrafiltered to 9% solids (w/w) and spray dried to 34% whey protein concentrate (WPC34). Aliquots of liquid whey were bleached at 60°C for 1 h (hydrogen peroxide, 250 ppm) immediately (no fat separation or pasteurization), before pasteurization and after fat separation, after pasteurization and fat separation, after storage at 3°C for 24 h, and after freezing at −20°C for 1 week. Aliquots of retentate were bleached analogously immediately and after storage at 3 or −20°C. Freshly spray dried WPC34 was rehydrated to 9% (w/v) solids and bleached. Bleaching efficacy was measured by extraction and quantification of norbixin. Proximate analyses and color analyses (Hunter Lab) were also conducted. Each experiment was replicated 3 times. Starter culture (fermentation), fat separation or pasteurization, or spray drying did not impact bleaching efficacy ($P < 0.05$). Cold or frozen storage decreased bleaching efficacy of fluid whey compared with immediate bleaching ($P < 0.05$). These results confirm that processing steps, particularly hold times, can influence bleaching efficacy.

Key words: whey, retentate, bleaching

M143 Impact of bleaching on flavor of 34% whey protein concentrate and benzoic acid concentration in dried whey proteins. M. A. Listiyani*, R. E. Campbell, R. E. Miracle, L. O. Dean, and M. A. Drake, *North Carolina State University, Raleigh.*

Previous studies have shown that bleaching negatively impacts flavor of 80% whey protein concentrate (WPC80) but bleaching effects on lower protein products have not been established. Benzoyl peroxide (BP), a whey bleaching agent, degrades to benzoic acid (BA) and may elevate BA concentrations in dried whey products. There is no legal limit in the US for BP use in whey, but international concerns exist. The objectives of this study were to determine the impact of hydrogen peroxide (HP) or BP bleaching on the flavor of WPC34 and to evaluate residual BA in commercial and experimental WPC bleached with and without BP. Cheddar whey was manufactured in duplicate. Pasteurized fat-separated whey was subjected to hot bleaching with either HP at 500 mg/kg, BP at 50 or 100 mg/kg, or no bleach. Whey was ultrafiltered and spray dried into WPC34. Color (L*a*b*) measurements and norbixin extractions were conducted to compare bleaching efficacy. Descriptive sensory and instrumental volatile analyses were used to evaluate bleaching effects on flavor. Benzoic acid was extracted from experimental and commercial WPC34 and commercial WPC80 and quantified by high performance liquid chromatography. The b* value and norbixin concentration of BP bleached WPC34 were lower than HP bleached and control WPC34 ($P < 0.05$). HP bleached WPC34 displayed higher cardboard flavor and had higher volatile lipid oxidation products than BP bleached or control WPC34 ($P < 0.05$). BP bleached WPC34 had higher BA concentrations than unbleached and HP bleached WPC34 ($P < 0.05$) and BA concentrations were also higher in BP bleached WPC80 compared with unbleached and HP bleached WPC80, with smaller differences than those observed in WPC34. Benzoic acid extraction from permeate showed that WPC80 permeate contained more BA than WPC34 permeate ($P < 0.05$). These results suggest that BP is more effective in color removal of whey and results in fewer flavor side effects compared with HP and that BA is removed by ultrafiltration and diafiltration.

Key words: whey, bleaching, flavor

M144 The influence of bleaching agent, solids concentration and temperature on bleaching efficacy and volatile components of fluid whey. A. J. Fox* and M. A. Drake, *North Carolina State University, Raleigh.*

Whey protein is desirable as a neutral flavored, uncolored powder. Fluid whey is often bleached to remove residual annatto and previous research has demonstrated that this process causes off-flavors in dried whey proteins. The objective of this research was to determine the impact of temperature, solids, and bleaching agent on bleaching efficacy and volatile components in fluid whey. A standard Cheddar cheese make-procedure was used to manufacture liquid whey at 6.7% solids. The whey was concentrated to 12% solids (w/v) and 80% protein (w/w) by ultrafiltration and diafiltration. Liquid whey or concentrated whey (retentate) were bleached using benzoyl peroxide (BP) at 100 mg/kg (w/w) or hydrogen peroxide (HP) at 250 mg/kg (w/w) at 5°C for 16 h or at 50°C for 1 h. An unbleached control was subjected to a similar temperature profile. The experiment was replicated 3 times. Annatto destruction (bleaching efficacy) among treatments was compared by solvent extraction and quantitation of norbixin of each treatment compared with an unbleached control. Volatile compounds were extracted and separated using solid phase microextraction gas chromatography mass spectrometry (SPME GC-MS). Bleaching efficacy of BP was higher than HP ($P < 0.05$) for fluid whey at both 5°C and 50°C. HP bleaching was significantly increased in retentate compared with liquid whey ($P < 0.05$). In retentate, there was no significant difference between bleaching with HP and BP at 50°C or 5°C ($P > 0.05$). Retentate bleached with HP at either temperature had significantly higher relative abundances of pentanal, hexanal, heptanal, and octanal than BP bleached retentate ($P < 0.05$). These results suggest that optimal bleaching of liquid whey is achieved using BP at 50°C and that optimal bleaching of retentate is achieved at 50°C with HP or BP. These results also suggest that bleaching with BP is less detrimental to flavor than bleaching with HP.

Key words: whey, bleaching, annatto

M145 Activation of lactoperoxidase for the bleaching of fluid whey. R. E. Campbell*[1], E. J. Kang[1], E. Bastian[2], and M. A. Drake[1], *[1]North Carolina State University, Raleigh, [2]Glanbia Nutritionals Inc., Twin Falls, ID.*

Lactoperoxidase (LP) is a heat stable peroxidase in raw milk that can generate oxidized substrates with antimicrobial activity. Activation of LP with low levels of hydrogen peroxide (HP) (5 – 10 ppm) is required

and this system has been used to preserve raw milk quality. Commercial bleaching of fluid whey with HP alone requires high concentrations (250 – 500 ppm HP) and recent studies have demonstrated that off flavors are generated during bleaching that carry-through to spray dried whey proteins. Bleaching of fluid whey with naturally present LP may be a viable alternative to traditional whey bleaching. The objective of this study was to monitor LP stability in fluid milk and whey, to determine the optimum level of HP for LP whey bleaching and to compare bleaching efficacy of fluid whey with LP to that of HP. Fluid Cheddar whey was manufactured in triplicate from pasteurized whole milk. LP activity was monitored in raw and pasteurized milk and in whey before and after pasteurization by UV-VIS spectrophotometry. The optimum concentration of HP (0 to 100 ppm) for LP activation was determined by monitoring loss of color in fluid whey via reflectance measurement. The optimum HP concentration for LP activity was 20 ppm. In subsequent experiments, fat separated whey was bleached at 35 or 50C with LP (with 20 ppm HP) or by the addition of 250 ppm HP. A control with no bleaching was also evaluated. Bleaching efficacy was determined by measuring norbixin destruction compared with the unbleached control and volatiles were measured by gas chromatography mass spectrometry (GCMS). LP was active in raw and pasteurized milk and whey, although concentrations decreased with pasteurization. Temperature did not affect bleaching efficacy ($P > 0.05$) while treatment (LP or HP) impacted bleaching efficacy ($P < 0.05$). Bleaching of fluid whey with LP (and 20 ppm HP) resulted in higher bleaching efficacy (color loss) than bleaching with HP alone at 250 ppm ($P < 0.05$). Fluid whey bleached with 250 ppm had higher concentrations of volatile lipid oxidation products compared with LP bleached or control whey. These results suggest that LP bleaching may be a viable and desirable alternative to HP bleaching for fluid whey.

Key words: bleaching, whey, lactoperoxidase

M146 Bleaching efficacy of ozone gas in liquid whey and its effects on flavor of 80% whey protein concentrate. T. J. Smith* and M. A. Drake, *North Carolina State University, Raleigh.*

Bleaching of whey is a necessary commercial practice but recent studies have demonstrated that hydrogen peroxide and benzoyl peroxide bleaching can cause off flavors. The objective of this study was to determine the viability of ozone as an alternative whey bleaching agent. Flavor effects and bleaching efficacy of ozone gas on whey and retentate were evaluated in benchtop experiments before pilot scale manufacture of 80% whey protein concentrate. Cheddar whey and retentate were produced in triplicate. Bleaching variables tested included bleaching temperature (35 and 60°C), ozone (200mg/h in 600mL whey) exposure time (15, 30, and 45 min), and whey solids (6.7 and 12%). Bleaching efficacy was evaluated by measurement of norbixin relative to an unbleached control. Based on benchtop results, hot bleaching of liquid whey with 1h ozone exposure was selected for WPC80 production. To ensure safety, ozone bleaching was performed at a lower level (1.6g/h in 94.5 L whey) and compared with a control (no bleaching) and hydrogen peroxide (HP) bleaching (250ppm). WPC80 was manufactured in triplicate. Bleaching of retentate with ozone was higher at 35°C compared with 60°C ($P < 0.05$); temperature did not affect liquid whey bleaching with ozone ($P > 0.05$). In benchtop studies, a 63% decrease in norbixin content was observed in fluid whey after 45 min ozone exposure. In pilot scale manufacture, WPC80 from HP bleached whey had a 27% norbixin destruction while that bleached with ozone had a 9% reduction. Ozone-treated WPC80 exhibited animal and flour/pasta flavors and HP bleached WPC80 was characterized by cabbage and fatty flavors. These flavors were not present in the control unbleached WPC80. Higher levels ($P < 0.05$) of nonanal and decanal were present in the ozone WPC80 while higher levels ($P < 0.05$) of pentanal, DMDS, hexanal, heptanal, 2-pentylfuran, and octanal were present in the HP WPC80 compared with the control WPC80. These results suggest that ozone bleaching does not represent a promising alternative to approved bleaching agents in whey protein production although it could possibly remain feasible at or close to saturation levels.

Key words: whey, bleaching, ozone

M147 The impact of sodium reduction on the flavor, texture and flavor chemistry of full fat and low fat Cheddar cheese. M. K. Kim*[1], R. E. Miracle[1], D. J. McMahon[2], and M. A. Drake[1], *[1]North Carolina State University, Raleigh, [2]Utah State University, Logan.*

Sodium and fat reduction are key issues for food processors. Salt plays a crucial role in the ripening of natural Cheddar cheese in both flavor and texture development. However, modest reductions in sodium may be acceptable and a quantitative study on the impact of various sodium reductions on flavor and texture development of Cheddar cheese has not been conducted. The objective of this study was to evaluate the role of salt reduction on the flavor and texture of full fat and low fat Cheddar cheese. Low fat and full fat Cheddar cheeses that contained 0.7%, 1.2%, 1.7%, 2.2% 2.7% or 3.25% (wet weight) salt were manufactured in triplicate at Utah State University. Cheeses were ripened at 8°C and samples were taken following 3, 6, or 9 mo for sensory and instrumental volatile analyses. A trained sensory panel (n = 10) documented flavor and texture attributes. Volatile compounds were extracted by solid phase microextraction and identified using gas chromatography mass spectrometry. Selected compounds were quantified using external standard curves. Consumer acceptance tests were conducted after 3 and 9 mo aging. Salty taste and to a lesser extent umami taste, increased with increasing sodium concentration ($P < 0.05$). Firmness of cheeses decreased with decreased sodium after 3 mo ripening and other attributes were impacted with further ripening. Aromatic flavor attributes of cheeses were not distinct at 3 mo ($P > 0.05$) but differences ($P < 0.05$) were documented as cheeses aged. Brothy and rosy flavors and bitter taste were associated with sodium reduction after 6 mo ripening in low fat cheeses and after 9 mo in full fat cheeses. Changes in flavor and texture attributes due to sodium reduction were larger for low fat cheeses compared with full fat cheeses. Cheeses with lower salt concentrations had higher relative abundances of volatile phenyl compounds compared with cheeses with 3.25% salt. Consumer acceptance of cheeses decreased when sodium was decreased by more than 50 percent. Sodium reduction alters flavor and texture properties of Cheddar cheeses and these changes are pronounced with ripening.

Key words: Cheddar cheese, sodium reduction, fat reduction

M148 Fortification of milk for Cheddar cheese manufacture using skim milk powder. A. C. Moynihan* and P. L. H. McSweeney, *University College Cork, Cork, Ireland.*

Using powders to fortify cheesemilk could have potential applications in ingredient cheese or to overcome problems caused by milk seasonality. The objective of this study was to make cheese from milk fortified with skim milk powder (SMP) and to determine its effect on cheese yield, composition, texture, meltability, proteolysis and microbiology. Skim milk (40 L) was fortified with 3.75 kg SMP to make a

milk stock with a higher casein content and the casein to fat ratio was standardized to 0.7 using cream. This mixture was added to cheese vats and made up to 50 L with pasteurized milk to give cheese milk with casein levels of 2.61% (CSMP), 2.86% (LSMP), 3.22% (MSMP) and 3.83% (HSMP) and Cheddar cheese was made therefrom. Significant differences ($P < 0.05$) were observed in moisture-adjusted cheese yields (9.76, 10.84, 12.06 and 14.99 kg/100kg milk for CSMP, LSMP, MSMP and HSMP, respectively). No significant difference ($P > 0.05$) was observed between the cheeses in terms of moisture in non-fat substances. pH values tended to be higher as SMP fortification level increased. Texture analysis showed that low level addition of SMP had no significant ($P > 0.05$) effect on the hardness values of the cheese throughout ripening compared with CSMP but higher levels of addition of powder resulted in increased hardness. The meltability of all cheeses increased with ripening time but HSMP and MSMP melted less than CSMP and LSMP cheeses. As cheese ripening progressed levels of proteolysis increased significantly ($P < 0.05$) in all cheeses but higher levels of SMP fortification resulted in slower proteolysis. Numbers of non-starter lactic acid bacteria (NSLAB) were higher in the fortified cheeses; as the level of powder addition increased so did the numbers of NSLAB. Fortifying Cheddar cheese with SMP had significant effects on yield, textural, melt, proteolytic and microbiological properties of the cheese without having major effects on its composition. Lower levels of fortification can give a cheese with similar properties to the control but with increased yield.

Key words: Cheddar cheese, skim milk powder, yield

M149 Rapid measurement of lactose concentration in cheese whey by using handheld blood glucose meter. A. C. Biswas*, J. K. Amamcharla, and L. E. Metzger, *Midwest Dairy Foods Research Center, Dairy Science Department, South Dakota State University, Brookings.*

Whey is a valuable byproduct of cheese production, and is used to manufacture a variety of whey based products. In addition to whey protein, lactose is an important component of whey, and influences the quality and cost of whey-based products. A blood glucose meter method was previously developed for determination of the lactose content of raw milk and process cheese. The objective of the current research was to modify the previously developed blood glucose meter method, and apply it to the analysis of whey. Additionally, a new generation ReliOn Confirm glucose meter was utilized. In the method, 1 g of whey was diluted with 20 g of 0.1 *M* phosphate buffer (pH 7.4). Five ml of diluted whey and 0.1 mL of β-galactosidase enzyme were mixed, and incubated at 40°C to hydrolyze the lactose into glucose and galactose. After 10 min, the sample was analyzed with 4 different lots of test strips to evaluate the variation between the lots. An individual calibration curve was developed for each test strips lot using the model whey solutions that had a constant protein content of 0.8%, and different lactose concentrations ranging from 2 to 6%. These model whey solutions were standardized and prepared by mixing ultra-filtered whey retentate, whey permeate, lactose powder, and water in different ratios to obtained the final concentration (2%, 3%, 4%, 5%, and 6%) of lactose. A universal calibration curve was also developed by pooling the data from all 4 test strips lots. Simultaneously, the calibration standards were analyzed for lactose concentration using an HPLC-based reference method. The slopes and intercepts of individual calibration curves were between 0.945 to 1.009, and −54.96 to −38.73, respectively. The slope and intercept of universal calibration curve was 0.978 and −46.775, respectively. Future study will focus on validation of the universal calibration curve equation for analysis of whey with a range of lactose concentration typically observed during cheese manufacture.

Key words: cheese whey lactose, rapid method, glucose meter

M150 Organic acid identification and quantification in low-fat Cheddar cheese by capillary zone electrophoresis. R. Kumar* and T. C. Schoenfuss, *University of Minnesota, Department of Food Science and Nutrition, St. Paul.*

Low fat cheese can lack important sensory attributes due to the reduction in fat. The biochemical changes during ripening are related to the development of characteristic flavor. When fat replacement ingredients are used in a cheese, these ingredients could be metabolized by culture and non-starter organisms to create flavor compounds. The objective of this study was the identification and quantification of organic acids in low-fat Cheddar compared with full-fat control by capillary zone electrophoresis using a commercial anion analysis kit (Beckman Coulter, Inc., Brea, CA). Eight organic acids (acetic, butyric, citric, formic, lactic, propionic, pyruvic and oxalic) were measured in cheese samples produced with and without whey protein concentrate (Avonlac 180, Glanbia Nutritionals, Monroe, WI) and polysaccharide fat replacers (Novagel RCN 15, FMC Biopolymer, Philadelphia, PA) and Pectin (XSS 100, Danisco USA Inc., New Century, KS). Separations were performed on a P/ACE MDQ capillary electrophoresis with indirect UV detection at 230 nm. Samples were prepared by solubilizing cheese in water, centrifuging and filtering supernatant before analysis. The separations were carried out on a 50 cm, 75μm i.d. bare fused silica capillary. The sample was injected with pressure at 3448 Pa (0.5 p.s.i.) for 10 s at 30kV with reverse polarity and separation was performed at 25°C. An internal injection standard (sodium octanoate) was used for the quantification of the anions. All quantifiable organic acids were present in significantly greater concentrations in low-fat cheese than full fat control. Among low fat cheeses, formic acid was significantly higher in Novagel treatment cheese and acetic acid was higher in cheese with whey protein concentrate. It was demonstrated that the anion analysis kit can be used effectively in identification and quantification of organic acids in cheese.

Key words: low fat cheese, organic acids, capillary electrophoresis

M151 Stability of sterilized micellar casein concentrates (MCC) during storage. A. Sauer* and C. I. Moraru, *Cornell University, Ithaca, NY.*

The use of micellar casein concentrates (MCC) obtained by membrane separation is receiving increasing interest from the dairy industry. Currently, there is a lack of knowledge regarding the storage behavior of sterilized MCCs. This work aimed at evaluating the stability, particularly the occurrence of aggregation and sedimentation, in sterilized MCCs during storage at 25°C. MCCs with casein concentrations of 5–10% were subjected separately to continuous-flow UHT treatment and in-container retorting, and subsequently stored for 8 weeks at 25°C. As control, non-heat treated MCC with added preservative (Broad Spectrum Microtabs II) was used. Sedimentation was evaluated by measuring the protein content in the bottom layer of the storage containers. Samples were analyzed weekly for protein content, particle size and pH. The study was performed in triplicate. Particle size in control samples increased up to wk 5 of storage, while particle sizes in retorted samples remained constant throughout storage. Control samples were stable for up to 8 weeks (no significant sedimentation was observed), while retorted samples showed significant sedimenta-

tion, with up to 22% increase of protein content in the bottom layer of the storage container. For the retorted samples, sedimentation was the least pronounced in the 10% MCC samples, and most pronounced in the 5% MCC samples. Very strong sedimentation was observed in all UHT treated samples, with large variability between replicates. To estimate sedimentation over prolonged storage, sedimentation kinetics was established for all samples. The rate of sedimentation for 10% MCCs in replicates 1 and 2 was 0.02% protein/day, in replicate 3 it was 0.06%protein/day. Overall, it was concluded that UHT treated MCC preparations were unstable during storage, and may require additional stabilization to increase their storage stability, while the retorted preparations were relatively stable. The results of this study provide valuable information about the storage stability of sterilized MCC obtained by membrane filtration, which can be used for the manufacture of shelf stable, protein rich beverages.

Key words: micellar casein concentrate, sterilization, storage stability

M152 Use of capillary gel electrophoresis for quantification of individual milk proteins in ultra- and microfiltration retentate. P. Salunke*, C. Marella, and L. E. Metzger, *Midwest Dairy Foods Research Centre, South Dakota State University, Brookings.*

Quantification of milk protein into various fractions has technological and functional significance. For determination of the casein (CN) and whey protein (WP) content of milk and milk products a multistep precipitation technique that includes non-casein nitrogen (NCN), non-protein nitrogen (NPN) and total nitrogen (TN) analysis is typically utilized. This method results in a crude fractionation of milk protein and does not quantify the individual protein fractions. However, capillary gel electrophoresis (CE) is emerging as an effective method for qualitative and quantitative separation of individual milk proteins based on molecular weight (MW). The objective of the present work was to utilizing CE to separate various protein fractions in skim milk, milk protein concentrate (MPC) and micellar casein concentrate (MCC), and compare the results to the traditional NCN, NPN and TN analysis. Three samples each of skim milk, MPC and MCC (9 total samples) were collected and CE was performed in triplicate on each sample using a Beckman P/ACE MDQ capillary electrophoresis system (Beckman-Coulter, Fullerton, CA) equipped with a UV detector set at 214nm. Separation was obtained using a 50µm bare fused silica capillary of 30.2cm. SDS-MW analysis kit (Beckman-Coulter) was used for the separation. The area of each peak was calculated from the electropherogram. The TP, NCN and NPN protein of each sample was also determined. The ratio of peak areas for αS1-CN: αS2-CN: β-CN: κ-CN: γ-CN as determined by CE was similar in the skim milk, MPC and MCC samples. The ratio of WP/true protein was significantly ($P < 0.05$) lower in MCC as compared with skim milk and MPC. Additionally the CN/True protein ratio obtained using CE was similar to the CN/True protein ratio determined with Kjeldahl analysis. The results indicate that CE can be used to determine the CN/True protein ratio of skim milk, MPC, and MCC and can be used to determine the relative concentration of individual milk proteins.

Key words: capillary electrophoresis, milk protein concentrate, micellar casein concentrate

M153 Incorporation of whey:buttermilk heat-denatured protein aggregates in model set-type yogurt. M. Saffon*[1], V. Richard[1], S. F. Gauthier[1], M. Britten[2], and Y. Pouliot[1], *[1]STELA Dairy Research Center, Institute of Nutraceuticals and Functional Foods (INAF), Université Laval, Québec, QC, Canada, [2]Food Research and Development Center (FRDC), Agriculture and Agri-Food Canada, St-Hyacinthe, QC, Canada.*

Previous work showed that it was possible to generate aggregated protein material by heating buttermilk in the presence of whey. It was hypothesized that addition of these protein aggregates would increase serum retention and improve firmness of yogurts. Whey and buttermilk protein mixtures (25:75) were adjusted to pH 4.6 and heated at 90°C for 25 min. Set-type model yogurts were prepared from milks standardized to 15% (w/v) total solids and 4.2% (w/v) protein using skim milk powder (SMP). Whey:buttemilk aggregates were introduced to substitute 40, 60, 80 or 100% of the proteins from SMP. Enriched milks were heated at 85°C for 20 min. After cooling at 42°C, milks were inoculated with a commercial yogurt starter (*S. thermophilus*, *L. bulgaricus*) and incubated until pH 4.6 was obtained. Syneresis was determined by centrifugation at 222 × *g* during 10 min at 4°C and texture properties were obtained by penetration using a TA-XT2 texture analyzer. All yogurt preparations were performed in triplicate and textural properties of yogurts were compared with those of control yogurt using *t*-tests. Addition of new aggregates significantly decreased ($P < 0.001$) forces of fracture, firmness, adhesiveness and relaxation. Syneresis was also increased. Substituting 60% of the proteins from SMP using aggregates had the least impact on the textural properties of yogurts. Particle size distribution analyses of milks before and after heating milks showed that unheated milks contained 2 populations of particles while heated milks contained only one population of particles. This suggests that whey:buttermilk aggregates may interact with milk protein during heating. Overall, our results show that whey:buttermilk aggregates can be used as protein ingredient in yogurt formulas, however, more work is needed to maximize heat-induced interactions between whey:buttermilk aggregates and milk proteins.

Key words: heat-denatured protein, yogurt, texture properties

M154 Linking environmental and sensory qualities of a Vermont artisan cheese. A. Greenbaum*[1], S. Carpino[2], M. Almena[1], S. Bosworth[1], P. Kindstedt[1], and A. Trubek[1], *[1]University of Vermont, Burlington, [2]CoRFiLaC, Ragusa, Italy.*

In collaboration with the Vermont Agency of Agriculture, Food and Markets, researchers at the University of Vermont have created the Taste of Place Initiative, involving research and outreach with cheesemakers to understand the quality of their product by identifying unique sensory characteristics. This particular research project investigates how the natural environment influences the final sensory characteristics of a particular alpine style farmstead cheese by identifying and characterizing key differences in sensory notes and chemical flavor compounds, and determining whether those differences are attributable to differences in the makeup of the pasture and practices of 2 Vermont artisan cheesemakers and their facilities. During this project SmartNose and gas chromatography-olfactometry analysis, sensory panels, observation, sample collection and cheesemaker interviews were conducted. First, pasture samples were collected from both farms on the same 2 d in early summer and 2 d in the fall. The pasture samples and aged cheese samples from 2 wheels of the cheese made the day of summer pasture collection and fall pasture collection were frozen and stored in a −32°C freezer until they were shipped to the CoRFiLaC lab in Ragusa, Sicily, and later analyzed using SmartNose, gas chromatography-olfactometry to identify similarities in volatile compounds between the pasture and corresponding cheese samples. A half-kilogram of each wheel of cheese sent for SmartNose and GC-O

analysis was also sampled during sensory analysis using Quantitative Descriptive Analysis. Preliminary results revealed overlaps across methodologies as similar descriptors found during QDA were defined during cheesemaker interviews and also correlated with environmental observation. The correlation between pasture and cheese samples has yet to be determined. By defining unique sensory characteristics of this artisan cheese, the results can impact struggling rural areas by keeping historically local products in production, thus creating rural employment and stabilizing rural population.

Graduate Student Competition: ADSA Production Division
Graduate Student Poster Competition - MS Division

M155 Chewing activities of dairy heifers precision-fed a low or high forage ration at four levels of dry distillers grain. F. X. Suarez-Mena*, G. J. Lascano, and A. J. Heinrichs, *The Pennsylvania State University, University Park.*

The objective of this study was to determine the effects of differing forage to concentrate ratios (F:C) and corn dry distillers grain with solubles (DDGS) inclusion rates on chewing behavior, rumen pH, and rumen fill in precision-fed dairy heifer rations. A split plot design with F:C as whole plot and DDGS inclusion level as sub-plot was administered in a 4-period (19 d) 4 × 4 Latin square. Eight rumen cannulated Holstein heifers (12.5 ± 0.5 mo and 344 ± 15 kg, age and BW respectively) housed in individual stalls were allocated to 2 F:C (50:50 LF or 75:25 HF; DM basis) and to a sequence of DDGS inclusion (0, 7, 14 and 21%; DM basis). Forage was a mix of 50% corn silage and 50% grass hay (DM basis). Diets were fed to provide equal amounts of nutrients to allow 800 g/d BW gain and fed 1X/d. Chewing behavior was visually monitored for 48 h at 5–min intervals. Rumen contents were sampled at –2, 0, 2, 4, 6, 8, 10, 12, and 20 h after feeding for pH determination. Total rumen evacuation was performed at –2 and 5 h after feeding. Statistical analysis was conducted using the MIXED procedure of SAS. DMI linearly decreased as DDGS increased (6.61to 6.11 ± 0.09 kg/d; $P < 0.01$). No differences were found for rumen pH. Time spent eating tended to be longer for HF (151 vs. 112 ± 14 min/d; $P = 0.09$) and was not different for DDGS inclusion. Ruminating time did not differ by F:C but linearly increased as DDGS increased (421 to 450 ± 15 min/d; $P = 0.03$). Total chewing time tended to be longer for HF (593 vs. 516 ± 28 min/d; $P = 0.10$) and to increase linearly as DDGS increased (553 to 579 ± 23 min/d; $P = 0.09$). Wet rumen digesta weight (46.6 vs. 37.6 ± 2.2 kg; $P = 0.03$) and volume (51.5 vs. 41.5 ± 2.5 L; $P = 0.03$) were greater for HF. Total chewing time increased by the addition of DDGS and higher F:C. DDGS influenced ruminating time with no effect on eating time while F:C affected eating time. Higher F:C increased rumen digesta weight and volume. F:C or DDGS levels in the ration did not affect rumen pH.

Key words: heifer, chewing, dry distillers grain with solubles

M156 Effect of one or two treatments of prostaglandin $F_{2\alpha}$ prior to Cosynch in lactating 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.*

Many dairies in the United States use $PGF_{2\alpha}$ treatment, as part of a presynchronization (Presynch) program. The objective of this experiment was to study the effects of one versus 2 $PGF_{2\alpha}$ Presynch treatments, before a Cosynch program. Analysis included: the effects on first service conception rates (FSCR), number of days open (DO), services per conception (SC), and days to first service (DFS). Lactating, Holstein cows (n = 748) were randomly assigned to the treatment group (n = 376; first treatment with $PGF_{2\alpha}$ between d 30 and 36 postpartum, second treatment with $PGF_{2\alpha}$ between d 44 and 50 postpartum) or the control group (n = 372; received one treatment with $PGF_{2\alpha}$ between d 44 and 50 postpartum). For both groups a cow found in estrous was bred and tracked for pregnancy. Data were further analyzed as bred before Cosynch treatment (n = 489) and completing Cosynch treatment (n = 259). Overall, there were no differences ($P > 0.05$) between the treatment and control groups in FSCR (0.43 ± 0.03 for both groups), DO (91.40 ± 1.96 and 91.67 ± 2.06), SC (2.00 ± 0.06 and 2.08 ± 0.06) and DFS (60.49 ± 0.51 and 59.77 ± 0.55). Of the cows removed from the experiment (n = 210) 47.9% were culled for reproduction and mastitis and 52.1% remained open, with no effect of treatment ($P > 0.05$). There was no difference ($P > 0.05$) between treatment and control for cows bred before completing Cosynch treatment (i.e., bred at observed estrus) including FSCR (0.45 ± 0.04 and 0.45 ± 0.03), DO (84.84 ± 0.2.33 and 85.13 ± 2.37), SC (2.00 ± 0.07 and 2.07 ± 0.08) and DFS (54.84 ± 0.47 and 54.30 ± 0.56), respectively. Further, no difference ($P > 0.05$) was found between treatment and control, among those completing Cosynch, in FSCR (0.38 ± 0.04 and 0.40 ± 0.04), DO (103.38 ± 3.33 and 104.41 ± 3.73), SC (2.02 ± 0.09 and 2.08 ± 0.11) and DFS (70.82 ± 0.24 and 70.46 ± 0.30). Finally, parity and day of Presynch treatment had no effect ($P > 0.05$) on any of the treatment groups. These results indicate, within the reproductive parameters studied, one $PGF_{2\alpha}$ Presynch was as effective as the 2 $PGF_{2\alpha}$ Presynch treatment.

Key words: prostaglandin $F_{2\alpha}$, presynchronization, Cosynch

M157 The effects of extruding wheat dried distillers grains with solubles with peas or canola meal on ruminal fermentation, nutrient digestion and milk production in lactating Holstein dairy cows. R. M. Claassen*, D. A. Christensen, and T. Mutsvangwa, *University of Saskatchewan, Saskatoon, Saskatchewan, Canada.*

The objective of this study was to examine the effects of feeding extruded and non-extruded mixtures of wheat dried distillers grains with solubles with peas (WP) or canola meal (WC) on ruminal fermentation, total tract nutrient digestion, and milk production in dairy cows. Eight Holstein cows (BW 712 ± 54 kg, 90 ± 31 DIM) were used in a replicated 4 × 4 Latin square design (28-d periods) with a 2 × 2 factorial arrangement of dietary treatments. Four cows in one Latin square were fitted with rumen cannulas for the measurement of ruminal fermentation characteristics. Treatment diets contained either WP or WC combinations fed in an extruded or non-extruded form (16% of DM intake). Diets were isonitrogenous (17.1% CP) and contained 50% concentrate and 50% forage (DM basis). DM intake was not affected ($P > 0.05$) by dietary treatment. Total tract digestibilities of ADF and NDF were not affected by dietary treatment; however, total tract digestibilities of crude protein ($P = 0.014$) and ether extract ($P = 0.002$) were higher, and that of DM tended ($P = 0.070$) to be higher for cows fed extruded when compared with those fed non-extruded diets. Total tract digestibility of ether extract tended to be higher ($P = 0.083$) in cows fed WC compared with those fed WP diets. Ruminal pH was higher in cows fed non-extruded WC compared with those fed extruded WC, but there was no difference in ruminal pH in cows fed WP diets (interaction; $P = 0.047$). Milk yield ($P = 0.021$) and milk protein yield ($P = 0.036$) were higher for cows fed WP compared with those fed WC diets. Milk contents of fat, protein and milk urea nitrogen, and milk fat yield were not affected by dietary treatment; however, milk lactose content was higher ($P = 0.013$) for cows fed the extruded compared with those fed non-extruded diets. In summary, these results indicate that the dietary inclusion of WP can potentially increase milk yield when compared with WC. Extrusion had positive effects on total tract nutrient digestion.

Key words: dairy cow, extrusion, wheat dried distillers grains with solubles

M158 Ruminal degradation and intestinal protein digestion of steam-flaked soybeans. H. R. Bruns*[1], K. J. Herrick[1], K. F. Kalscheur[1], D. J. Schingoethe[1], R. Rosenboom[2], G. Doppenberg[2], and A. R. Hippen[1], *[1]South Dakota State University, Brookings, [2]Deluxe Feeds, Sheldon, IA.*

This research used in situ and in vitro techniques to evaluate the rumen degradability and intestinal digestibility of steam-flaked soybeans (Deluxe Feeds – EnRG Flakes; Sheldon, IA) as well as investigate the effect of particle size on protein and dry matter degradability of steam-flaked soybeans (SFSB). In the first experiment, 3 cannulated, lactating Holstein cows were used to determine rumen protein degradability of SFSB, solvent extracted soybean meal (SSBM), expeller soybean meal (ESBM) and raw, whole soybeans (WSB). The WSB and SFSB were ground through a 2-mm screen and all feeds were ruminally incubated in Dacron bags for 0, 2, 4, 8, 16, 24 or 48 h. Rumen undegradable protein (RUP) was least for WSB, similar for SFSB and SSBM and greatest for ESBM (20.7, 28.3, 30.1, and 52.5%; $P < 0.01$). Intestinally absorbable dietary protein (IADP) ranged widely with WSB being the least absorbable followed by SFSB, SSBM and ESBM (12.6, 23.6, 29.0 and 51.5%; $P < 0.01$). Total digestibility of dietary protein (TDP) was least for WSB followed by SFSB and was greatest for SSBM and ESBM (92.0, 95.4, 98.9 and 99.3%; $P < 0.01$). These results indicated that SFSB are similar to SSBM with regards to ruminal degradability, and have greater overall digestibility than WSB. Previous in situ determinations suggested that particle size may influence rumen degradability parameters of SFSB, thus, a second in situ study evaluated the effects of particle size of SFSB on rumen degradability. In this study, 4 particle sizes (2mm grind, 4mm grind, coarsely chopped, or whole) were compared as described above. Rapidly and potentially degradable protein (fractions A and B) disappearance was similar for all treatments while acid detergent-insoluble protein (fraction C) was greatest in 2mm and 4mm particle sizes and least in chopped and whole SFSB (10.5, 9.9, 6.2, and 6.0%; $P < 0.01$). RUP increased with particle size (30.3, 30.8, 40.8 and 42.2%; $P < 0.01$). Overall, this research demonstrates that decreasing the particle size of SFSB also decreases RUP. Additionally, maintaining whole SFSB results in RUP values greater than that of SSBM and more similar to that of ESBM.

Key words: steam-flaked soybeans, degradability, particle size

M159 A simulation assessment of long-term nitrogen runoff reduction from dairy pastures. R. White* and J. L. Capper, *Washington State University, Pullman.*

A 20-yr assessment was run simulating a pasture on a dairy to determine the effect of various harvesting techniques on Nitrogen (N) removal from the system. The aim was to identify a treatment that resulted in the greatest uptake of N by plant matter thereby diminishing N loss through runoff. Grass, shrubs and trees were modeled to function as they would in a riparian system, grass diffused water to allow absorption by soil, whereas shrubs and trees functioned to absorb nutrients. The pasture was located next to a dairy from which runoff inputs were given as N, Carbon and water sources. Other inputs to the system were historical data for monthly rainfall, temperature and soil attributes. The output was expressed as N runoff from the soil profile. The model was run over 20 yrs to view the long-term consequences of treatments. Mowing, grazing and planting were hypothesized to stimulate a grass density increase inhibiting water flow from the system while pruning and burning plants were thought to stimulate growth and increase nutrient uptake from the soil. These hypotheses were tested via 5 treatments: mowing grass to a stubble height of 0.1 m^2, pruning 1 m^2 from trees and 0.5 m^2 from shrubs, planting 90 kg of grass/acre, grazing of 450 kg of cattle/acre, and burning 70% of the biomass. A total of 4.335 kg N per acre was calculated to runoff during the 20-yr time period. Annual planting in October, burning before yr 5 and pruning after yr 3 were all found to significantly decrease N runoff. When grazing during the spring N runoff increased to 5.16 kg; however, during the winter, runoff did not significantly increase. Mowing did not change N runoff. The most effective reduction resulted from annual fires in the first 5 yrs, pruning annually in August starting in yr 7, grazing cattle annually starting in yr 6 and annual planting of grass in October. This combination of treatments resulted in a runoff reduction to 1.09 kg N, nearly a 75% decrease. This reduction shows that good riparian area management, including use by cattle, can reduce N runoff from dairy pastures.

Key words: nitrogen, runoff, dairy

M160 Characterization of management practices utilized by low somatic cell count Kentucky dairy herds. A. E. Sterrett* and J. M. Bewley, *University of Kentucky, Lexington.*

Recent market changes have renewed interest in lowering bulk tank SCC, particularly in the southeastern United States where the highest SCC in the country is observed. The objective of this research was to summarize management practices utilized by Kentucky dairy herds with low SCC. Herds with an annual mean SCC < 250,000 cells per mL were identified from DHIA and milk cooperative records. A 54 question survey was mailed to 71 producers with 48 producers (67.6%) responding. Herd size ranged from 25 to 750 cows with a mean (±SD) of 144.96 ± 297.39. Mean (±SD) DHIA SCC and producer-reported SCC were 190,333 ± 36,281 (n = 27) and 223,475 ± 71,257 (n = 40) cells per mL, respectively. The most common management practices incorporated by these producers were post-dipping (100%, n = 47), drying teats before attaching milkers (95.8%, n = 46), pre-dipping (91.7%, n = 44), dry treating all quarters of all cows (85.4%, n = 41), incorporating DHIA as a SCC management tool (83.3%, n = 40), using individual towels to dry teats (77.1%, n = 37), receiving bulk tank SCC (77.1%, n = 37), trimming hooves at least annually (75.0%, n = 36), performing a milking system evaluation annually (72.9%, n = 35), and vaccinating for mastitis pathogens (68.8%, n = 33). Of the mastitis vaccines used, J-Vac (Merial Ltd., Duluth, GA) was most common (40.6%, n = 13), followed by J-5 Bacterin (Pfizer Inc., New York, NY) (25.0%, n = 8), Endovac-Bovi (Immvac Inc., Columbia, MO) (15.6%, n = 5), and Lysigin (Boehringer Ingelheim, St. Joseph, MO) (15.6%, n = 5). When asked to identify the management practice that contributed the most to their low SCC level, the most frequently cited practices were (1) keeping cows and facilities clean (n = 31), (2) maintaining dry, clean bedding (n = 14), (3) adhering to a consistent milking routine (n = 10), (4) forestripping (n = 7), and (5) pre- and post-dipping (n = 6). Producers with different housing strategies were represented in this study including freestalls, tie-stalls, compost bedded packs, bedded packs, and no housing. Results of this survey may be used to promote best management practices among other producers attempting to lower SCC.

Key words: best management practices, low SCC, dairy survey

M161 Evaluation of an electronic cow-side glucose meter for diagnosing insulin resistance in Holstein dairy cows. J. A. M. Wittrock*[1], T. F. Duffield[1], S. Riuzzi[2], and S. J. LeBlanc[1], *[1]University of Guelph, Guelph, Ontario, Canada, [2]University of Padua, Padova, Italy.*

The purpose of this study was to evaluate the diagnostic performance of a hand-held electronic glucometer (Precision Xtra; Abbott) for cow-side use in dairy cattle. This device has been validated for measuring blood concentrations of β-hydroxybutyrate in dairy cows. This study was designed to assess the accuracy of whole blood glucose measurements from the glucose meter relative to a reference chemical analyzer in a diagnostic lab. Additionally, the suitability of the glucometer to classify cows as insulin resistant with a glucose tolerance test (GTT) was evaluated with the ratio of (glucose concentration at 80 min after dextrose infusion/concentration before infusion) > 1.05 being defined as insulin resistant. Blood analyzed in the lab were duplicate samples taken from the same cows at the same time, from either serum with the preservative sodium fluoride (gray top tube, the gold standard for glucose analysis) or without any additives (red top tube). Blood samples were collected from cows at time points between 3 wk before and after calving, with the GTT being conducted at 1 or 3 wk before, or 1 week after parturition. There was a strong correlation in 366 samples from 65 cows between the Precision Xtra and serum from samples preserved with NaF ($R^2 = 0.84$, $P < 0.0001$), and in 746 samples from 89 cows between the Precision Xtra and blood without additives ($R^2 = 0.88$, $P < 0.0001$). In 284 glucose-tolerance tests, the Precision Xtra had a sensitivity of 64% and specificity of 92% ($P < 0.0001$) for correctly diagnosing insulin resistance. Dichotomizing at various cut points to identify the optimal test threshold, a cut point of 0.91 for the insulin resistant ratio yielded sensitivity of 90% and specificity of 87% relative to serum preserved with NaF and analyzed in a diagnostic lab. With the identification of a more suitable cut point, and the strong correlation between glucose concentrations obtained from whole blood by the Precision Xtra and serum glucose concentrations, the hand-held glucometer appears suitable for rapid measurement of glucose including glucose tolerance and insulin resistance under field conditions in dairy cattle.

M162 Effect of treatment with human chorionic gonadotropin (hCG) on day 5 after timed artificial insemination (TAI) on fertility in lactating Holstein cows. R. W. Bender*, A. B. Nascimento, A. H. Souza, H. Ayres, R. R. Araujo, J. N. Guenther, and M. C. Wiltbank, *Department of Dairy Science, University of Wisconsin - Madison, Madison.*

Reproductive management programs that synchronize ovulation can result in a smaller than normal follicle potentially resulting in inadequate progesterone (P4) concentrations after AI. The present analysis combining 5 field studies tested the hypothesis that an injection of hCG on d 5 after TAI will raise circulating P4 in diestrus, and consequently improve pregnancies per AI (P/AI). Lactating Holstein cows (n = 2979) from 6 commercial dairy herds in WI had synchronized ovulation and TAI after Presynch-Ovsynch or Double Ovsynch for first AI and Resynch-32 for later AIs, stratified by parity, and breeding number; and then randomly assigned to 2 groups: control (no further treatment, n = 1519) or hCG (Chorulon; 2,000 IU [in 4 of the herds] or 3,300 IU [in 2 herds]; n = 1460). In a subset of cows, blood samples were collected on d 5 and 12 after TAI for analysis of serum P4. Pregnancy was diagnosed by ultrasound at 35 ± 3d after AI. Binomial data were analyzed with Proc Glimmix of SAS with farm and cow treated as random effects. The Mixed procedure of SAS was used to evaluate P4. Circulating P4 concentrations were similar ($P > 0.05$) on d 5, but greater ($P = 0.001$) in hCG (5.3 ng/mL) compared with control cows (4.3 ng/mL) on d 12. Overall Pregnancies/AI (P/AI) was greater ($P = 0.01$) in cows treated with hCG (41.9%; 612/1460) than control cows (37.0%; 562/1519). Interestingly, a 3-way interaction among treatment, parity, and times bred was observed. In primiparous cows, there was greater ($P = 0.013$) P/AI in first service cows treated with hCG (56.2%; 176/313) than controls (46.3%; 152/328). In second service primiparous cows there was greater ($P = 0.012$) P/AI in hCG (40.5%; 90/222) than control (29.2%; 63/216) cows. However, multiparous cows treated with hCG (n = 925) had similar P/AI as controls (n = 975) for both first ($P = 0.26$; 40.5% vs. 37.1%) and later services ($P = 0.13$; 29.6% vs. 34.6%). Thus, targeted use of hCG on Day 5 after TAI increases the circulating P4 on d 12 post AI and enhanced fertility in primiparous cows at both first and later services, but did not increase fertility in older cows.

Key words: hCG, cow, Ovsynch

M163 Evaluation of three-dimensional accelerometers to monitor motion changes relative to estrus behavior. W. A. Smith*, J. M. Bewley, and W. J. Silvia, *University of Kentucky, Lexington.*

Three-dimensional (3D) accelerometers may be used as an estrus detection aid by monitoring changes in cow leg or neck movement. Limited research has been conducted to characterize the changes in movement captured by accelerometers for monitoring estrus behavior. The objective of this study was to utilize a motion index (MI), provided by a commercially available accelerometer, to describe estrus behavior. IceTag (IceRobotics Ltd., Edinburgh, Scotland, UK) accelerometers were attached to 15 Holstein or crossbred cows (DIM 40 to 90) at the University of Kentucky Coldstream Dairy Research Farm. Three IceTags were attached to each cow with high grade Velcro (right rear leg, left front leg, and neck). Cows were synchronized using an OVSYNCH protocol preceded by G6G. The first injection of prostaglandin F2α (PGF) was administered 40 to 90 days postpartum. The OVSYNCH protocol was modified by omitting the last injection of GnRH, allowing for the synchronized expression of estrus. Transrectal ultrasonography was utilized to track follicular development. Beginning 72 h after PGF, behavior observations were recorded. Human observers recorded times when cows were mounting (MG, n=116) other cows and being mounted (MD, n=167), for an 8 h period or until estrus ended. The MI was used to describe the degree of motion (0= no motion), and is defined as total 3D acceleration. A rolling mean (± 2 min) MI was calculated for each estrus event (RME). The GLM procedure of SAS was used to compare RME to the motion index during periods where no estrus behavior (NE) was observed. Least Square Means (LSM ± SE) RME for MD events were significantly higher than LSM for NE (0.847 ± 0.043 ($P < 0.01$), 0.733 ± .038 ($P < 0.01$), 0.05 ± 0.004 ($P < 0.01$) for front leg, hind leg, and neck, respectively). The LSM (± SE) RME for MT events were significantly higher than LSM for NE (0.748 ± 0.043 ($P < 0.01$), 0.727 ± 0.048 ($P < 0.01$), 0.055 ± 0.005 ($P < 0.01$), respectively). Motion index is a useful indicator of estrus behavior.

Key words: estrus behavior, accelerometers, estrus detection

M164 Effects of hutches and fortified waste milk on growth and health in preweaned Holstein dairy calves. . K. L. Machado*[1], R. E. James[1], M. L. McGilliard[1], and T. J. Earleywine[2], *[1]Department of Dairy Science, Virginia Polytechnic Institute and State University, Blacksburg, [2]Land O Lakes Animal Milk Products, Shoreview, MN.*

Large California dairies often find it economical to feed pasteurized waste milk and house calves in elevated wooden crates. The objective of this field study in 2 herds was to evaluate the influence of diet and housing type on growth and morbidity in 84 Holstein heifer calves

in a 2 by 2 factorial experiment. Calves were housed in either plastic hutches or elevated wooden crates with slatted floors. Diets consisted of pasteurized waste milk or the same waste milk supplemented to provide approximately 454 g of additional milk replacer solids containing 25% protein and 10% fat (LOL Balancer) twice daily. Calves were randomly placed in 1 of 4 treatment groups 48 h after birth and were monitored until weaning (60 d of age). Body weights and hip heights were measured at time of enrollment and weaning. Milk samples of pasteurized waste milk were obtained to measure standard plate count 332,171 ± 733,487 cfu/ mL, percent of fat 3.51 ± 0.59, protein 3.13 ± 0.30, and total solids 11.64 ± 1.05. All calves were fed 3.12 L via bottle at 0730 and 1530 h. Calves were monitored daily for respiratory and digestive illness and treated according to protocols. Origin of dairy had no impact on weight gain or hip height. Housing ($P = 0.05$) and diet ($P = 0.01$) affected weight gain, but there was no interaction. Least squares weight gain means for crate and hutches were 0.52 ± 0.024 and 0.59 ± 0.024 kg/d, respectively. Least squares weight gain means for waste milk and balancer were 0.52 ± 0.024 and 0.60 ± 0.024 kg/d, respectively. Calves housed in crates fed balancer had similar gain to calves housed in hutches fed waste milk. Housing or diet did not affect hip height (0.196 ± 0.007). A nonparametric test of maximum fecal score showed no effect due to housing or diet. Calves fed pasteurized waste milk supplemented with balancer or calves housed in plastic hutches had more rapid daily weight gain than calves housed in crates or fed waste milk. The importance of this advantage warrants economic evaluation.

Key words: calves, diet, housing

M165 Effect of postpartum diseases on reproduction of grazing dairy cows. E. S. Ribeiro*, F. S. Lima, H. Ayres, L. F. Greco, R. S. Bisinotto, M. Favoreto, R. S. Marsola, A. P. A. Monteiro, W. W. Thatcher, and J. E. P. Santos, *University of Florida, Gainesville.*

Objectives were to determine the incidence of postpartum diseases and their impact on reproduction of grazing dairy cows subjected to timed AI at the beginning of the breeding season. A total of 957 cows were evaluated in the postpartum period and incidence of diseases recorded. At calving, dystocia, twin birth, stillbirth, and retained placenta were recorded and grouped as calving problem. On d 7 ± 3 and 14 ± 3 postpartum, cows were evaluated for metritis and blood was sampled and analyzed for concentrations of NEFA and BHBA. Cows were considered in severe negative energy balance if NEFA >0.70 mEq/L, and with subclinical ketosis if BHBA >10 mg/dL in at least one of the 2 samples. Clinical endometritis was evaluated on d 28 ± 3 postpartum by scoring the vaginal mucus, and uterine cytology was collected on d 49 ± 3 for detection of subclinical endometritis. Ovaries were scanned on d 35 ± 3 and 49 ± 3 postpartum. Other diseases were also recorded. Cows were then categorized as healthy, when no clinical or subclinical disease was diagnosed, or as having a single or multiple disease events. The body condition was scored on d 7 ± 3, 35 ± 3, 85 ± 3 and 115 ± 3. Cows received timed AI at d 85 ± 3. Pregnancy per AI (P/AI) was determined 30 and 65 d after AI. Data were analyzed using PROC Logistic of SAS with either individual or categories of diseases. Incidence of disease was high and it was associated with reductions in the proportion of cyclic cows and pregnancy per AI. Calving problems and uterine diseases reduced maintenance of pregnancy in grazing dairy cows.

Table 1. Incidence of health problems and their impact on reproduction at first AI

Category	Incidence	Cyclic	Pregnant d 30	Pregnancy loss
Health	41.8	91.6[a]	70.9[a]	10.4
1 case of disease	31.1	90.8[a]	61.4[b]	9.0
> 1 case of disease	27.1	82.2[b]	48.5[c]	15.0
Disease				
Calving problem	8.2	83.6	44.8*	26.9*
Metritis	5.7	73.9*	38.6*	31.2*
Clinical endometritis	14.7	90.2	54.1	20.6*
NEFA > 0.7mEq/L	20.0	82.5*	45.6*	6.6
Subclinical ketosis	35.4	88.1	56.8*	8.3

[a,b,c]Different superscripts differ within a column ($P < 0.05$). *Different from health cows ($P < 0.05$).

Key words: disease, grazing, fertility

Graduate Student Competition: ADSA Production Division
Graduate Student Poster Competition - PhD Division

M166 Effects of using protective cover sheaths at the time of AI on fertility of lactating dairy cows. S. Bas*, G. M. Schuenemann, A. Hoet, E. Gordon, D. Sanders, and K. N. Galvao, *Department of Veterinary Preventive Medicine, The Ohio State University, Columbus.*

The objective of this study was to evaluate the effectiveness of using a disposable sheath protector (SP) on top of the regular AI sheath to minimize contamination of the AI catheter (AIC) on pregnancies per AI (PAI) in lactating dairy cattle. Services (n = 2843) during spring (67%) and summer (33%) from lactating Holstein cows [primiparous (PRIM; n = 1158) and multiparous (MULT; n = 1062)] in 3 commercial herds were included in this study. Animals were presynchronized with 2 injections of PGF2α (PG) given 14 d apart (starting at 26 ± 3 DIM) followed by Ovsynch (GnRH-7d-PG-56 h-GnRH-16 h-Timed AI) or Cosynch (GnRH-7d-PG-72 h-GnRH+Timed AI) 12 d later. Cows presenting signs of standing estrus at any time during the protocol were AI while the remaining cows were subjected to Timed-AI. At the time of AI, services were randomly (every other cow) assigned to 1 of the 2 groups: 1) with (TRT; n = 1405) or 2) without (CON; n = 1438) the use of SP. In TRT, the AIC protected with a SP was introduced into the vagina and only the AIC was manipulated through the cervix into the uterine body for semen deposition. CON cows were AI without the use of SP. Sterile cotton swab samples were collected from the AIC (n = 102) immediately after AI (from TRT and CON) for bacteriology. Pregnancy diagnosis was determined by ultrasonography 40 ± 5 d after AI. Data were analyzed using GLIMMIX (PAI) and FREQ (culture) procedures of SAS. Swab samples revealed that the use of SP was effective in minimizing contamination of the AIC at the time of AI in TRT (51.9%) compared with CON cows (98%; $P < 0.05$). Overall, PAI was greater ($P = 0.01$) for cows in TRT (30.1 ± 1.7%) than in CON (25.4 ± 1.9%). Results from this study suggested that the use of SP reduced contamination of the AIC at the time of AI and improved PAI in lactating dairy cows. To achieve consistent reproductive outcomes over time, the cleanliness of the AI procedure and equipment should not be compromised for convenience.

Key words: dairy cattle fertility, AI, sheath protector

M167 Metabolism of ruminally dosed butyrate and lactose in lactating dairy cows. K. J. Herrick*[1], A. R. Hippen[1], K. F. Kalscheur[1], D. J. Schingoethe[1], S. C. Moreland[2], and J. E. van Eys[2], *[1]South Dakota State University, Brookings, [2]Nutriad Inc., Elgin, IL.*

The objective of this research was to investigate the effect of ruminal butyrate on metabolites of lactating dairy cows. Jugular catheters were inserted into 4 ruminally-fistulated Holstein cows (45.5 ± 2.1 kg milk/d; 152.5 ± 26.9 DIM) in a 4 × 4 Latin square with 3-d periods. At d-1 of each period, 2 h after feeding, cows were ruminally dosed with one of four treatments: 2 L of water (CON), 1 g/kg BW of lactose (LAC), 1 g/kg BW of butyrate (1G), or 2 g/kg BW of butyrate (2G). Sodium butyrate was the source of butyrate and NaCl was added to CON, LAC and 1G to provide equal amounts of sodium as the 2G treatment. All treatments were dissolved in 2 L of water. Serial blood samples were collected at −2, −1, −0.5, 0, 0.25, 0.5, 0.75, 1, 1.5, 2, 3, 4, 6, and 8 h relative to dosing. Samples of rumen fluid were collected at similar intervals. Area under the curve (AUC) was calculated using the pre-dosing values as a baseline to determine treatment response (see table). Butyrate had a significant ($P < 0.05$) effect on plasma glucose and β-OHB and altered rumen VFA. There were no significant ($P > 0.05$) changes in AUC for plasma insulin or NEFA, but there were numerical differences. Milk protein (2.60, 2.85, 2.82 and 3.13%), MUN (11.5, 9.5, 11.8 and 13.4 mg/dL), and fat yield (1.58, 2.29, 1.95 and 1.63 kg/d) for the CON, LAC, 1G and 2G treatments respectively were affected ($P < 0.05$) 24 h post dosing. Rumen pH (6.1, 5.9, 6.3 and 6.6) was increased ($P < 0.01$) by butyrate while AUC for rumen ammonia (−8.1, −22.3, −38.1 and −35.6 mg/dL•h) decreased ($P < 0.01$). Results demonstrate that butyrate dosed in the rumen increases plasma β-OHB and decreases blood glucose.

Table 1. Least squares means of AUC responses by dairy cows to butyrate or lactose

	Treatment[1]				
Metabolite	CON	LAC	1G	2G	SEM
Blood					
Glucose (mg/dL•h)	91.7[a]	−18.7[b]	−76.7[bc]	−131.4[c]	27.3
β-OHB (mM•h)	2.91[b]	2.37[b]	22.3[a]	33.4[a]	3.88
Insulin (μIU/L•h)	−4.9	79.3	68.5	1132.8	651.8
NEFA (μM•h)	−1061.5	−1189.0	−813.0	−523.1	484.1
Rumen					
Acetate (mM•h)	−82.2	93.2	37.3	−39.7	54.8
Propionate (mM•h)	−22.3[ab]	13.3[a]	−3.8[ab]	−32.7[b]	14.8
Butyrate (mM•h)	−14.1[c]	11.4[c]	169.0[b]	575.9[a]	30.9

[1]Least squares means with different superscripts within row differ (P<0.05).

Key words: butyrate, lactose, ketone

M168 Antioxidant activity of calf milk replacers. M. A. Soberon*, D. J. R. Cherney, and R. H. Liu, *Cornell University, Ithaca, NY.*

A milk replacer (MR) is designed to mimic the nutritional benefits of milk in an effort to nourish a newborn calf, reduce calf mortality, strengthen immunity and increase animal life span and productivity. Antioxidants (AO) can enhance immune defense by reducing oxidative damage, but milk replacers are traditionally not formulated for AO activity. The objective of this study was to compare total AO activities of bovine milk with 6 calf MR (Table 1), varying in amount and source of fat and protein. MR was donated by Milk Products, Inc. Milk was obtained from the Cornell Dairy Research Farm bulk tank, representing milk produced within 24 h by 455 cows. MR was mixed to 150 g/L with 40°C, purified water. All samples were extracted in triplicate. Following hexane lipid extraction, both milk and MR samples were extracted 5 times with ethyl acetate, and then evaporated and reconstituted with 70% methanol/water. Samples were assessed for total AO activity using the peroxyl radical scavenging capacity assay where each sample was diluted to 5 descending concentrations, plated in triplicate. Ascorbic and gallic acids were standards for each plate. Results for total AO activity are expressed as umol of vitamin C equivalent(VCE)/mL of milk or reconstituted MR. The only known distinguishing feature of MR A, which exhibited the highest total AO activity (86.0 umol VCE/mL; $P < 0.001$) is its soy protein whereas natural bovine milk (52.7 VCE/mL) is distinguished by its increased fat content. Fat ($P = 0.057$) as opposed to protein ($P = 0.140$) content

may have an effect on AO activity. Total fat content may explain the difference between the 2 MR with similar amounts of NeoTec4, a commercial essential fatty acid supplement, (44.2 umol VCE/mL versus 14.9 umol VCE/mL). Future research is warranted to compare MR with a broader range of fat content as well as the effect of additional compounds in milk that may impact AO activity.

Table 1. Characterization of milk and milk replacers

ID	Description	Protein Source	Animal Fat, %	Vegetable Fat, %	VCE, umol[1]	SE
A	21% CP, 20% fat	50% milk, 50% soy	100	0	86.0[a]	1.92
Milk	Bovine milk; 27% CP, 29% fat	milk	100	0	52.7[b]	1.92
B	NeoTec4; 22% CP, 20% fat	milk	98.4	1.56	44.3[c]	1.92
C	20% CP, 20% fat	milk	100	0	16.1[d]	2.35
D	NeoTec4; 28% CP, 18% fat	milk	98.6	1.39	14.9[d]	1.92
E	28.5% CP, 15% fat	milk	100	0	12.1[d]	1.92
F	5% plasma; 22% CP, 20% fat	animal	100	0	10.5[d]	1.92

[1]Means with different superscript differ, $P < 0.001$.

Key words: antioxidant, milk replacer, calf

M169 In situ ruminal degradability of diets, dried distillers grains with solubles and soybean meal under different rumen conditions. 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 in situ degradability of diets, distillers grains with solubles (DG) and soybean meal (SBM) under different ruminal conditions. Four Holstein cows with ruminal fistulae were assigned to a 4 × 4 Latin square in a 2 × 2 factorial arrangement of treatments. Diets contained low forage (LF; 41% of diet DM) or high forage (HF; 60% of diet DM) and DG 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 DG from 0% DG diets to formulate 18% DG diets. Dacron bags containing DG, SBM, and dietary TMR were incubated in duplicate in the rumens of the cannulated cows at 0, 2, 4, 8, 12, 24, 48, and 72 h on d 15 each period. Each TMR was incubated only in cows assigned to the corresponding diet. Rumen passage rate (Kp) was greater for HF (6.2 vs. 6.6%/h) and 0 DG (6.5 vs. 6.3%/h) diets. Effective degradability (ED) of DM for TMR was lower for 18% DG diets (64.8 vs. 62.7%). Similarly, ED of DM for DG (55.8 vs. 55.0%) and SBM (72.0 vs. 70.1%) were lower in 18% DG diets. For TMR, ED of NDF was greater in HF (28.0 vs. 34.5%) and 18% DG diets (29.9 vs. 32.6%) whereas ED of NDF for DG was greater in HF diets (37.1 vs. 40.4%). ED of CP for TMR was lower in HF (54.7 vs. 53.3%) and 18% DG diets (54.9 vs. 53.0%). Similarly, ED of CP for DG was lower for HF (50.6 vs. 48.6%) and 18% DG diets (50.1 vs. 49.0%). For SBM, CP was degraded to a lower extent for the 18% DG diets (62.7 vs. 60.4%). Results suggest that forage and DG concentration in diets affect ruminal degradability of nutrients.

Table 1.

	ED, %					
	LF	LF	HF	HF		
Feed	0DG	18DG	0DG	18DG	SEM	P^1
TMR-DM	64.8	62.5	64.8	63.0	0.74	D
NDF	27.7	28.2	32.0	37.0	1.54	F, D, F×D
CP	54.9	54.5	55.0	51.6	0.93	F, D, F×D
DG -DM	55.7	55.2	55.9	54.8	0.71	D
NDF	38.1	36.2	40.3	40.5	1.42	F
CP	51.0	50.1	49.3	47.9	0.59	F, D
SBM-DM	71.4	70.7	72.5	69.4	0.99	D, F×D
CP	62.6	61.4	62.8	59.4	1.19	D

[1]F or D = Forage or DG effect; F×D = Forage and DG interaction ($P < 0.05$).

Key words: distillers grains, forage, in situ

M170 Effect of air-flow controlled chambers and cows of contrasting feed efficiency on methane emission. C. Arndt*[1], M. A. Wattiaux[1], J. M. Powell[2], and M. J. Aguerre[1], *[1]Department of Dairy Science, University of Wisconsin, Madison, [2]USDA-ARS U.S. Dairy Forage Research Center, Madison, WI.*

The objective of this study was to determine the effect of chamber on methane (CH_4) emission, the number of days needed for adaption to chambers (using DMI as an indicator), and CH_4 emission between 2 high feed efficient (HE) and 2 low feed efficient (LE) cows (2nd parity, 101±11 DIM) as determined by MY/DMI. Emission of the 4 individual cows was measured in 4 chambers in a modified tie-stall barn. Cows were rotated among chambers every 4 d and measurements during each 4 d period included DMI, MY, and CH_4 emission (average duration of CH_4 measurements 18.5 h/d, using a Photo-acoustic Multi-gas Monitor; Innova Model 1412). All cows were fed the same TMR at 0800h and were milked twice daily. Data was analyzed as a 4x4 Latin square design with proc mixed procedure of SAS assuming cow efficiency as fixed treatment effect (1 df), cow within feed efficiency as random effect (2 df term used to test cow efficiency), days as repeated measures, and chamber and period as blocking factors. Chamber did not affect CH_4 emission ($P = 0.38$). An effect of period and period by day interaction ($P < 0.05$) was observed for DMI. Dry matter intake was greater in period 4 (28.8 kg/d) than in period 1 and 2 (averaged 26.3 kg/d), but not period 3 (27.4 kg/d). Although no consistent patterns were detected, DMI differed among days within all periods except period 4. These results suggest that cows were adapted to chambers by the beginning of period 4, although rotation among chambers may have extended required time for adaptation. Compared to LE cows, HE cows (1.90 vs. 1.52 (MY/DMI); $P = 0.01$) tended to have a greater MY (50.3 vs. 42.2 kg/d; $P = 0.06$), lower CH_4 emission (802 vs. 1000 g/d; $P = 0.08$), CH_4/DMI (30.3 vs. 36.0 g/kg; $P = 0.10$), CH_4/MY (16.0 vs. 23.7 g/kg; $P = 0.01$), and $CH_4/(NE_l+NE_m)$ (19.3 vs. 24.5 g/Mcal; $P = 0.02$). Although the effect of feed efficiency was tested against 2 degrees of freedom only, our preliminary results suggested that HE was associated with lower CH_4 emission. In addition, designs of future experiments do not require rotation of treatments among the chambers, which had no effect on CH_4 measurements in this study.

Key words: methane, feed efficiency, chambers

M171 Comparison of two resynchronization protocols initiated at different intervals after insemination on fertility in lactating dairy cows. R. G. S. Bruno*[1,2], J. G. N. Moraes[3], J. A. Hernández-Rivera[1,2], K. J. Lager[1,2], P. R. B. Silva[3], A. L. A. Scanavez[3], L. G. D. Mendonça[3], R. C. Chebel[3], and T. R. Bilby[1], *[1]Texas AgriLife Research and Extension Service, Texas A&M System, College Station, [2]Department of Agricultural Science, West Texas A&M University, Canyon, [3]Department of Veterinary Population, University of Minnesota, St. Paul.*

The objective of this study was to evaluate effects of 2 resynchronization timed AI (TAI) protocols beginning at different intervals after AI on fertility in dairy cows. Lactating cows from 2 dairies located in TX (n = 2233) and MN (n = 3077) were assigned to 1 of 4 TAI protocols 17 ± 3 d after AI. All cows were examined for pregnancy 31 ± 3 d after AI. Cows assigned to EOV or OV received the OvSynch56 starting 24 or 31 d after AI, respectively. Cows assigned to EGGPG or GGPG received a presynchronizing GnRH 17 or 24 d after AI, respectively, 7 d before the start of OvSynch56. Any cow observed in estrus was AI on the same day. Ovaries were examined and blood was sampled for progesterone concentration (P4) on day of first GnRH and PGF of Ovsynch56. Pregnancy was diagnosed at 31 and 66 d after resynchronized AI. Fewer EGGPG ($P < 0.01$) and more OV ($P < 0.01$) cows were re-inseminated in estrus (EGGPG = 23.7, GGPG = 49.0, EOV = 41.6 and OV = 57.6%). Treatment did not affect ($P > 0.66$) P/AI at 31 or 66 d for cows re-inseminated in estrus. Cows re-inseminated in estrus, however, had greater ($P < 0.01$) P/AI at 31 (40.0 vs. 27.5%) and 66 d (36.0 vs. 23.9%) than cows that received TAI. Among cows completing the TAI protocols, EOV reduced ($P < 0.03$) P/AI at 31 d (EOV = 22.2, EGGPG = 30.3, GGPG = 28.3, OV = 28.7%). Overall P/AI at 31 d after AI was reduced ($P < 0.01$) in EOV (29.3%) compared with other treatments (OV = 34.6, EGGPG = 33.3, and GGPG = 34.3%). However, treatment did not affect ($P = 0.11$) P/AI 66 d after re-insemination (EOV = 26.1, EGGPG = 29.4, GGPG = 30.4, OV = 30.4%). On day of first GnRH of Ovsynch56, more EGGPG and GGPG cows had CL (EGGPG = 83.8, GGPG = 88.8, EOV = 76.6, OV = 73.2%, $P < 0.01$) and P4 > 1ng/mL (EGGPG = 63.1, GGPG = 76.3, vs. EOV = 50.0, OV = 59.0%, $P < 0.01$). However, percentage of cows ovulating to first GnRH of Ovsynch56 was not affected ($P = 0.91$) by treatment. In conclusion, early start of resynchronization and presynchronization with GnRH reduced number of cows re-inseminated in estrus. Neither the timing nor the resynchronization protocol affected overall P/AI.

Key words: dairy cows, GGPG, resynchronization

M172 Antimicrobial usage on large herds in Wisconsin. L. Oliveira* and P. L. Ruegg, *University of Wisconsin, Madison.*

The objective of this study was to describe the antimicrobial usage on dairy herds in Wisconsin. A survey was conducted (March to August, 2010) in 50 dairy herds with >200 lactating animals. The questions included information about inventory and expansion, production, clinical and subclinical mastitis, dry-off therapy, pre-calving heifers, respiratory disease, uterine infections, foot problems, diarrhea, calves, and feeding. A total of 33,935 lactating cows were included, herd size ranged from 170 to 2,728 lactating cows, and daily milk production per cow was 33 kg. Occurrence of mastitis, respiratory diseases, and uterine infection were reported for all participants, but only 36% (n = 18) reported occurrence of diarrhea in adult cows. Dry cow therapy was used in all herds and 46% (n = 23) of the herds had used the same treatment over the last 5 years; preferred drugs were penicillin and streptomycin (n = 37 farms). Internal teat sealant was used in 84% (n = 42) of farms but only 16% (n = 8) use external sealant. Eight intramammary antimicrobials were used to treat mastitis and the most common were ceftiofur (n = 45 farms) and pirlimycin (n = 29 farms). Almost all farms use systemic antimicrobial to treat clinical mastitis, and the preferred drug was ampicillin (n = 20 farms). On 14% (n = 7) of the dairy herds, sulfadimethoxine was used to treat mastitis. On 40% (n = 20) of the herds, pre-calving heifers were treated with antimicrobials to treat or prevent mastitis. For respiratory disease in adult cows, farmers used from 1 to 5 drugs, and preferred drugs were ceftiofur and florfenicol. For uterine infection and foot problems, the preferred drugs were ceftiofur and ampicillin. For disease in calves such as respiratory disease and diarrhea, the preferred drug used was tulathromycin. On 22% of farms, calves were fed with medicated milk replacers; on 50% of farms, calves were fed with medicated calf starter. Results showed that antimicrobials were used extensively on dairy herds and ceftiofur was the most widely used. Further investigation will quantify antimicrobial drug usage on farms.

Key words: antimicrobial usage, dairy farm, disease

M173 Milk production, milk composition and first service pregnancy rate in lactating Holstein cows fed a lipid-encapsulated supplement containing *trans*-10, *cis*-12 and *cis*-9, *trans*-11 conjugated linoleic acids. C. L. Bailey*, R. G. Morell, B. L. Fisher, B. F. Jenny, G. T. Gentry, K. R. Bondioli, R. A. Godke, and C. F. Hutchison, *Louisiana State University Agricultural Center, Baton Rouge.*

Primiparous (n = 15) and multiparous (n = 24) Holstein females were randomly allotted to experimental diets after stratification by previous (cows) or expected (heifers) milk production, lactation number and expected date of parturition. Cows received a corn silage based TMR enriched with either a lipid-encapsulated supplement containing trans-10, cis-12 and cis-9, trans-11 conjugated linoleic acids (CLA) or a rumen-protected calcium salts of palm oil. Diets were formulated to be isoenergetic and isonitrogenous and to provide 100 g per hd/d supplement to respective treatment diets from parturition through 118 ± 14 DIM. Milk yield was assessed at each of 2 daily milkings by electronic meters and milk composition was analyzed weekly from consecutive AM and PM milk samples. Cows were estrous synchronized for fixed-time artificial insemination (FTAI; 98 ± 8 DIM) using a modified Double Ovsynch protocol. Pregnancy status was assessed at 34 ± 5 d of gestation by transrectal ultrasound or return estrus was recorded. Milk yield, milk composition and BW were analyzed using the GLM procedure and pregnancy status was analyzed using chi-squared (SAS). Body weight was similar between treatment groups ($P \geq 0.76$) at 12 ± 2 DIM (610 ± 16 kg) and 94 ± 2 DIM (620 ± 17 kg). Mean weekly milk yield was greater ($P = 0.002$) for cows fed CLA (38.5 ± 0.5 kg) compared with cows fed Ca salts (36.3 ± 0.5 kg). Percent milk fat ($P < 0.001$) and milk fat yield ($P = 0.002$) were reduced in cows fed CLA compared with cows fed Ca salts (3.25 vs. 3.92 ± 0.05%; 1.33 vs. 1.53 ± 0.04 kg, respectively). Percent protein ($P = 0.24$), protein yield ($P = 0.35$), energy corrected milk ($P = 0.98$) and 3.5% fat corrected milk ($P = 0.08$) were not influenced by dietary treatment. First service pregnancy rate was similar ($P = 0.30$) between cows supplemented CLA (n = 8/16, 50.0%) and Ca salts (n = 5/17, 29.4%), respectfully. The lipid-encapsulated CLA appears to be a viable supplement for lactating cows and deserves further investigation.

Key words: dairy cows, dietary fat supplementation, milk production

M174 A hoof biopsy procedure of front and rear claws for gene expression analysis and its relation to locomotion in dairy cows. J. S. Osorio*, E. F. Garrett, B. C. Fraser, D. E. Graugnard, J. K. Drackley, and J. J. Loor, *University of Illinois, Urbana.*

Lameness represents a significant health problem and one of the main causes of death in dairy cows in the USA. Impacts of environmental and dietary factors such as floor system hoof trimming, and dietary carbohydrate overload have been assessed through behavioral indicators including time budgets and locomotion scores, as well as hoof appearance and incidence and severity of hoof diseases. Evaluation of post-mortem corium tissue has generated important information at the molecular level on these effects. The current experiment was conducted to evaluate a biopsy procedure to extract tissue specimens through the hoof wall between the epidermis and pedal bone of dairy cows via regional anesthesia. The aims of the experiment were to: 1) determine the feasibility of performing hoof biopsies without impairing locomotion or inducing pathological alterations of affected tissues; 2) evaluate the feasibility of using biopsied tissue for RT-PCR by analyzing quantity and purity of extracted RNA; and 3) compare relative expression by claw position of genes involved in cell differentiation, proliferation, inflammation, and keratin formation. Biopsies were performed on 6 Holstein cows yielding 2 tissue specimens per cow from front and hind limbs. Cows were monitored for lameness daily for 7 d after biopsy and then weekly for 8 wk. Total RNA yield from tissue was within acceptable ranges (4.64–23.84 ug). Preliminary analysis by claw position showed that the transcription regulator NFKB1 had greater expression ($P = 0.02$) in front than rear claws. Also, within medial and lateral hind claws there was a tendency ($P = 0.09$) for greater expression of NFKB1 in lateral claws. Other genes of interest included SOD2, KLF10, NR3C1, SAA3, STAT3, MYD88, and TLR4. Lameness assessment after biopsies did not reveal difficulty in the cow's locomotion. Overall, results suggest that this hoof biopsy procedure was suitable to obtain and analyze laminar corium tissue at the molecular level. Further research using this procedure on peripartal cows is warranted, for example to assess the effects of prepartal plane of nutrition on hoof transcriptomics.

Key words: laminitis, gene expression, biopsy

M175 Variation in failure of passive transfer and growth rates of calves on 38 farms in British Columbia. G. B. Bond, M. A. G. von Keyserlingk, G. Zobel*, and D. M. Weary, *Animal Welfare Program, University of British Columbia, Vancouver, BC, Canada.*

Two basic indicators of success in calf rearing programs are failure of passive transfer (FPT) of immunoglobulins from colostrum, and growth rates, but little data are available to producers to benchmark their performance against industry norms. The aim of this study was to describe variation among farms in FPT, calf weight gains during the milk-feeding period (<8 wk of age), and weight gains of older heifers (11 to 20 mo of age). Thirty-eight farms were randomly selected in the lower Fraser Valley region of British Columbia within the criteria that herds were registered Holsteins, using the DHI recording system, and with a minimum of 50 heifer calves born per yr. Blood was sampled from 10 calves (2 wk old or less) per farm, and FPT defined as age corrected serum protein < 5.5 g/dL. Heart girth tapes were used to estimate BW (using 14 ± 5 pre-weaned calves and 17 ± 6 older heifers per farm); gains were estimated using the within-farm slope from the line equation, BW = age. Serum protein averaged 5.9 ± 0.4 g/dL. FPT averaged 31 ± 25%; 7 of the 38 farms had 100% success, but on 10 farms more than 50% of the calves failed. ADG pre-weaning averaged 0.7 ± 0.2 kg/d, but was highly variable (among farm range 0.4 to 1.2 kg/d). ADG for older heifers averaged 0.8 ± 0.1 kg/d, and was less variable (among farm range 0.6 to 1.0 kg/d). These results provide benchmarking data for producers, and illustrate that low rates of FPT and gains averaging 1 kg/d are achievable for farms in this region.

Key words: calf welfare, benchmarking, on-farm assessment

M176 Comparisons of udder health and milk quality in North Carolina organic and conventional pasture-based dairy herds. K. Mullen*, L. Gentry, R. Lyman, S. Washburn, and K. Anderson, *North Carolina State University, Raleigh.*

This observational study compared milk quality and herd health management of 7 organic and 7 conventional dairies in North Carolina. Published comparisons between organic and conventional dairy systems with regard to milk quality are sparse for the southeastern region of the United States. Management practices vary between organic and conventional dairies because of differences in farming philosophy and in government regulations. Organic dairies are prohibited from using certain drugs and antibiotics that are commonly used on conventional dairies. The objective of this study was to elucidate the relationship between management type and milk quality. To assess milk quality, milk samples were aseptically collected from each quarter of each cow in the milking herd at the time of sampling and somatic cell scores were obtained for individual cows. A total of 4988 quarter milk samples (2608 conventional, 2380 organic) were collected from 1247 cows (652 conventional, 595 organic). Milk samples were cultured and bacterial growth was identified using protocols consistent with those of the National Mastitis Council. The proportion of cows with positive microbiological results did not differ ($P > 0.10$) between organic (56.1%) and conventional (52.9%) dairies. However, differences in species present in positive cultures were observed: conventional herds had significantly more (22.4% vs. 15.3%, $P < 0.01$) coagulase-negative staphylococci infections per cow whereas organic herds had more *Corynebacterium* sp. (12.9% vs. 4.1%, $P < 0.01$) and *Staphylococcus aureus* (12.6% vs. 8.1%, $P < 0.01$) infections per cow. Conventional herds did have a lower proportion of infected quarters (27.0% vs. 36.3%, $P < 0.001$). Somatic cell scores did not differ between organic (3.0 ± 0.1) and conventional (3.0 ± 0.1) herds. Despite differences in herd management, milk culture results and SCS measurements were remarkably similar between organic and conventional NC dairies compared for this study.

Key words: mastitis, comparison, organic

M177 Effect of conjugated linoleic acid supplementation on in vitro bovine embryo production and cryopreservation. V. A. Absalón Medina*[1], S. J. Bedford Guaus[1], R. O. Gilbert[1], L. C. Siqueira[2], G. Esposito[3], A. Schneider[4], S. H. Cheong[1], and W. R. Butler[1], *[1]Cornell University, Ithaca, NY, [2]Universidade Federal de Santa Maria, Santa Maria, RS, Brasil, [3]Università degli Studi di Napoli Federico II, Portici, Napoli, Italia, [4]Universidade Federal de Pelotas, Pelotas, RS, Brasil.*

Conjugated linoleic acid isomers (CLAs) and other polyunsaturated fatty acids can affect the membrane lipid profile and signaling in cells thereby altering their function. The objectives were systematic evaluation of in vitro supplementation of CLA isomers (c9,t11 and t10,c12) on bovine oocytes or parthenotes (experiment 1) and fertilized preimplantation embryos (experiment 2 and 3) and to assess the optimal dose(s), and/or developmental stages during culture. The effects of CLAs on

embryonic survival after vitrification (experiment 4) were also evaluated. A total of 6267 oocytes were used in this project. Higher doses (50, 100, 200 μM) of CLA during in vitro maturation (IVM), or during the entire in vitro embryo culture (IVC) were compared with lower doses (15, 25, 50 μM) for effects before and after activation on subsequent development of bovine parthenotes. Low doses of both isomers tested the effect of CLAs on performance of fertilized embryos during IVM/IVC. Experiment 3 examined lowest doses (15, 25 μM) of CLA at specific stages during culture (i.e., IVM vs. IVC only) and finally, resistance to cryopreservation viz. post thaw survival rates of vitrified embryos supplemented with CLA was assessed. Overall, parthenotes and preimplantation embryo blastocyst rates (~35%) were not different among low CLAs levels ($P > 0.05$). Although low CLA resulted in better blastocyst rates for fertilized embryos, higher CLAs concentration (≥100 μM) reduced blastocyst rates to 7–15%. Vitrifying embryos after supplementation with 100 μM c9,t11 for a short period of time resulted in high survival rates comparable to the vitrified control (38 and 35%, respectively), but importantly the development of thawed embryos was comparable to control embryos not undergoing cryopreservation (total cell count equaled 161 ± 43 vs. 174 ± 39 [$P > 0.05$], respectively). In conclusion, no beneficial effect of supplemental CLA was found on embryo performance, however, inclusion of 100 μM c9,t11 before vitrification improved post thaw survival and development of bovine embryos.

Key words: CLA, parthenogenetic activation, bovine in vitro fertilization

M178 Net requirements of calcium and phosphorus for gain of Nellore and Nellore x *Bos taurus* crossbreds. M. P. Gionbelli*[1], M. I. Marcondes[1,3], S. C. Valadares Filho[1,3], L. F. Prados[1], and M. L. Chizzotti[2], *[1]Universidade Federal de Viçosa, Viçosa, MG, Brazil, [2]Universidade Federal de Lavras, Lavras, MG, Brazil, [3]Instituto Nacional de Ciência e Tecnologia - Ciência Animal, Brazil.*

This study aimed to understand and estimate net requirements of calcium (Ca) and phosphorus (P) for gain of Nellore and crossbred Nellore × *B. taurus* cattle. A database containing 283 animals from 11 comparative slaughter studies was used. There were 190 Nellore and 93 Nellore × *B. taurus*, being 99 intact males, 115 steers, and 69 heifers. Allometric and quadratic regression models were used to describe the relationship between Ca and P in the equivalent EBW (EQEBW, kg). It was also determined the point at which there was no more significant addition of these mineral in the EQEBW by the linear plateau method. This represents the point at which the net requirements of these minerals for gain are considered equal to zero. Allometric and quadratic equation allowed equal adjustments, although quadratic equation represents better the biological deposition of Ca and P. There was a linear reduction in the net requirement of Ca and P per unit of gain due to the increase of animal weight (Table 1). The plateaus of deposition of Ca and P were observed at 413 kg of EQEBW (470 and 497 kg of SBW for Nellore and Crossbred, respectively) for Ca and 412 kg of EQEBW (468 and 495 kg of SBW for Nellore and Crossbred, respectively) for P. Therefore, utilization of a common plateau for Ca and P at 412 kg of EQEBW is suggested. The effects of gender and genetic group were not tested, however the breed impact seems to be well controlled, given that the EQEBW adjusts the degree of maturity. We conclude that the net requirements for Ca and P in Nellore and Crossbred decrease with the increase of BW and reaches zero with 412 kg of EQEBW. Acknowledgment: Sponsored by INCT-Ciência Animal, Brazil.

Table 1. Allometric and quadratic equations and net requirements for Ca and P for Nellore and Crossbred cattle

Mineral	Model	Equation
Calcium	Allometric	Ca_{EBW} (kg) = 0.17 × $EQEBW^{0.60}$
		NRG_{Ca} (g) = EBG × (102 × $EQEBW^{-0.40}$)
	Quadratic	Ca_{EBW} (Kg) = 0.2 + 0.024 × EQEBW – 0.0000225 × $EQEBW^2$
		NRG_{Ca} (g) = EBG × (24 – 0.045 × EQEBW)
Phosphorus	Allometric	P_{EBW} (kg) = 0.042 × $EQEBW^{0.71}$
		NRG_P (g) = EBG × (29.8 × $EQEBW^{-0.29}$)
	Quadratic	P_{EBW} (Kg) = – 0.3 + 0.013 × EQEBW – 0.0000119 × $EQEBW^2$
		NRG_P (g) = EBG × (13 – 0.0238 × EQEBW)

Key words: allometric, quadratic, beef

M179 Effects of maternal body condition and breeding season forage type on beef heifer growth. J. D. Patterson*[1], M. L. Looper[2], B. C. Williamson[1], and C. F. Rosenkrans[1], *[1]University of Arkansas, Fayetteville, [2]USDA/ARS DBSFRC, Booneville, AR.*

Gestational malnutrition of the dam may affect postnatal growth of offspring. Our objective was to determine effects of forage type grazed during conception and body condition (BC) during pregnancy of cows on heifer growth. Brahman-influenced cows (n = 40; BCS = 5.9 ± 0.1) were assigned to graze either common bermudagrass (CB) or toxic tall fescue (E+) during a 60-d breeding season; BC was assessed at d 0, 30, and 60 of the breeding season. Cows were classified into 1 of 2 BCS change categories: gain/maintain (n = 22 cows; mean gain = 0.8 BCS units) or lose (n = 18 cows; mean loss = 1.1 BCS units) BC during the first 2 trimesters of pregnancy. Cows were managed to achieve marginal (BCS = 4.3 ± 0.8) or good (BCS = 6.3 ± 0.8) BC during the last trimester. Birth weight of heifers was recorded. During development, heifers were equally assigned to CB or E+ and weaning weight (WW), hip height (HH), hip width (HW), pelvic height (PH), pelvic width (PW), and pelvic area (PA) were measured at 9 to 10 mo of age. Influence of forage, BC, and BC change on heifer growth was determined by ANOVA. Cows grazing E+ had heifers weighing less ($P < 0.01$) at birth (32.7 ± 0.8 kg) compared with heifers from cows grazing CB (35.6 ± 0.6 kg). Change in BC of cows during the first 2 trimesters did not influence ($P > 0.10$) birth weight, WW, HW, PH, PW or PA; HH tended ($P = 0.12$) to be increased in heifers (117 ± 1 cm) from cows losing BC during the first 2 trimesters compared with heifers (115 ± 1 cm) from cows gaining BC. Heifers (244 ± 7 kg) from cows in good BC tended ($P < 0.10$) to have heavier WW than heifers (228 ± 7 kg) from cows in marginal BC during the last trimester. Actual BCS of cows during the last trimester was correlated ($P < 0.05$) with birth weight (r = 0.34), WW (r = 0.40), HW (r = 0.38), and tended ($P < 0.10$) to be correlated with heifer HH (r = 0.27). Consumption of toxic tall fescue during breeding may reduce birth weight of subsequent offspring. Further, BC loss in cows late in gestation can decrease WW of their calves. Improper nutrition during conception, gestation, or both may impact postnatal growth.

Key words: beef cow, body condition, postnatal growth

M180 Effects of colostrum intake and pre-weaning nutrient intake on post-weaning feed efficiency and voluntary feed intake. F. Soberon* and M. E. Van Amburgh, *Cornell University, Ithaca, NY.*

Non-nutritional factors in colostrum have long been recognized as valuable for the development of the newborn calf, however, the benefits of colostrum intake surpass those related to the immune system. We hypothesized that some of the non-nutritional factors in colostrum as well as the nutrient availability during the pre-weaning period have permanent effects on feeding behavior or efficiency of nutrient utilization. Calves were fed either 2 L (n = 19) or 4 L (n = 32) of pooled colostrum, within 1 h of birth. Calves receiving 4 L of colostrum were fed another 2 L of colostrum 12 h after the first feeding while the calves fed 2 L were fed 2 L of milk replacer (MR, 28% CP, 15% fat, Excelerate, MSC). Plasma IgG content was determined for all calves 24 to 48 h after the first colostrum feeding. After the second feeding, all calves were fed MR by an automated feeder (Förster-Technik). Half of the calves on each colostrum treatment were allowed to consume 4 L/ d of MR while the other half were allowed to consume up to 12 L/d and intake was recorded by the feeders. Calves had access to a calf starter. All calves were weaned at 52 d and offered the same ration and DMI was recorded daily for 1 mo post weaning. All calves had plasma IgG concentrations above 12 mg/mL. Treatment comparisons were made using the mixed procedures of SAS and significance was determined at $P < 0.05$. Calves fed 4 L MR had similar ADG pre-weaning regardless of colostrum (0.35 ± 0.04 kg/d, $P = 0.56$). However, calves offered 12 L/d MR demonstrated greater ADG when they had 4 L of colostrum at birth (0.78 kg/d vs. 0.55 kg/d, $P < 0.01$). Also, during the post-weaning period, calves fed 4 L colostrum had greater DMI than calves receiving 2 L of colostrum independent of previous MR intake (2.8 vs. 2.2 kg/d;

$P = 0.01$). Calves that received 4 L of colostrum also had greater feed efficiency regardless of MR treatment (0.38 vs. 0.32 kg gain:kg DM, $P = 0.02$). We concluded that some non-nutritional components of colostrum are altering metabolic programming responsible for regulating appetite and nutrient utilization in calves.

Key words: colostrum, feed efficiency, appetite

M181 Interactions of residual feed intake and other performance parameters of Japanese Black (Wagyu) bulls. M. McGee*[1], C. M. Welch[1], J. B. Hall[2], and W. Small[3], *[1]University of Idaho, Moscow, [2]University of Idaho Nancy M. Cummings Research, Education, and Extension Center, Carmen, [3]AgriBeef Snake River Farms, American Falls, ID.*

Wagyu cattle are unique due to a propensity for accumulation of extraordinary levels of intramuscular fat as animals mature. Unfortunately, the Wagyu breed exhibits slow growth and poor feed efficiency. Objectives of the present study were to characterize these performance parameters, to accumulate data describing performance of Wagyu cattle, and to improve growth and feed efficiency while simultaneously optimizing marbling. Ninety–2 yearling Wagyu and Wagyu cross bulls were evaluated for residual feed intake (RFI) and other performance variables during a 70-d RFI test. Individual daily feed intake (GrowSafe, Alberta, Canada) and BW gain (BW measured at the beginning and end of test and at 2-wk intervals) were recorded. During the test period, bulls were fed a corn–based TMR (1.90 Mcal/kg NEm, 1.25 Mcal/kg NEg, 15.05% CP) formulated to match the nutritional equivalent of the diet fed to finishing Wagyu cattle. The RFI was positively correlated with DMI (r = 0.56; $P < 0.0001$) and F:G ratio (r = 0.49; $P < 0.0001$) but was not correlated with ADG, metabolic BW, ultrasound REA, or ultrasound rib fat. There was a tendency toward a favorable correlation between RFI and IMF (r = −0.17; $P = 0.11$). To facilitate further analysis, bulls were classified into RFI groups as efficient (n = 32), marginal (n = 34), and inefficient (n = 26), based on deviations from the mean RFI value. The RFI groups exhibited differences in F:G ratio ($P = 0.003$), and DMI ($P < 0.0001$), but there were no differences for metabolic BW, ADG, or ultrasound estimates of IMF, REA, and rib fat. The inefficient group had greater DMI ($P < 0.0001$) and F:G ratio ($P = 0.0003$) than the efficient group. The marginal group also had greater DMI ($P < 0.0001$) than the efficient group. This phenotypic evaluation of Wagyu bulls provides an indication that RFI is related to other measures of intake and feed efficiency, however does not influence growth and carcass performance. It is expected that accumulation of these data as greater numbers of bulls are characterized will facilitate simultaneous improvements in feed efficiency, BW gain, and optimized marbling in Wagyu cattle.

Key words: Wagyu, residual feed intake, efficiency

M182 Feeding or passive transfer of Anti-IL-10 peptide antibodies suppresses growth and feed efficiency in chicks. J. M. Sand*, J. Abazi, T. Fullmer, and M. E. Cook, *University of Wisconsin-Madison, Madison.*

Previous work from our lab showed that feeding antibody to the pro-inflammatory protein secretory phospholipase A2 (sPLA2) increased chick growth and feed efficiency (Cook ME, 2004 J. Appl. Poult. Res. 13:106–119). Here we attempt to suppress chick growth rate and or feed efficiency using an antibody to chicken interleukin-10 (IL-10), a cytokine responsible for downregulation of inflammatory processes. Egg antibody directed against 4 hydrophilic, antigenic, and accessible peptides of IL-10 were produced in Single Comb White Leghorn laying hens and measured using ELISA. Egg yolks were collected and lyophilized; the yolk powder was then added to feed at 3.41 g/kg feed to determine chick response. Treatment differences were determined using a 2-sided *t*-test. Anti-IL-10 peptide 4 (EPTCLHFS) suppressed growth in a study of mixed-sex chicks 6% (20/treatment, $P = 0.03$) whereas anti-IL-10 peptide 3 (EKMDENGI) decreased feed efficiency 3% in a study of mixed-sex chicks (35/treatment, $P = 0.069$). Hens producing the anti-IL-10 antibodies were artificially inseminated and chicks were hatched to determine the effects of passive transfer of anti-IL-10 peptides on growth and response to a lipopolysaccharide (LPS) challenge. Day-old mixed-sex chicks from hens producing any anti-IL-10 peptide antibodies (25 chicks/group) were smaller than chicks from adjuvant-injected controls (23 chicks) (3.4 to 9%, $P < 0.05$). Weight gain was reduced approximately 7% in chicks from hens injected with peptides 3 and 4 ($P = 0.08$). Chicks with passive anti-peptide 2 (VLPRAMQT) and anti-peptide 4 had reduced weight following LPS injection compared with saline-injected controls ($P = 0.05$). In summary, the feeding or passive transfer of antibody to specific peptides on chicken IL-10 reduced the rate of gain and may serve as a host targeted model for mimicking immune regulation of growth.

Key words: interleukin-10, inflammation, growth

M183 Empty body composition of Nellore bulls classified for residual feed intake. E. F. M. Bonilha[1], F. L. Araújo[2], S. F. M. Bonilha*[1], and R. H. Branco[1], *[1]Instituto de Zootecnia, Sertãozinho, São Paulo, Brazil, [2]Universidade Federal de Viçosa, Viçosa, Minas Gerais, Brazil.*

Residual feed intake (RFI) is an efficiency measure calculated as the difference between DMI observed and estimated based on metabolic BW and ADG. High RFI animals (less efficient) consume more than expected to a certain ADG, while the low RFI ones (more efficient) consume less than expected. This study aimed to evaluate empty body composition (EBC) of Nellore bulls classified in divergent levels of RFI. The experiment was conducted at Instituto de Zootecnia, Sertãozinho/São Paulo/Brazil, with 33 Nellore bulls, which were previously evaluated for RFI. From 60 evaluated bulls, 15 were classified as low RFI (≤mean + 0.5 SD) and 18 as high RFI (≥mean + 0.5 SD). Animals were slaughtered when they reached the minimum of 4 mm of subcutaneous fat thickness, with an average of 399 kg for BW and 18 mo for age. The EBC was obtained after grinding, homogenizing, sampling, analyzing, and combining blood, hide, head, feet, viscera, and carcass. Empty body percentages of water, ether extract (EE), protein, and ash were determined. Data were analyzed by GLM of SAS and means were compared by Tukey test at 5% of probability. There was no significant difference ($P = 0.9526$) in empty BW, showing that low and high RFI animals had similar body sizes. No significant differences were detected for empty body percentages of water ($P = 0.1266$), EE ($P = 0.6663$), protein ($P = 0.2800$), and ash ($P = 0.4627$), showing that low RFI animals (more efficient), for the same body composition, had a lesser feed intake, which contributes to the system economic viability.

Table 1. Means of empty BW, percentages of water, EE, protein, and ash in Nellore bulls from divergent levels of RFI

	Low RFI	High RFI	CV (%)	*P*-value
n	15	18	—	—
EBW, kg	367	366	12.5	0.9526
Water, %	63.9	63.1	2.39	0.1266
EE, %	13.6	14.0	15.5	0.6663
Protein, %	17.7	18.3	8.66	0.2800
Ash, %	4.76	4.67	7.69	0.4627

Key words: feed efficiency, body fat, body water

M184 Body and carcass fat of Nellore bulls classified for residual feed intake. S. F. M. Bonilha*[1], R. H. Branco[1], K. Zorzi[2], M. E. Z. Mercadante[1], J. N. S. G. Cyrillo[1], and L. A. Figueiredo[1], *[1]Instituto de Zootecnia, Sertãozinho, São Paulo, Brazil, [2]Universidade Federal de Viçosa, Viçosa, Minas Gerais, Brazil.*

Efficiency of food utilization is directly related to production system profitability, because food is the major cost in intensive beef production. Residual feed intake (RFI), expressed as the difference between DM intakes observed and estimated by a regression equation as a function of metabolic BW and ADG, is a measure of feed efficiency and can be a tool to reduce beef production costs. The study objective was to evaluate differences in body and carcass fat of Nellore bulls from low (≤mean - 0.5 SD; n = 32) and high (≥mean + 0.5 SD; n = 27) RFI levels. The experiment was conducted at Instituto de Zootecnia - Sertãozinho/São Paulo/Brazil, with 59 Nellore bulls finished in individual pens until they reach 4 mm of subcutaneous fat thickness (FT), assessed by ultrasound in LM, and slaughtered with averages of 447 kg for BW and 20 mo for age. The KPH was collected and weighed and FT was measured at 11th rib of LM. A steak sample of LM, with 2.5 cm of thickness, was removed from 11th rib for LM ether extract (LMEE) determination on a DM basis. Data were analyzed using GLM procedure of SAS, and means were compared using *t* test. The RFI variation was 0.740 kg of DM/d, with averages of −0.330 ± 0.034 and 0.410 ± 0.037 kg, respectively, for low and high RFI animals. No differences were detected between low and high RFI animals for slaughter BW (442 ± 11.1 and 454 ± 12.1 kg; $P = 0.4615$) and HCW (271 ± 7.30 and 279 ± 7.95 kg; $P = 0.4608$), respectively, showing that more and less efficient animals had similar body sizes. For KPH, FT, and LMEE, no significant differences were found between low and high RFI animals. The KPH averages were 8.88 ± 0.596 and 9.72 ± 0.649 kg ($P = 0.3447$); FT averages were 4.29 ± 0.281 and 4.37 ± 0.306 mm ($P = 0.8413$); and LMEE averages were 40.8 ± 1.24 and 39.7 ± 1.35% ($P = 0.5463$), respectively for low and high RFI animals, showing that more and less efficient animals had similar body and carcass fat content.

Key words: beef cattle, fat thickness, feed efficiency

M185 Describing DMI and growth patterns in beef steers during the finishing period. N. Vargas Jurado*[1], G. Scaglia[2], W. S. Swecker[1], D. A. Fiske[1], J. P. S. Neel[3], J. P. Fontenot[1], and R. M. Lewis[1], *[1]Virginia Tech, Blacksburg, VA, [2]Louisiana State University, Iberia Research Station, Jeanerette, [3]USDA-ARS, Beaver, WV.*

Feed intake is central to animal production systems, as it impacts efficiency and represents a substantial fraction of the total costs. The objectives of this study were to: (i) assess feed intake, weight gain, and feed efficiency in Angus crossbred steers during finishing on a total mixed diet; and, (ii) describe the pattern of their growth using the Brody function. The experiment was conducted at a research farm in western Virginia. Feed intake and BW data were collected on 18, 22, and 11 steers in 2005, 2006, and 2007, respectively. Animals were on average 420 d of age, and weighed 357 kg, when housed in a drylot with access to an individual feeding system (Calan Gate System, American Calan, NH). Across years, steers were fed a similar diet (9.7% CP and 15.6% NDF DM) ad libitum for 90 to 128 d. Daily feed intake (DFI), ADG, and feed conversion ratio (FCR) were evaluated. In addition, mature size (A), daily rate of growth (k), and initial BW at the start of the study (W_0), were estimated by fitting the Brody function $W_t = A - ((A - W_0)*\exp(kt))$, where W_t is weight at time t. Mean DFI were 15.4 ± 0.1, 16.6 ± 0.1, and 17.6 ± 0.1 kg/d, for 2005, 2006, and 2007, respectively, with significant differences among years ($P < 0.001$). Growth rate was constant (linear) over the finishing period ($P < 0.001$; $R^2 = 0.93$). The mean ADG in 2006 (1.25 ± 0.09 kg/d) was less ($P < 0.01$) than in 2005 (1.66 ± 0.07 kg/d) and 2007 (1.53 ± 0.13 kg/d). Mean FCR was better ($P < 0.01$) in 2005 (10.0 ± 0.4) than in 2006 (13.1 ± 0.7), with 2007 intermediate (12.1 ± 1.1). The estimates of A and k, the 2 key parameters of the Brody function, were similar across years: A was 742 ± 158, 734 ± 298, and 730 ± 269 kg while k was 0.0065 ± 0.0041, 0.0065 ± 0.0110, and 0.0072 ± 0.0092/d, for 2005, 2006, and 2007, respectively. The correlation between A and k was −0.99, indicating a strong relationship between their estimated values. Differences in intake, ADG, and FCR were observed among years although cattle genotype and husbandry were similar. Even with those differences, the Brody function appeared to provide a useful general description of growth in steers during the finishing period.

Key words: Brody function, cattle, feed intake

M186 Effects of heat stress on proliferation, protein turnover, and levels of heat shock protein mRNAs in cultured porcine muscle satellite cells. E. Kamanga-Sollo, M. Pampusch, M. White, M. Hathaway*, and W. Dayton, *University of Minnesota, St. Paul.*

It is well established that heat stress (HS) negatively impacts growth rate in swine. Although reduced feed intake undoubtedly plays a significant role in this reduction, studies in laboratory animals and other non-swine species indicate muscle growth also is affected by heat-stress-related alterations in muscle physiology. Heat shock proteins (Hsp) may play an important role in regulating rate and efficiency of muscle growth. The effects of HS on rates of satellite cell proliferation, protein synthesis, and protein degradation may play an important role in determining the rate and extent of muscle growth. We have examined the effects of mild HS (40.5°C for 48 h) on rates of proliferation (^{3}H-thymidine incorporation rate), protein synthesis (^{3}H-phenylalanine incorporation), and protein degradation (^{3}H-phenylalanine release from pre-labeled cultures) and on levels of Hsp90, Hsp70, and Hsp25/27 mRNA (qRT-PCR) and protein in cultured porcine muscle satellite cells (PSC). Data were analyzed using the mixed procedure of SAS. When significant interactions were detected ($P < 0.05$), least squares means were separated using LSD tests. Mild HS of PSC cultures resulted in 2.5-, 1.4-, and 6.5-fold increases ($P < 0.05$) in the levels of Hsp90, Hsp70, and Hsp25/27 mRNAs, respectively, relative to the levels in control cultures. Levels of Hsp 90, 70, and 25/27 proteins were also increased in HS PSC cultures compared with those in control cultures. Proliferation rates in HS PSC cultures were 35% lower ($P < 0.05$) than those in control cultures. Protein synthesis rates in HS fused PSC cultures were 85% higher ($P < 0.05$) than in control cultures and protein degradation rates in HS fused PSC were 23% lower ($P < 0.05$) than in control cultures. In light of the crucial role satellite cells play in postnatal muscle growth, the HS-induced changes

we have observed in rates of proliferation, protein turnover, and in levels of Hsp mRNA and protein in PSC cultures indicate that mild HS affects the physiology of PSC in ways that could affect muscle growth in swine.

Key words: porcine, satellite cell, heat stress

M187 Effects of increased protein and energy fed in milk replacer and heat stress on growth parameters of neonatal Holstein bull calves. A. J. Krenek*[1], G. A. Holub[1], T. A. Tomaszewski[1], and C. C. Stanley[2], *[1]Texas A&M University, College Station, [2]Land O Lakes Purina Feed, Amarillo, TX.*

The objective was to evaluate if calves fed 6 L of milk replacer with higher protein levels (HPMR; 1135 g/d, 28% CP, 20% fat) had improved performance compared with calves fed 4 L of a conventional milk replacer (CMR; 454 g/d, 20% CP, 20% fat) in heat stress and non-heat stress environments. Holstein bull calves (n = 52) < 3 d of age were assigned to a 2 X 2 factorial trial based on initial BW, physical health score, and total serum protein levels to either a heat stress (HS) or non-heat stress environment (NHS), with one half of each environment receiving HPMR and the other half receiving CMR. The study was conducted for 56 d from June 19 to August 13, 2010. The average thermal heat index (THI) was calculated for each day by averaging the 24 recorded temperatures and % relative humidity. The 56-d average, low, and high range THI for the HS were 79, 67, and 86 respectively, while THI for the NH were 69, 66, and 74 respectively. Weekly measurements of BW, body length (BL), hip width (HW), wither height (WH), heart girth (HG), and hip height (HH) were measured and ADG and average daily change were calculated. Water consumption (WC) and starter intake (SI) were measured daily. Data were analyzed using Proc Mixed of SAS 9.2. Calves on HPMR had a greater ($P < 0.01$) WH, HG, BL, HH, and ADG than the CMR calves (1.81 VS. 1.28 ± 0.004), (0.20 vs. 0.14 ± 0.009), (0.27 vs. 0.22 ± 0.01), (0.37 vs. 0.28 ± 0.008), and (0.82 vs. 0.58 ± 0.04) respectively. Calves in HS had a greater ($P < 0.01$) WC than the NHS calves (4365.56 vs. 2526.97 ± 102.2), respectively. The HPMR calves also had a greater WC ($P < 0.01$) than the CMR calves (4235.6 vs. 2656.96 ± 102.2), respectively. The CMR calves had a greater SI ($P < 0.05$) than HPMR calves (942.38 vs. 435.99 ± 0.39), respectively. There was no significant difference in growth parameters in HS or NHS in calves of like feeding strategies. The increased amount of protein and energy fed in the HPMR treatment did have an effect on WH, HG, HH, BL, WC, SI, and ADG.

Key words: calf, milk replacer, heat stress

M188 Indirect methods for estimation BW of crossbreed Holstein-Jersey heifers. B. C. Matos*, C. M. M. Bittar, W. R. S. Mattos, and L. F. Silveira, *University of São Paulo, University of Sao Paulo, USP/ESALQ, Piracicaba, SP, Brazil.*

This study's aim was to develop an estimation equation of BW on prepubertal Holstein-Jersey heifers from measures of growth parameters, and to compare them with the values obtained by mechanic scale and classical prediction equations described in the literature. Biweekly, 12 heifers of ~90 d of age were evaluated for BW, withers height (WH), hip width (HW), and heart girth (HG). The measures were taken until the animals attained 280 to 300 kg of BW. Regression analyses to estimate BW from measurements of growth parameters were developed using Proc Reg of SAS (1999). Regression analysis estimates and classical prediction equations were also used to estimate BW of heifers of different ages. Analysis of variance of estimated and mechanical scale data was performed using Proc GLM of SAS, with the average values compared by the Tukey test, and significance level of 5%. The measurement of HG presented the best coefficient of determination (R^2) with BW values. Linear regression resulted in lower R^2 values, especially for WH and HW. There were no statistical effects ($P > 0.05$) for the estimation measure. However, significance was found for age and interaction of age and estimation measure ($P < 0.001$). For the age range of 3 to 5.9 mo only WH linear regression overestimated the values of BW ($P < 0.05$). During the period of 6 to 7.9 mo the linear regressions of WH, HG, and HW overestimated the BW in relation of those found on a mechanical scale ($P < 0.05$). Estimating BW by classical prediction equations numerically underestimated the BW values as compared with the scale values. For the age range from 11 to 13 mo, WH and HW linear regression underestimated the BW of dairy heifers. Use of HG, WH, and HW measurements and classical prediction equations for BW estimation of crossbred dairy heifers was efficient, indicating that use of these measures, in lieu of a mechanical scale, may support improvements in on-farm management of nutrition and reproduction.

Key words: estimate method, growth, growth parameter

M189 Effects of rice or wheat straw as ingredients in a TMR on Holstein heifer growth. R. E. Rauch*[1,2], G. A. Nader[2], P. H. Robinson[2], and L. J. Erasmus[1], *[1]University of Pretoria, Pretoria, South Africa, [2]University of California, Davis.*

Rice straw (RS) is not common in dairy heifer rations, partly due to its low NE value and tough physical properties. To compare 2 RS harvesting methods (sickle chop or slicer baled), 5 dairies received ~12 t of each and a survey was conducted to compare dairyman experiences. The best RS (slicer baled) was used in a Latin square study with 2 treatments (i.e., RS- and wheat straw (WS)-based diets, both at 18% DM), 2 periods of 28 d and 4 pens of ~180 Holstein heifers each (age 14 to 18 mo) to compare effects on DMI, digestibility, BCS, and growth. The general linear model (GLM) procedure of SAS was used for statistical analyses. The RS heifers had a lower DMI (9.5 vs. 11.1 kg/d, $P < 0.01$) but greater ($P < 0.01$) digestibility of DM (57.8 vs. 52.4%), CP (57.6 vs. 54.5%), fat (82.2 vs. 78.4%), and ADF (40.4 vs. 36.9%, $P = 0.01$). The RS had lower intakes of digestible DM, aNDFom (amylase-treated ash-free NDF), and fat (5.5 vs. 6.0 kg/d, $P = 0.09$; 2.16 vs. 2.41 kg/d, $P = 0.04$; 0.26 vs. 0.28 kg/d, $P = 0.0497$, respectively). Change in BCS, tailhead height (TH), and hip width (HW) was lower for RS than WS (−0.0141 vs. +0.008 units/30 d, $P < 0.01$; 0.44 vs. 1.28 cm/30 d, $P < 0.01$ and 0.68 vs.1.63 cm/30 d, $P = 0.01$, respectively). A heifer frame score (HFS) was developed to create a 2-dimensional measure of skeletal growth while removing effects of BCS change on HW, as: HFS = corrected HW x TH, where: corrected HW (mm) = HW - BCS correction (BCS*c*), and BCS*c* (mm) = (3.2 x BCS) + (0.8 x age in mo) - 6.09. The BCS*c* was determined using a calliper to measure pin bone skin and fat thickness. The RS heifers had lower HFS change (3.82 vs. 8.46 cm^2/30 d, $P < 0.01$) and calculated NE output (i.e., NE_M, growth based on HFS, BCS loss/gain, and fetal growth), and diet NE concentration than WS (10.5 vs. 13.5 Mcal/d, $P < 0.01$; 1.10 vs. 1.21 Mcal/kg DM, $P = 0.049$, respectively). Lower feed efficiency with RS may be due to increased rumen retention time and fermentation energy loss (e.g., methane), a difference in DCAD for WS and RS diets (264.9 vs. 319.9 mEq (Na^+K-Cl^-S)/kg), or compensatory growth of WS heifers, as they had been fed a RS diet before the study.

Key words: rice straw, wheat straw, heifer growth

M190 Effects of pre-weaning nutrient intake in the developing mammary parenchymal tissue and fat pad. F. Soberon* and M. E. Van Amburgh, *Cornell University, Ithaca, NY.*

The mammary gland is considered to grow at an isometric rate during the first 2 mo of life followed by an allometric rate until peri-puberty. Multiple reports describe an association between growth rate before puberty and altered mammary gland development, primarily due to an increase in the size of the fat pad while parenchymal growth is restricted. Twelve dairy heifer calves were fed either a constant amount of a 28% CP 15% fat milk replacer (MR) per day equivalent to 0.18 Mcal intake energy/kg $BW^{0.75}$ (Control, n = 6) or 0.3 Mcal intake energy/kg $BW^{0.75}$ (Enhanced, n = 6). All calves had full access to water and calf starter. Calves were harvested at 54 ± 2 d. The Control group consumed 32.6 kg of MR and 6.7 kg of calf starter and the Enhanced group consumed 69.5 kg of MR and 1.9 kg of calf starter. Initial and final BW for the Control and Enhanced treatments were 39.2, 61.0, 39.7, and 83.2 kg, respectively. At harvest, weights of liver, kidneys, pancreas, whole skinned mammary gland, and mammary parenchyma were measured. Growth rate was calculated for each organ as the change in organ weight as a percentage of BW. Treatment comparisons were made using the mixed procedures of SAS and significance declared at $P < 0.05$. The mammary glands with Enhanced treatment were heavier at harvest ($P < 0.01$) and when calculated as %BW, resulted in 4x greater parenchymal growth. We conclude that in early life, the mammary gland is responsive to nutrient intake and this differs from post-weaning mammary growth responses. Based on differences in nutrient supply, allometric growth was initiated pre-weaning. Understanding which cells are responding to nutrient supply may aid in understanding the effect of early life nutrient intake on future milk production.

Table 1.

	Control	Enhanced	SE	*P*-value
ADG (kg/d)	0.39	0.82	0.03	<0.01
Pancreas (g)	32.90	29.47	4.39	0.61
Pancreas, %BW	0.06	0.04	0.01	0.11
Liver (kg)	1.35	2.35	0.82	<0.01
Liver, %BW	2.23	2.84	0.09	<0.01
Kidney (g)	183.60	319.72	33.29	0.02
Kidney, %BW	0.30	0.38	0.03	0.09
Whole mammary (g)	75.48	337.58	29.14	<0.01
Mammary gland, %BW	0.12	0.41	0.03	<0.01
Parenchyma (g)	1.10	6.48	1.00	<0.01
Parenchyma, % of gland	1.35	1.90	0.37	0.30
Parenchyma, %BW	0.002	0.008	0.001	<0.01

Key words: mammary gland, growth

M191 Effect of diet metabolizable protein:metabolizable energy ratio on growth parameters and mammary gland development of crossbred Holstein-Jersey heifers reared on an accelerated growth program. B. C. Matos*, C. M. M. Bittar, W. R. S. Mattos, G. B. Mourao, and L. F. Silveira, *University of Sao Paulo, USP/ESALQ, Piracicaba, SP, Brazil.*

The aim of this trial was to evaluate the effect of metabolizable protein:metabolizable energy (MP:ME) ratio in diets based on tropical grasses and concentrate composed of by-products formulated for high growth rate during the prepubertal phase on growth parameters and mammary gland development of Holstein-Jersey heifers. Twelve heifers (90 d of age) were housed in individual pens, with free access of water and shade. Heifers were allocated to control (MP:ME = 39 g/Mcal) and high MP:ME ratio (MP:ME = 44.5 g/Mcal), according to a completely randomized statistical design. Biweekly, heifers were weighed on a mechanical scale until BW had attained between 280 and 300 kg, the expected weight of puberty. Measures of withers height (WH), hip width (HW), and heart girth (HG) were also taken. Monthly, size and length of teats were measured, and blood samples were collected for progesterone analysis. Heifers were considered pubertal when levels of progesterone were > 1.0 ng/mL. The MP:ME ratios observed were higher than those first predicted by NRC (2001), with values of 44.39 and 52.98 g/Mcal, respectively for control and high MP:ME treatment. The average value of DMI was 5.3 ± 1.8 kg DM/d with no effect of diet ($P < 0.05$). Body weight, HW, HG, and WH increased during the experiment ($P < 0.05$) and were not influenced by treatment. Measures of mammary gland development increased ($P < 0.05$) during the experimental period however no statistical effect of diet was found. The age at puberty of treatments occurred at 10.6 and 11.4 mo, respectively for high MP:ME and control; no effect of diet was observed. Measurement of growth parameters and mammary gland development were not influenced by diet MP:ME ratio. Increasing values were a result of animal growth. Formulating diets for prepubertal dairy heifers based on MP:ME requirements is efficient because it minimizes the occurrence of protein deficiency, which might occur in growing heifers, especially in mammary and skeletal tissues.

Key words: growth parameter, puberty, heifer

M192 Milk diet affects glucose transporters in skeletal muscle of neonatal calves. U. Schönhusen, C. Rehfeldt, J. Steinhoff-Wagner, and H. M. Hammon*, *Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany.*

Colostrum feeding improves glucose status in neonatal calves by stimulating intestinal glucose absorption. Elevated systemic glucose availability may also lead to an altered substrate flux between tissues. We have tested the hypothesis that gene and protein expression of facilitative glucose transporters GLUT1 and GLUT4 in skeletal muscle depends on milk diet. Calves were fed twice daily either colostrum (C; n = 7) or a milk-based formula with same nutrient density as colostrum, but no biologically active factors (F; n = 7). Amounts fed per meal were 4% of BW on d 1 and 5% of BW on d 2 to d 4. Nutrient and lactose contents of C and F were identical. On d 4, calves were slaughtered 2 h after feeding. Masseter (M), longissimus dorsi (LD) and semitendinosus (ST) muscles were removed for measurement of mRNA and protein expression of GLUT1 and GLUT4 by real-time PCR and SDS PAGE immunoblot, respectively. Muscles were classified as oxidative and glycolytic according to isocitrate dehydrogenase (ICDH) and lactate dehydrogenase (LDH) activities. Data were analyzed by the Mixed Model of SAS with diet, muscle, and diet × muscle interaction as fixed effects and individual calves as random effect. ICDH was highest ($P < 0.001$) and LDH was lowest ($P < 0.001$) in M; ICDH tended to be higher ($P < 0.1$) and LDH tended to be lower ($P < 0.1$) in ST than in LD. Protein expression of GLUT4 was highest ($P < 0.001$) in M and protein expression of GLUT1 was higher ($P < 0.05$) in LD than in M. For GLUT4, protein expression in M, LD, and ST tended to be higher ($P < 0.1$) in C than in F, whereas gene expression was lower ($P < 0.05$) in ST and tended to be lower ($P < 0.1$) in LD of C compared with F. Gene expression of GLUT1 in ST was higher ($P < 0.05$) in F

than in C. Elevated GLUT4 protein expression in C than in F is in line with previously shown higher postprandial plasma concentrations of insulin after colostrum feeding, probably resulting in a greater insulin-stimulated glucose uptake in oxidative as well as glycolytic muscles. The elevated mRNA expression of GLUT4 in glycolytic muscles of F vs. C may point at a compensatory transcriptional response to lower protein expression.

Key words: calf, muscle, glucose transporter

Lactation Biology 1

M193 Essential amino acids significantly contribute to the energy status in short-term MAC-T cell cultures. V. S. Lyman[1], M. L. Bell[1], W. A. D. Nayananjalie*[1], E. M. England[1], J. A. D. R. N. Appuhamy[2], and M. D. Hanigan[1], *[1]Virginia Polytechnic Institute and State University, Blacksburg, [2]University of Guelph, Guelph, ON, Canada.*

Acetate is a major energy source for ruminant mammary glands. Supplementation of AA increases milk protein synthesis, but the mammary glands have been found to take up some essential AA (EAA) beyond requirements for protein synthesis. Catabolized AA contribute to the energy supply of mammary cells. The in vivo contribution to ATP production is small, but that may not be the case in vitro. The present study was designed to investigate the effects of acetate and EAA on ATP levels and phosphorylation of AMP-activated protein kinase (AMPK). Reduced AMPK phosphorylation is indicative of improved energy status. A bovine mammary epithelial cell line, MAC-T was incubated in glucose free Dulbecco's Modified Eagle's Medium Ham's Nutrient Mixture F-12 (DMEM/F12) with 0 or 3.5 m*M* EAA and 0 or 5 m*M* acetate in a 2 × 2 factorial arrangement with 3 replicates. All media contained 10 ng/mL insulin. Cells were harvested after 1 h of incubation in treatment media and cell lysates were subjected to analysis for ATP (μmol/mg of protein) and total protein (mg/ml) content. The experiment was repeated on a different day and the cell lysates were subjected to Western immunoblotting analysis of AMPK phosphorylation state (phosphorylation at Thr172: total AMPK). Supplementation of EAA increased ($P = 0.07$) ATP content in MAC-T cells by 27% (60.4 ± 4.1 vs.78.2 ± 4.6 μmol/mg of protein) whereas added acetate was noneffective ($P = 0.46$). Consistent with the ATP results, EAA supplementation reduced ($P = 0.04$) phosphorylation of AMPK by 33% (0.95 ± 0.10 vs. 0.64 ± 0.10) whereas added acetate was associated with a numerical ($P = 0.20$) decline of 21% (0.89 ± 0.10 vs. 0.70 ± 0.10). There were no significant interactions between acetate and EAA on the ATP content or the phosphorylation of AMPK. ATP concentrations were highly correlated (r = - 0.90) with AMPK phosphorylation. In MAC-T cells, AMPK phosphorylation was responsive to ATP concentrations as observed in other cell types. Essential AA were much more potent in eliciting an ATP and AMPK response suggesting that these cells have limited ability to metabolize acetate.

Key words: amino acids, energy status, mammary cells

M194 Mammary uptake of fatty acids varying in chain length and unsaturation supplied by intravenous triglyceride infusion. J. A. Stamey*, J. K. Suagee, C. Caldari-Torres, and B. A. Corl, *Virginia Tech, Blacksburg.*

Supplementing dairy cows with feeds rich in omega-3 fatty acids does not readily increase excretion in milk fat of dairy cows. Previous results demonstrated that very long chain omega-3 fatty acids are primarily transported in the phospholipid fraction of blood, making them largely unavailable to the mammary gland for enrichment of milk fat. Our objective was to compare fatty acids of increasing chain length and unsaturation delivered intravenously as triglyceride emulsions to uncover any regulation of fatty acid uptake by the mammary gland. Late lactation dairy cows were assigned to a completely randomized block design to prevent carryover effects. Cows were fed a total mixed ration formulated to meet nutrient requirements and allowed an acclimation period of 5 d. Treatments were intravenous triglyceride emulsions enriched with oleic, linoleic, linolenic, or docosahexaenoic acid and were delivered continuously at 16 mL/h for 72 h. Each treatment supplied 30 g/d of the target fatty acid. Treatments did not affect feed intake, milk yield, or milk composition. Each target fatty acid demonstrated increased proportion in plasma triglyceride. Increases of target fatty acids, especially linolenic and docosahexaenoic, were evident in plasma phospholipid and cholesterol ester fractions, suggesting re-esterification in the liver. Transfer efficiencies were 31.6, 46.4, and 13.0%, and d 3 total milk fatty acyl yields were 37.5, 19.4, and 3.9 g (±1.36 pooled SEM) for linoleic, linolenic, and docosahexaenoic acid. Variation in oleic acyl yield prevented calculation of oleic acid transfer efficiency. Mammary uptake of fatty acids was reduced with increased chain length and unsaturation. Both liver and mammary mechanisms might regulate transfer of long chain polyunsaturates.

Key words: fatty acid, lipid metabolism, transfer efficiency

M195 Conjugated linoleic acid-induced milk fat depression in lactating ewes is accompanied by reduced expression of genes involved in mammary lipid synthesis. M. Hussein*[1], K. H. Harvatine[2], W. M. P. B. Weerasinghe[3], L. A. Sinclair[3], and D. E. Bauman[1], *[1]Cornell University, Ithaca, NY, [2]Pennsylvania State University, University Park, [3]Harper Adams University College, Newport, Shropshire, UK.*

Conjugated linoleic acids (CLA) are produced during rumen biohydrogenation and exert a range of biological effects. The t10, c12 CLA isomer is a potent inhibitor of milk fat synthesis in lactating dairy cows and some aspects of its mechanism have been established. CLA-induced milk fat depression (MFD) has also been observed in small ruminants and our objective was to examine the molecular mechanism in lactating ewes. Multiparous lactating ewes (n = 16) were fed a basal ration (0.55:0.45 concentrates to forage; dry matter basis) and randomly allocated to 2 treatments. Treatments were zero CLA (Control) or 15 g/d of lipid-encapsulated CLA supplement containing c9, t11 and t10, c12 CLA isomers in equal proportions. Treatments were for 10 wk and CLA supplement provided 1.5 g/d of t10, c12. There were no effects on milk yield or milk composition for protein or lactose at wk 10 of the study ($P > 0.1$). In contrast, CLA treatment decreased both milk fat percent ($P < 0.01$) and milk fat yield (g/d) ($P = 0.07$) by almost 22%. The de novo synthesized fatty acids (FA) (<C16) decreased in proportion (15%) and daily yield (27%) due to CLA treatment ($P < 0.05$). In addition, the proportion of preformed FA (>C16) increased ($P < 0.05$) and there were numerical decreases in the yields of 16 carbon FA (15%) and >16 carbon FA (6%). Consistent with the FA pattern, mRNA abundance of FASN, ACACA and SCD1 decreased by 35 to 45% in the CLA-treated group ($P < 0.05$). Similarly, CLA treatment decreased mRNA abundance of GPAT ($P = 0.15$) and DGAT1 ($P = 0.09$), genes involved in fatty acid esterification, by almost 30%. The mRNA abundance for SREBP-1 and INSIG1, genes involved in regulation of transcription of lipogenic enzymes, was decreased by almost 60% with CLA treatment ($P < 0.05$). Furthermore, mRNA abundance of LPL decreased by almost 30% due to CLA treatment ($P = 0.06$). In conclusion, the mechanism for CLA-induced MFD involved the SREBP transcription factor family and a coordinated downregulation in transcript abundance for lipogenic enzymes involved in mammary lipid synthesis.

Key words: CLA, lactation, mammary

M196 Characterization of a novel bovine mammary epithelial cell line. P. Bernier-Dodier*[1,2], G. Tremblay[1], and P. Lacasse[2], *[1]Université de Sherbrooke, Sherbrooke, QC, Canada, [2]AAFC-Dairy and Swine Research and Development Centre, Sherbrooke, QC, Canada.*

Milk contains several cell types, including exfoliated mammary epithelial cells. Since the available bovine cell lines poorly differentiate at best (meagre milk proteins expressions and leaky tight junctions), we have isolated primary mammary epithelial cells from milk for in vitro experimentations. Although a high proportion of contaminant immune cells were initially present, they were rapidly loss since they have a relatively short survival time. Out of the 7 isolations accomplished, one cell population, isolated from the milk of a Holstein cow at approximately 200 DIM, was successfully maintained in culture for a prolonged period. Interestingly, those epithelial cells have survived and to proliferated for at least 50 passages without any sign of senescence, suggesting that they have spontaneously immortalized. Because only a small number of bovine mammary epithelial cell (BMEC) lines are currently available, we undertook the characterization of this novel cell line named HERA-2. Their epithelial origin was confirmed by an immunohistochemical detection of cytokeratins and by PCR detection of the cytokeratin-18 gene expression. The bovine origin of the cell line was confirmed by karyotype analysis of 12 cells and by sequencing the gene *cytochrome C oxidase I*. At all the tested passages, the HERA-2 cells formed tight inter-cellular junctions as evaluated by transepithelial electrical resistance measurement that generally reached more than 1500 ohm*cm^2. When the HERA-2 cells are cultured on matrigel in presence of lactogenic hormones (prolactin, dexamethasone and insulin), they form mammospheres and duct-like structures. Up to now, none of the culture conditions tested was able to induce significant expression of lactogenic differentiation markers (αs1-casein, β-casein and α-lactalbumin encoding genes). In conclusion, the HERA-2 is a novel BMEC line that could constitute a good alternative to the MAC-T cells since they were not immortalized with the SV-40 large T-antigen. Their use as a model could facilitates the study on the regulation bovine mammary cells functions.

Key words: mammary gland, tight junction

M197 Further study on the role of SREBP-1 in lipogenesis in bovine mammary epithelial cells. L. Ma* and B. A. Corl, *Virginia Tech, Blacksburg.*

Sterol regulatory element binding proteins (SREBPs) are transcription factors that regulate lipid metabolism. Among the 3 isoforms, SREBP-1a, −1c and −2, SREBP-1a and −1c regulate fatty acid synthesis. The objective of this study was to further determine the role of SREBP-1 in regulating lipogenesis in bovine mammary epithelial cells (MAC-T cells). Cells were seeded to plates at a density of 2×10^4 cells/cm^2 and incubated in basal medium (DMEM+10% FBS) overnight. Then cells were transfected with small interfering RNAs (siRNA) against SREBP-1 (SSI), a random sequence as negative control (NEG), and no siRNA as untreated control (UNT), according to protocol (Dharmacon Inc.). After 48 h, cells were harvested for real-time quantitative PCR, immunoblotting, and radiolabeled-oleate incorporation assays. Our previous study showed that SREBP-1 mRNA and SREBP-1 proteins were reduced by SREBP-1 siRNA significantly ($P < 0.0001$). Acetate incorporation and mRNA expression of de novo lipogenic enzymes (acetyl-CoA carboxylase (ACC) and fatty acid synthase (FAS)) also decreased with SSI ($P < 0.001$). In the current study, we observed a significant reduction in mRNA expression of acyl-CoA synthetase short-chain family member 2 (ACSS2), isocitrate dehydrogenase 1 (IDH1), and fatty acid binding protein 3 (FABP3) ($P < 0.0001$). The protein expression of stearoyl-CoA desaturase 1 (SCD1) and ACC was decreased as well. Although we did not observe any reduction in triglyceride synthetic enzymes in previous study, phosphatidic acid phosphatase-1(Lipin1) mRNA level dropped with SSI treatment. However, adipophilin (PLIN2) had a 3.5-fold increase. De novo fatty acid synthesis starts with acetate which is converted to acetyl-CoA by ACSS2. Acetyl-CoA is used to synthesize malonyl-CoA by ACC, and FAS is responsible for fatty acid chain elongation. IDH1 generates NADPH as a reducing equivalent for de novo lipogenesis. In conclusion, SREBP-1 regulates lipogenesis in MAC-T mainly through de novo lipogenic enzymes. 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-1, small interfering RNA, bovine

M198 Capturing circadian mammary gene expression of cows using RNA from milk fat globule. J. Crodian*, T. Casey, and K. Plaut, *Purdue University, West Lafayette, IN.*

The overall objective of this study was to measure mammary gene expression over a circadian cycle in the lactating cow. Rather than isolating RNA from repeated mammary biopsies, total RNA was isolated from the cytoplasmic crescent of the milk fat globule. Three lactating Holstein cows were housed in tie stalls with water and feed provided ad libitum. Cows at 125 d into lactation with an average SCC of 105,000 were milked every 4hrs over a 48hr period. Milk samples were analyzed by DHIA for %fat, %protein, %lactose and MUN. Milk fat was separated by centrifugation and total RNA was isolated using QIAZOL. qPCR analysis was performed and expression of ACACA (acetyl-CoA carboxylase α), CSN2 (β-casein), PER2 and ARNTL were measured. Expression of core clock genes, PER2 and ARNTL showed diurnal variation (Table 1), with peak (16–20h; dark phase) and trough (32–36h; light phase) of expression significantly different ($P < 0.05$). Although ACACA and CSN2 showed diurnal variation, peak and trough of gene expression were not different. Diurnal patterns of MUN and %fat were also evident. Mean peak of %fat (4.18+/−0.11; 32–36h; light phase) and trough (3.52+/−0.17; 16–20h; dark phase) were different ($P < 0.01$), and opposite in phase of PER2 and ARNTL. These results suggest that mammary clock genes and milk components exhibit circadian rhythms.

Table 1. Fold change in gene expression relative to average expression across 48 hrs (log base 2*).

Time (h)	PER2*	SEM	ARNTL*	SEM
0	−0.48	0.56	−1.18	0.69
4	0.51	0.06	−0.19	0.37
8	1.29	0.12	0.30	0.52
12	1.44	0.12	0.21	0.45
16	1.30	0.20	0.41	0.27
20	1.30	0.35	0.55	0.30
24	−0.74	0.38	−0.15	0.32
28	−0.41	0.70	−0.06	0.10
32	−2.75	0.64	−1.22	0.74
36	−2.31	0.74	−0.56	0.35
40	−0.16	0.29	0.47	0.21
44	0.49	0.35	−0.02	0.43
48	0.50	0.56	1.44	0.09

Key words: circadian, mammary, gene expression

M199 Expression of PEPCK isoforms in the mammary gland of dairy goats is regulated by insulin status. S. J. Mabjeesh*[1], A. Sahmay[2], N. Argov-Agrman[1], C. Sabastian[1], and B. J. Bequette[3], *[1]The Robert H. Smith Faculty of Agriculture, Food and environment, The Hebrew University of Jerusalem, Rehovot, Israel, [2]Institute of Animal Science, The Volcani Center, Bet Dagan, Israel, [3]University of Maryland.*

Phosphoenolpyruvate carboxykinase (PEPCK) isoforms (c, cytosolic; m, mitochondria) are expressed in the liver and mammary gland. PEPCK-c is a rate-controlling enzyme for gluconeogenesis and glyceroneogenesis whose activity is decreased by insulin, whereas PEPCK-m expression is constitutive and functions to channel lactate towards gluconeogenesis. We hypothesized that the increase in milk protein but decrease in milk lactose and fat when the hyperinsulinemic-euglycemic clamp (HIEC) is applied to dairy goats is due to a decrease in expression of mammary PEPCK-c mRNA. Late lactation goats (n=4;150 ± 30 DIM) were subjected to saline infusion and HIEC (104 µg insulin/h) for 4-d periods in a 2×2 cross-over design. Goats were milked two times per day and milk yields and components were determined. On day 4 of each period, a mammary biopsy (~1g) was taken from an udder half for expression of PEPCK-m and -c mRNA by rtPCR. Plasma insulin increased (P< 0.002) 3.5-fold due to the HIEC and euglycemia was maintained. The HIEC decreased (P < 0.005) DMI (40%) and milk yield (26%). Whereas milk fat content was not affected, HIEC increased (P < 0.001) milk protein content (2.82% vs. 3.09%) but decreased (P < 0.001) milk lactose content (4.22% vs. 4.03%). Expression of PEPCK-m mRNA was 8-fold higher (P < 0.031) than PEPCK-c. The HIEC decreased PEPCK-c mRNA 7-fold but increased PEPCK-m mRNA by 30%. These results demonstrate that insulin regulates mRNA expression of mammary PEPCK isoforms, and this may underlie the changes in milk component synthesis observed when the HIEC is applied.

Key words: insulin, casein, goat

Nonruminant Nutrition: DDGS

M200 Amino acids and energy utilization in zero tannin faba bean and co-fermented wheat and corn distillers dried grains with solubles (DDGS) fed to growing pigs. E. Kiarie*[1], R. K. Kahindi[1], P. Lopez[2], C. Furedi[2], and C. M. Nyachoti[1], *[1]University of Manitoba, Winnipeg, MB, Canada, [2]The Puratone Corporation, Niverville, MB, Canada.*

Nutritional characterization of locally available feedstuffs may stimulate their inclusion in swine diets and contribute to whole farm nutrient management programs. We determined the nutritive value of Manitoba grown zero-tannin fava beans (ZTFB, < 1% tannin) and co-fermented wheat and corn DDGS (wcDDGS) from a local ethanol plant. Corn DDGS (cDDGS) was also included for comparison. In Exp. 1, 6 ileal-cannulated barrows (BW = 29.3 kg) were fed 3 diets in a replicated 3 × 3 Latin square design to determine the apparent (AID) and standardized (SID) ileal digestibility of AA. The 3 diets contained either ZTFB or wcDDGS or cDDGS as the sole source of AA. The SID was calculated using values of basal endogenous AA losses from our previous studies. In Exp. 2, 12 intact barrows (BW = 22.5 kg) were fed 4 diets in a 2 15-d period crossover design to determine DE and ME contents of the test ingredients by difference method. The diets were a basal corn-based diet or the basal diet with corn replaced by 46% ZTFB or wcDDGS or cDDGS. The concentrations (DM basis) of GE (kcal/kg), CP (%) and Lys (%) in ZTFB were 4,136, 27 and 1.6, respectively; corresponding values for wcDDGS were 5,175, 31.5 and 0.85. The ZTFB had higher ($P < 0.05$) SID of Lys (83.2%) compared with wcDDGS (72.1%) and cDDGS (67.8%); as a result the SID content (g/kg DM) of Lys in ZTFB (13.5) was greater ($P < 0.05$) than that of either wcDGGS (6.03) or cDDGS (6.68). The DDGS samples had higher ($P < 0.05$) SID and contents of sulfur AA (Met and Cys) compared with ZTFB. The ME content (kcal/kg DM) of ZTFB (3,548) was lower ($P < 0.05$) than that of cDDGS (3,851) whereas the ME content of wcDDGS (3,669) was similar ($P > 0.05$) to that of ZTFB or cDDGS. The results show that ZTFB has higher digestible Lys whereas wcDDGS has higher digestible sulfur AA but both ingredients have comparable ME content. Thus, a blend of these 2 ingredients can serve as excellent source of AA and energy for swine.

Key words: energy and nutrient utilization in swine, zero tannin faba beans, co-fermented wheat and corn DDGS

M201 Glucanase, xylanase and microbial inoculants improve feeding value of DDGS for liquid-fed finishing pigs. C. L. Zhu*, M. Rudar, D. Wey, and C. F. M. de Lange, *University of Guelph, Guelph, ON, Canada.*

Fiber degrading enzymes and microbial inoculants are likely more effective in improving the feeding value of DDGS in liquid feeding than in conventional dry feeding systems. A study was conducted to determine the impact of feeding corn DDGS steeped with exogenous enzymes (xylanase and glucanase) or microbial inoculants (*Pediococcus* in Exp. 1 and *Enterococcus* plus *Bacillus* in Exp. 2) on growth performance, nutrient digestibility, and carcass and meat quality in finishing pigs. A total of 384 Yorkshire pigs (192 in each Exp; initial BW 66 kg; 4 gilts and 4 barrows per pen; equal number of pens per treatment) were liquid-fed corn and soybean meal based diets containing 30% DDGS (DM basis) using a computerized liquid feeding system. The DDGS was mixed with water (17% DM basis) and steeped in one of 4 fermentation tanks, representing 4 treatments: (1) control, DDGS only, (2) DDGS+enzymes, (3) DDGS+inoculants, (4) DDGS+enzymes+inoculants. Samples of supernatants were taken after at least 48 h of steeping for analysis. Fecal samples were collected at 90 kg BW for determining apparent nutrient digestibility, using titanium as an indigestible marker. At the final BW (110 kg) carcass quality was evaluated according to the Canadian grading scheme. Responses to treatments were similar in Exp. 1 and 2 ($P > 0.05$). Steeping DDGS with enzymes, inoculants and enzymes plus inoculants increased ($P < 0.05$) lactic acid content in the supernatants (for all responses treatments 1 to 4, respectively: 1.69, 1.94, 1.98, and 2.37%; SE 0.10). Steeping DDGS with enzymes, inoculants or enzymes plus inoculants increased ($P < 0.05$) ADG (1.04, 1.15, 1.16, and 1.22, kg/d; SE 0.02) and ADFI (2.50, 2.73, 2.78, and 2.87, kg/d; SE 0.05). A numerical increase ($P = 0.07$) in digestibility of N was observed (82.0, 83.7, 84.0 and 84.2%; SE 0.60). Hot carcass weight, back fat depth, loin depth and estimated carcass lean yield did not differ among treatments ($P > 0.05$). Through steeping and using fiber degrading enzymes or microbial inoculants the feeding value of DDGS for liquid fed finishing pigs was improved.

Key words: pigs, liquid feeding, DDGS fermentation

M202 Determination of dry matter content in feces of pigs fed three different sources of DDGS. K. Kock* and C. Hostetler, *South Dakota State University, Brookings.*

An experiment was conducted to determine the differences in dry matter output between 3 different sources of DDGS. A total of 72 crossbred barrows were placed in metabolism crates at an average initial body weight of 55.2 kg. Dietary treatments were either a corn-based basal diet with no DDGS (Control; n = 9) or the basal diet with 30% DDGS from one of 3 commercially available sources (Diets A, B and C; n = 21 respectively). Pigs were fed their respective diets at 3% of BW for 9 d before a 4 d collection period. During the 4 d collection period, pigs were fed half their ration twice daily and all feces were collected once per day at the morning feeding. Feces were weighed, pooled within pig and frozen until analysis of dry matter content. Dry matter content was determined by drying approximately 1 kg of the pooled sample in a forced air oven at 70°C for 48 h. There was no difference between treatments in total dry matter intake over the entire 4 d collection period (5.89, 5.94, 5.98 and 6.00 kg for Control, A, B and C respectively; $P > 0.1$). There was a significant difference between treatments for total manure output (0.99 vs. 1.94, 1.73 and 1.95 kg for Control vs. A, B and C respectively; $P < 0.01$), resulting in approximately 1.5 to 2 times the amount of manure from pigs fed diets containing DDGS compared with the corn only diet. Additionally, there were differences due to treatment in manure %DM (53.6 vs. 44.6, 46.7 and 45.5 for Control vs. A, B and C respectively; $P = 0.04$) and total DM output (531 vs. 847, 798 and 872 kg for Control vs. A, B and C respectively; $P < 0.01$) which is an increase of approximately 50% in DM output compared with corn only diets. However, there was no difference between sources of DDGS in total manure output, manure %DM or total DM output. These data indicate that diets containing DDGS add a significant amount of volume to manure output; therefore, manure storage facilities may reach capacity more quickly when feeding a high level of DDGS in swine diets.

Key words: swine, DDGS, dry matter

M203 Effects of dietary enzyme fermented wheat on growth performance, nutrient digestibility, blood characteristics, and fecal noxious gas emission in growing pigs. X. Y. Guo*, H. Y. Baek, and I. H. Kim, *Dankook University, Cheonan, Choognam, South Korea.*

This research was conducted to evaluate the effect of dietary enzyme fermented wheat (FW) on growth performance, nutrient digestibility, blood characteristics, and fecal noxious gas in growing pigs. A total of 120 pigs with initial BW of 29.6 ± 1.9 kg [(Landrace × Yorkshire) × Duroc] were randomly allotted into 1 of 5 dietary treatments with 6 replicate pens per treatment and 4 pigs per pen. Every pen was equipped with semi-automatic feeder and nipple drinker. The pigs were housed in an environmental controlled, slatted-floor facility in 30 adjacent pens and were allowed ad libitum access to feed and water. The temperature and humidity of animal house were maintained at 24°C and 60%, respectively. This experiment lasted for 6 wk. Pigs were fed a common corn-soybean meal based diet for a 3 d adjustment period and then fed experiment diets. The experiment diets were formulated based on corn-soybean meal with FW at different levels of 0%(FW0), 5%(FW5), 10%(FW10), 15%(FW15) and 20%(FW20). All experiment diets contained a total of 20% of wheat. The FW were treated by protease (26,014 U/g), amylase (7,176 U/g) xylanase (799 U/g), cellulose (5,204 U/g) and a-galactosidase (176 U/g) for 72 h. Pigs fed FW15 diet had higher ADG than pigs fed FW0 diet ($P < 0.05$), however, no difference was observed in ADFI and G:F among all dietary treatments ($P > 0.05$). Apparent total tract digestibility (ATTD) of DM and N in FW10, FW15 and FW20 treatments were higher (84.63, 84.60, 84.47 vs. 82.40%, $P < 0.05$) than that in FW0 group. Concentrations of blood glucose, RBC, WBC and lymphocyte percentage were not affected ($P > 0.05$) by dietary FW. There was no difference ($P > 0.05$) in fecal noxious gas concentration (H_2S, Acetic acid and NH_3) among all treatments. In conclusion, ADG can be improved by FW15 and ATTD of DM and N can be enhanced by FW10, FW15 and FW20.

Key words: fermented wheat, growing pigs, growth performance

M204 The effect of enzyme fermented corn on growth performance, nutrient digestibility, blood profile, and fecal gas emission in growing pigs. P. Y. Zhao*, S. C. Kim, and I. H. Kim, *Dankook University, Cheonan, Choongnam, South Korea.*

This study was conducted to evaluate the effect of fermented corn (FC) on growth performance, nutrient digestibility, blood profile, and fecal gas concentration in growing pigs. A total of 96 pigs [(Landrace × Yorkshire) × Duroc] with an average initial BW 24.4 ± 1.1 kg were used in a 6 wk trial. All pigs were randomly allotted to 1 of 4 treatments (6 replicate pens per treatment with 4 pigs per pen). The experiment lasted for 6 wk. Treatments included: 1) CON (0% FC), 2) FC1 (10% FC), 3) FC2 (20% FC) and 4) FC3 (30% FC). All treatment diets contained 30% corn. The FC was pre-treated xylanase, cellulose and hemicellulase. Data were subjected to the GLM procedures and Duncan multiple range test was used to compare the means of the treatments. The FC were treated by protease (26,014 U/g), amylase (7,176 U/g)xylanase (799 U/g), cellulose (5,204 U/g) and a-galactosidase (176 U/g) for 72 h.There were no differences on growth performance among all dietary treatments during the overall period. Apparent total tract digestibility (ATTD) of DM and energy were higher in FC2 than CON, FC1, and FC3 throughout the experiment (83.37 vs. 81.36, 80.17, 81.72; 86.81 vs. 84.01, 82.59, 84.28%; $P < 0.05$). Blood glucose concentration in FC1 treatment was decreased compared with CON treatment (106.75 vs. 114.72 mg/dl; $P < 0.05$) and there were no differences on white blood cells (WBC), red blood cells (RBC) counts, and lymphocyte percentage among all the dietary treatments. Fecal H_2S measured on d 5 and 7 was reduced (6.7, 6.6 vs. 8.6; 6.9, 7.0 vs. 8.6 mg/kg; $P < 0.05$) in FC2 and FC3 treatments compared with CON. Acetic acid was lower (21.8, 23.5 vs. 25.8 mg/kg; $P < 0.05$) in FC2 and FC3 treatments than CON treatment on d 7. In conclusion, feeding enzyme fermented corn in growing pig diet improves nutrient digestibility without any negative effect on growth performance and meat quality. Furthermore, fermented corn can reduce fecal noxious gas emission content.

Key words: fermented corn, growing pigs, nutrient digestibility

M205 Effects of enzyme fermented oat on growth performance, digestibility, blood profile, and fecal gas emission of growing pigs. S. Zhang*, J. M. Lee, and I. H. Kim, *Dankook University, Cheonan, Choongnam, South Korea.*

The objective of this study was to evaluate the effects of enzyme fermented oat (FO) on growth performance, digestibility, blood profile, and fecal gas in growing pigs. A total of 125 pigs [(Landrace × Yorkshire) × Duroc] with an average initial BW of 20.5 ± 0.8 kg were used in a 6 wk growth trial, and were allotted to 5 dietary treatments in a randomized complete block design. There were 5 pens per treatment with 5 pigs per pen. Dietary treatments included: 1) CON (100% nature oat), 2) FO1 (75% nature oat + 25% FO), 3) FO2 (50% nature oat + 50% FO), 4) FO3 (25% nature oat + 75% FO) and 5) FO4 (100% FO). The oats, before added to diets, were treated by protease (26,014 U/g), amylase (7,176 U/g) xylanase (799 U/g), cellulose (5,204 U/g) and a-galactosidase (176 U/g) for 72 h. Data were subjected to the GLM procedure of SAS. In result, there was no difference in growth performance (ADG, ADFI, and G:F) among dietary treatments ($P > 0.05$). Apparent total tract digestion (ATTD) of DM was higher in FO2 group than CON group throughout the experiment ($P < 0.05$), as well as no difference was observed among FO2, FO3 and FO4 groups ($P > 0.05$). ATTD of energy was higher in FO2, FO3 and FO4 than CON group, throughout the experiment ($P < 0.05$). Plasma glucose concentration, red blood cell (RBC) and white blood cell (WBC) counts, and lymphocyte percentage did not differ among treatments. No difference was observed in fecal gas (H_2S, Acetic acid, NH_3). In conclusion, the FO has a beneficial effect on the ATTD of DM and energy.

Key words: fermented oat, growing pigs, growth performance

M206 Effects of emulsifier and multi-enzyme on growth performance, organ weight, meat quality and blood characteristics in broilers. S. C. Kim*, H. J. Kim, and I. H. Kim, *Dankook University, Cheonan, Choongnam, South Korea.*

This study was conducted to evaluate the effects of emulsifier and multi-enzyme on growth performance, organ weight, meat quality and blood characteristic in broilers. A total of 672 Ross 308 broilers with an initial BW of 34 ± 5 g were allotted into 1 of the 6 treatments (16 broilers per pen and 7 replicate pens per treatments). Dietary treatment included: 1) PC (basal diet), 2) NC (basal diet - 100 kcal down spec.), 3) R05 (NC + 0.05% emulsifier), 4) R10 (NC + 0.10% emulsifier), 5) E05 (NC + 0.05% multi-enzyme), and 6) E10 (NC + 0.10% multi-enzyme). The experiment lasted for 35 d. Data were subjected to the GLM procedures and Duncan multiple range test was used to com-

pare the means of the treatments. Overall the experiment, BWG was higher in R10 and E10 treatments than NC treatment (1,454, 1,446 vs. 1,358 g; $P < 0.05$). Liver weight was higher in E10 treatment than NC and R10 treatments (3.75 vs. 2.45, 2.54%; $P < 0.05$). Spleen weight was increased in R05, E05 and E10 treatments compared with PC, NC and R10 treatments (0.16, 0.14,0.18 vs. 0.09, 0.10, 0.10%; $P < 0.05$). Breast muscle weight was higher in PC, R05 and E05 treatments than E10 treatment (9.86, 9.28, 9.20 vs. 7.24%; $P < 0.05$). Abdominal fat weight was greater in E10 treatment than other treatments (2.12 vs. 1.28, 0.51, 1.24, 1.16, 1.12%; $P < 0.05$). NC treatment had a higher WHC than other treatments (80.67 vs. 73.83, 69.71, 68.08, 63.86%; $P < 0.05$). Lightness of breast meat was higher in NC treatment than that in PC, R10 and E05 treatments (64.33 vs. 57.12, 57.92, 58.17%; $P < 0.05$). In drip loss, NC treatment was higher compared with PC, R05, R10 and E05 treatments on d1 (6.52 vs. 2.70,, 3.51, 3.56, 2.97%; $P < 0.05$), NC treatment was higher compared with PC and E05 treatments on d3 (14.74 vs. 8.75, 8.26%; $P < 0.05$), and NC treatment was higher compared with PC treatment on d5 (18.29 vs. 10.50%; $P < 0.05$). In conclusion, the dietary supplementation emulsifier and multienzyme can bring benefit on BWG, relevant organ weight, WHC, breast meat color and drip loss.

Key words: broilers, emulsifier, multi-enzyme

M207 Hydrolysis of native starches by gastric enzymes in vitro: 1. Relationship between starch hydrolysis and organic matter digestibility. O. O. Adeleye*[1], A. D. Ologhobo[1], P. A. Iji[2], and O. A. Adebiyi[1], *[1]Department of Animal Science, University of Ibadan, Department of Animal Science, University of Ibadan Ibadan, Oyo State, Nigeria, [2]School of Environmental and Rural Sciences, University of New England, School of Environmental and Rural Sciences, University of New England Armidale, NSW, Australia.*

An investigation was carried out using a 2-step enzymatic model simulating foregut digestibility to study the relationship between starch hydrolysis and organic matter digestibilities of different native starches. Starches of sago, rice, wheat, corn, sweetpotato, arrowroot and potato as well as sweetpotato meal, cassava pulp and tapioca were selected based on their starch content ranging from 575.1 to 846.3mg/g OM. Substrates were incubated in a pepsin/HCl solution for 1.5 h and subsequently in potassium phosphate buffer containing pancreatin and amylase for 1, 2, 3 and 6 h. Hydrolyzed starch and residual organic matter were measured at each time point. Starch hydrolysis ranged from 9.8% in potato starch to 85.5% in sago starch with their corresponding organic matter digestibilities of 22.36% and 95.04% respectively at 6 h of incubation. Relationship between starch hydrolysis and organic matter digestibility for all substrates could be described by: Starch hydrolysis (mg/g OM) = −93.1 + 0.91 × organic matter digestibility at incubation time t, $R^2 = 0.8$. While relationship between starch hydrolysis and organic matter digestibility for individual substrates were described with R^2 ranging from 0.8 to 0.99. Organic matter digestibility was also seen to precede the take off of starch hydrolysis for all substrates studied confirming that digestion of non-starch fractions occurred prior and simultaneously with starch hydrolysis. Variations in starch hydrolysis for the different substrates were attributed to their granular sizes and crystalline structures.

Key words: starch hydrolysis, organic matter digestibility, in vitro

M208 Performance of 1- to 42-day-old broilers fed diets containing multienzyme complex and lipid sources. G. do Valle Polycarpo*[1], A. C. Pezzato[1], V. C. da Cruz[2], J. R. Sartori[1], V. B. Fascina[1], F. B. de Carvalho[1], F. Vercese[1], N. C. Alexandre[1], L. P. Centenaro[1], I. M. G. P. de Souza[1], P. G. Castelo[1], E. M. Muro[1], W. T. da Silva[1], V. C. Pelícia[1], P. C. de Araujo[1], *[1]São Paulo State University, Botucatu Campus, Botucatu, São Paulo, Brazil, [2]São Paulo State University, Dracena Campus, Dracena, São Paulo, Brazil.*

This work was carried out at the São Paulo State University, Botucatu Campus, Brazil, with the aim of evaluating the performance of broilers fed diets containing a multienzyme complex (MeC) and different lipid sources from 1 to 42 d of age. A total of 840 1-d-old male Cobb chicks were housed, allotted in a completely randomized design featuring a 2 × 2+2 factorial arrangement, 2 lipid sources (soybean oil and poultry fat) with 2 inclusion levels (2% and 4%) in feeds supplemented with MeC; and 2 control treatments without added lipids – a positive control using MeC-supplemented feed, and a negative control without added MeC. There were 4 replications with 35 broilers per experimental unit (density = 14 birds/m^2). Mean initial chick weight was 44.55 g. The different feeds featured similar energy and AA levels within each breeding phase, and were formulated based on corn and soybean meal. Water and feed were supplied ad libitum. There was no interaction ($P > 0.05$) between lipid source and inclusion level for the following studied variables: BW, ADG, ADFI and G:F. Birds fed diets containing lipids in feed showed greater ($P < 0.01$) BW and ADG than those fed lipid-free diets. Lipid sources did not influence ($P > 0.05$) broiler performance, which can be attributed to the higher ratio of unsaturated and polyunsaturated fatty acids in poultry fat as compared with other animal fat sources, making it an excellent alternative to soybean oil. The inclusion of 4% lipid in feed led to greater ($P < 0.01$) BW (2.812 g vs. 2.701 g), ADG (2.768 g vs. 2.657 g) and ADFI (4.827 g vs. 4.579 g) compared with 2% inclusion, which demonstrates that incorporating higher levels of oil into feed benefits growth and increases intake. G:F was not influenced ($P > 0.05$) by the treatments. The inclusion of 4% lipid in feed increases ADG and BW of birds, regardless of lipid source. Diets without lipid inclusion – with or without MeC – show inferior performance to the others.

Key words: poultry fat, soybean oil

M209 Carcass and cuts yield, and abdominal fat level in 42-day-old broilers subjected to diets containing multienzyme complex and lipid sources. A. C. Pezzato*[1], G. do Valle Polycarpo[1], V. C. da Cruz[2], J. R. Sartori[1], V. B. Fascina[1], F. Vercese[1], N. C. Alexandre[1], L. P. Centenaro[1], I. M. G. P. de Souza[1], P. G. Castelo[1], E. M. Muro[1], W. T. da Silva[1], A. C. Stradiotti[1], M. K. Maruno[1], F. Barros de Carvalho[1], *[1]São Paulo State University, Botucatu Campus, Botucatu, São Paulo, Brazil, [2]São Paulo State University, Dracena Campus, Dracena, São Paulo, Brazil.*

This work was carried out at the experimental slaughterhouse of the São Paulo State University, Botucatu Campus, Brazil, with the aim of evaluating carcass yield, cuts and abdominal fat level in broilers fed diets containing multienzyme complex (MeC) and different lipid sources at 42-d of age. A total of 840 1-d-old male Cobb chicks were housed in 24 boxes at an experimental aviary, with density equal to 14 birds/m^2. The broilers were raised from 1 to 42 d of age in a completely randomized design featuring a 2 × 2+2 factorial arrangement, 2 lipid sources (soybean oil and poultry fat) with 2 inclusion levels (2% and 4%) in feeds supplemented with MeC; and 2 control treatments without added lipids – a positive control using MeC-supplemented feed, and a negative control without added MeC. There were 4 replications with 35 broilers per experimental unit. The different feeds featured similar

energy and AA levels within each breeding phase, and were formulated based on corn and soybean meal. Water and feed were supplied ad libitum. At 42 d of age, 5 birds per replication were slaughtered following an 8-h fast to determine carcass and cuts yield, and abdominal fat percentage. Carcass yield was determined by considering the weight of the dressed and eviscerated carcass (without feet, head and neck) in relation to live fasting weight obtained just before slaughter. For the other cuts (breast, drumstick and thigh, back and abdominal fat), yield was calculated in relation to eviscerated carcass weight. The treatments did not influence ($P > 0.05$) any of the variables. Multienzyme complex and lipid sources do not influence carcass and cuts yield, or abdominal fat level of broiler chickens.

Key words: poultry fat, soybean oil

M210 Effect of dietary phytase on performance, digestive enzymes and intestinal morphology in weaned pigs. M. C. Shields*[1], E. van Heugten[1], C. H. Stahl[1], A. J. Moeser[2], P. W. Plumstead[3], and M. H. Borgmann[1], *[1]Department of Animal Science, North Carolina State University, Raleigh, [2]Department of Clinical Sciences and Molecular, Biomedical Sciences, College of Veterinary Medicine, North Carolina State University, Raleigh, [3]Danisco Animal Nutrition, Marlborough, Wiltshire, UK.*

This study was designed to evaluate the effect of an *E. coli* phytase on weaned pig performance, trypsin and chymotrypsin activity in the small intestine, and intestinal morphology. Pigs (n = 40; BW = 9.72 ± 0.36 kg) were weaned at 21 d of age and housed individually. Pigs were acclimated and fed a common starter diet for 14 d before being assigned to 1 of 5 dietary treatments. Treatments consisted of a positive control diet (PC) without phytase (0.6% total P and 0.29% available P) and a negative control diet (NC) (0.45% total P and 0.14% available P) supplemented with 1 of 4 levels of phytase (0, 500, 1000, 2000 FTU/kg). Diets were corn-soybean meal based with 1.2% SID lysine and fed in mash form for 2 wk. Phytase supplemented at 2000 FTU/kg diet tended to increase ADG in a step-wise manner with increasing phytase dose ($P = 0.10$) to the highest phytase dose of 2000 FTU/kg. Increasing dietary phytase content linearly improved G:F ratio ($P < 0.05$; 0.52, 0.57, 0.59, 0.78 for 0, 500, 1000 and 2000 FTU of phytase, respectively). Phytase supplementation also tended to decrease linearly ADFI ($P = 0.07$; 0.78 0.73, 0.73, 0.67 kg/d). As dietary phytase increased, there was a numerical increase in duodenal trypsin activity (quadratic $P = 0.13$; 79.3, 97.8, 133.7, 108.9 units/mg protein). Phytase supplementation did not impact ileal trypsin ($P = 0.83$) or chymotrypsin activity ($P = 0.44$). Phytase linearly decreased duodenal villi height ($P = 0.03$; 310, 191, 193, 177 µm). Ileal villi height was lower for PC than NC ($P < 0.05$; 150.3 vs. 177.8 µm), and duodenal ($P = 0.07$; 55.6 vs. 67.0 µ) and ileal ($P = 0.09$; 54.2 vs. 62.3 µ) villi width tended to be lower for PC compared with NC, but they were not impacted by phytase. Dietary treatments did not impact crypt depth in the duodenum ($P = 0.84$) or ileum ($P = 0.19$). Phytase supplementation did not affect pH in the stomach ($P = 0.92$), duodenum ($P = 0.38$) or ileum ($P = 0.29$). Duodenal pH was increased ($P = 0.05$) in PC (5.92) when compared with NC (5.62). In conclusion, phytase improved nursery pig performance, increased trypsin activity in the duodenum, and decreased duodenal villi height in weaned pigs.

Key words: phytase, pigs, enzymes

M211 Effect of carbohydrolase complex and phytase combined in corn-soybean meal diet for pigs. M. Ceccantini*[1], B. V. Freitas[2], M. M. Mota[3], N. B. Petroli[3], C. C. Silva[3], C. S. S. Araujo[2], and L. F. Araujo[3], *[1]Adisseo, Sao Paulo, SP, Brazil, [2]FMVZ/USP, Pirassununga, SP, Brazil, [3]FZEA/USP, Pirassununga, SP, Brazil.*

This experiment was conducted to evaluate the effect of a multiple enzyme complex containing carbohydrolases and 6-phytase (Rovabio Max AP, Adisseo) on the performance and carcass characteristics of pigs fed a corn-soybean meal diet. 96 barrows (7 wk old) were assigned to a randomized block design and fed 3 experimental diets with 8 replicates (4 pigs/pen) for 100 d. The positive control diet was a standard diet formulated to meet the requirement of all nutrients, while the negative control diet was reformulated with reductions in energy (85 kcal ME/kg at initial phase, and 65 kcal ME/kg at the other phases), 3% of protein, 3% of digestible AA, 0.15% of Av.P, and 0.10% of Ca. The treatments were: T1- Positive control diet, T2 - Negative control diet supplemented with enzyme, T3- Negative control diet. At 100 d, one barrow/pen was slaughtered and fat thickness, muscle thickness, lean meat and muscle color were measured. For the purpose of distribution of pig carcasses into commercial classes according to SEUROP system methods, which is a method that classifies carcass according to lean percentage, all carcass sides were categorized into different classes (S, > 60%; E, 55 to 60%; U, 50 to 55%; R, 45 to 50%; O, 40 to 45%; and P, < 40% carcass lean). Barrows fed a diet supplemented with enzymatic complex showed better ADG (0.875, 0.913, and 0.856, respectively), G:F (2.44, 2.34, 2.46, respectively), and lower fat thickness (29, 24, and 26 mm respectively) than other treatments ($P < 0.05$). None of treatments resulted in classification of carcasses into the meat class of highest meat ratio (S) or lowest meat ratios (P). However, the use of the enzyme complex resulted in higher carcass ratio U (12.5, 37.5, and 12.5% respectively) than other treatments, and positive control treatment showed higher carcass ratio O (75, 25, and 37.5%, respectively). There was no difference to the other characteristics. The results indicated that dietary enzyme supplementation in corn and soybean meal based diet is efficient in reducing costs, by reducing nutrients requirements, without compromising performance and carcass characteristics.

Key words: carcass characteristics, enzymatic complex, performance

M212 Effects of β-glucan and probiotics (*Bacillus subtilis* and Kefir) supplementation on growth performance, blood profile, relative organ weight and meat quality in broiler chickens. J. H. Jang*, L. Yan, and I. H. Kim, *Dankook University, Cheonan, Choongnam, South Korea.*

This study was conducted to determine β-glucan and probiotics (*Bacillus subtilis* and Kefir) on growth performance, blood profile, relative organ weight and meat quality in broilers. A total of 315 Ross 308 broilers with an initial BW of 46 ± 5 g were allotted into 1 of 7 treatments (15 broilers per pen and 3 replicate pens per treatment). Dietary treatments included: 1) NC, basal diet (antibiotics-free diet); 2) PC, NC + 40 mg/kg avilamycin; 3) B, NC + 0.1% β-glucan; 4) P, NC + 0.1% *Bacillus subtilis*; 5) K, NC + 0.1% Kefir; 6) BP, NC + 0.1% β-glucan + 0.1% *Bacillus subtilis*; and 7) BK, NC + 0.1% β-glucan + 0.1% Kefir. The experiment lasted for 35 d. Data were subjected to the GLM procedures of SAS and Duncan's multiple range test was used to compare the means of the treatments. On d 21, broilers in PC, B, P, K, BP and BK treatment had a higher ($P < 0.05$) ADG than broilers in NC treatment group. On d 35, broilers fed BP had a higher ($P < 0.05$) ADG than those fed NC diet. Overall, ADG in PC, B, P, K, BP and BK treatments was higher ($P < 0.05$) than that in NC treatment. G:F was higher ($P < 0.05$) in PC treatment group compared with NC treatment group. The BP treatment increased ($P < 0.05$) relative liver weight. Broilers in BK treatment group had a higher ($P < 0.05$) relative breast meat and gizzard weight than those in NC treatment group. Broilers fed PC, B, BP and BK diets had a higher ($P < 0.05$) redness than those fed NC diet. Furthermore, the yellowness was higher ($P < 0.05$) in BP treatment than in K treatment. On d 5 and 7, drip loss was decreased ($P < 0.05$) by dietary supplementation of 0.1% β-glucan + 0.1% Kefir. Cooking loss was lower ($P < 0.05$) in BP and BK treatment groups than that in NC treatment. In conclusion, dietary supplementation of β-glucan and/or probiotics could increase the growth performance of broilers and 0.1% β-glucan along with 0.1% Kefir could improve broiler′s relative organ weight and meat quality.

Key words: β-glucan, probiotics, broiler

M213 Effects of caprylic acid and *Yucca schidigera* extract supplementation on growth performance, nutrient digestibility, fecal microflora and blood profiles in growing pigs. B. U. Yang*, S. Zhang, and I. H. Kim, *Dankook University, Cheonan, Choongnam, South Korea.*

This study was conducted to evaluate the effects of caprylic acid and *Yucca schidigera* extract supplementation on growth performance, nutrient digestibility, excreta microflora and blood profiles in growing pigs. A total of 120 [(Landrace × Yorkshire) × Duroc] pigs with a initial body weight (BW) of 23.3 ± 1.74kg was used in a 6–wk experiment. Pigs were randomly allotted to 1 of 6 treatments with 5 replicate pens per treatment and 4 pigs per pen. Dietary treatments included: 1) NC (Antibiotic free diet), 2) PC (NC + 0.01% Apramycin), 3) B1 (NC + 0.05% Caprylic acid + 0.05% Yucca extract), 4) B2 (NC + 0.1% Caprylic acid + 0.1% Yucca extract), 5) B3 (NC + 0.15% Caprylic acid + 0.15% Yucca extract) and 6) B4 (NC + 0.2% Caprylic acid + 0.2% Yucca extract).Overall the experiment, pigs fed the B2 had a greater ADG and G:F but lower ADFI than those fed the NC diet ($P < 0.05$). The ATTD of DM and N was higher in B2, B3, B4 and C1 treatments than that the NC treatment ($P < 0.05$). and ATTD of energy was higher in B4, C1, B3, PC, B2 and B1 groups than that in NC group ($P < 0.05$). The number of *Lactobacillus* was greater in B2 treatment than that in NC, PC and B4 treatments ($P < 0.05$). NC had a higher *E. coli* number compared with other treatments ($P < 0.05$), further more PC and B3 treatments had a lower *E. coli* concentration than B1, B2 and C1 treatments ($P < 0.05$). The total protein concentration in the blood was increased in B1 treatment ($P < 0.05$). Moreover, the IgG concentration was increased in both B1 and C1 treatments compared with the NC treatment ($P < 0.05$). NC treatment had a higher HDL-cholesterol concentration than B3 and C1 treatments ($P < 0.05$), furthermore LDL-cholesterol concentration was higher in B3, B1 and PC treatments compared with the other treatments ($P < 0.05$). It is concluded that caprylic acid and *Yucca schidigera* extract at level of 0.1 or 0.2% can improve growth performance, nutrient digestibility, fecal microflora and blood profiles in growing pigs.

Key words: caprylic acid, growing pigs, yucca extract

M214 Effect of fructooligosaccharide and levan on growth performance, nutrient digestibility, blood characteristic and diarrhea in growing pigs. L. Yan*, X. Y. Guo, and I. H. Kim, *Dankook University, Cheonan, Choongnam, South Korea.*

A total of 100 commercial cross-bred pigs [(Duroc × Yorkshire) × Landrace, weaned at 21 d, BW = 5.97 ± 0.46 kg] were allocated to 1 of 5 treatments [4 replicates with 5 pigs per pen (3 barrows and 2 gilts)] to determine the effects of fructooligosaccharide (FOS) and levan (LV) on growth performance, nutrient digestibility, blood characteristic and diarrhea in weaning pigs. The experiment lasted for 6 wk. The experimental treatments were: 1.NC, basal diet; 2.PC, NC + 0.01% apramycin; 3. LV, NC + 0.1% levan; 4. BM, NC + 0.1% FOS and 5. LB, NC + 0.05% levan + 0.05% FOS. Data were subjected to the GLM procedures and Duncan multiple range test was used to compare the means of the treatments. Pigs fed PC, BM and LB diets led to a higher (410, 399, 394 vs. 306 g; $P < 0.05$) ADG than the NC diet during 0–14 d. Dietary supplementation of 0.1% FOS increased (402 vs. 327 g; $P < 0.05$) the ADG compared with the NC treatment through the entire period. No difference ($P > 0.05$) was observed on the ADFI and G:F among treatments in the present study. Administration of PC, BM and LB led to higher (84.38, 85.82, 85.42 vs. 78.71; 81.33, 82.73, 83.69 vs. 77.27; 83.43, 86.14, 86.27 vs. 78.91%; $P < 0.05$) DM, N and energy digestibility compared with the NC treatment at the end of 14 d. A lower diarrhea score was detected for the BM treatment compared with the NC treatment during 0–7 d ($P < 0.05$). No difference was observed on the ($P > 0.05$) blood characteristic in the current study. In conclusion, the inclusion of levan or fructooligosaccharide could benefit the growth performance and nutrient digestibility during 0–14 d. Administration of fructooligosaccharide decreased the diarrhea scores and increased the growth performance when the entire period was evaluated.

Key words: fructooligosaccharide, growth performance, levan

M215 Effects of dietary sodium stearoyl-2-lactylate supplementation on growth performance, nutrient digestibility, and blood profiles in growing pigs. B. U. Yang*, H. Y. Baek, and I. H. Kim, *Dankook University, Cheonan, Choongnam, South Korea.*

This study was conducted to evaluate the effects of dietary sodium stearoyl-2-lactylate (SSL) supplementation on growth performance,

nutrient digestibility, and blood profiles in growing pigs. A total of 144 [(Landrace × Yorkshire) × Duroc] pigs with an initial BW of 24.62 ± 1.32 kg were used in a 6-wk experiment. Pigs were randomly allotted to 1 of 6 treatments. Dietary treatments included: 1) PC (basal diet), 2) PCS (basal diet + 0.05% SSL), 3) P50 (50 kcal/kg down spec design (−50 kcal/kg comapred with basal diet)), 4) P50S (P50 + 0.05% SSL), 5) P100 (100kcal/kg down spec design (−100 kcal/kg comapred with basal diet)) and 6) P100S (P100 + 0.05% SSL). There were 6 replicates per treatment with 4 pigs per pens (2 barrows and 2 gilt). Throughout the experimental period, pigs fed the PC, PCS and P50S treatments had greater ADG than those fed the P100 diets (647, 680, 671 vs. 671 g; $P < 0.05$). Average daily gain was decreased as SSL level increased (680, 671 vs. 658 g; $P = 0.025$). Pigs fed P100S diet had greater blood glucose concentration than those fed the PC and PCS diets (90.8 vs. 77.2, 79.3 mg/dL; $P < 0.05$). The blood glucose concentration was increased as energy source decreased (78.3, 83.0 vs. 88.65 mg/dL; $P = 0.018$). However, the triglyceride concentration was decreased as SSL level increased (46.8, 46.0 vs. 45.8mg/dL; $P = 0.022$). In conclusion, SSL at level of 0.05% can improve growth performance and blood profiles in growing pigs.

Key words: blood profile, growing pigs, growth performance

M216 Effect of dietary zootechnical feed additive supplementation on sow and litter performance. D. Solà-Oriol*[1], P. S. Agostini[1], S. L. Vinokurovas[1], B. T. Lund[2], and J. Gasa[1], *[1]Universitat Autònoma de Barcelona, Bellaterra, Spain, [2]Chr. Hansen, Hørsholm, Denmark.*

The aim of the present study was to evaluate the effect of Bioplus 2B supplementation of sows' diet on sows and litter performance. Bioplus 2B is a zootechnical additive containing *B. licheniformis* and *B. subtilis* in a 1:1 ratio. A total of 72 crossbred sows were fed one of 2 experimental treatments from matting to 21 d of lactation. Treatments were: control diet (CTL, n = 35) and CTL + 0.4 ppm of Bioplus 2B (B2B, n = 37). Cereal and soybean meal based diets were formulated to contain 12.2 MJ/kg ME and 6.23 g/kg Lys during gestation and 13.1 MJ/kg ME and 8.93 g/kg Lys during the lactation. At matting, sows were distributed into 2 experimental treatments according to parity number, BW, BCS and backfat (BFP2). Sow BW, BCS and BFP2 were individually monitored at 0, 35 and 110 d of gestation and at 21 d post-farrowing. Feed intake was individually adjusted according to BCS (every 3 wk during gestation) and an ad libitum feeding program was used during lactation. Total feed intake (TFI) of sows was individually recorded during gestation and lactation. Sow and litter performance was controlled until 21 d of age. Litters were standardized in number and weight by cross fostering within each treatment. No difference in BCS or BFP2 was observed between treatments during gestation and lactation periods ($P > 0.10$). Lower and higher TFI was observed for sows fed B2B than those fed CTL diets for the gestation (320 vs. 336 kg; $P < 0.05$) and lactation (129 vs. 121 kg $P < 0.05$), respectively. The total piglets born and piglets born alive was not afected ($P > 0.10$) by the treatments used. A reduction of stillbirth piglets and piglets dead during the suckling period was observed for the sows fed the B2B diet than those fed the CTL diet (1.27 vs.. 2.05 and 1.32 vs.. 2.09; $P < 0.01$, respectively). Total mortality rate during lactation tended to be reduced for the B2B supplemented sows (9.6 vs.. 14.6%; $P = 0.105$). No differences were observed on the number of piglets weaned, litter weight at weaning, or weaning to oestrus interval ($P > 0.10$). It is concluded that B2B may improve sow farrowing performance by reducing piglet mortality at farrowing.

Key words: feed additive, sow, stillborn

M217 Effect of a wheat dextrin and a fructooligosaccharide as prebiotics on nursery pig performance. V. G. Perez*, H. Yang, T. R. Radke, and D. P. Holzgraefe, *ADM Alliance Nutrition Inc., Quincy, IL.*

The wheat dextrin (PMD) and fructooligosaccharide (FOS) selected for this experiment were used as prebiotics to promote pig growth. Both PMD and FOS were added in nursery diets at the dose recommended by their vendors to determine whether or not they have additive effects on promoting pig performance. The experiment was a randomized complete block design; blocks were 3 categories of initial BW. Treatments had a 2 (0 vs.. 0.2% PMD) × 2 (0 vs.. 0.1% FOS) factorial arrangement. Each treatment was replicated with 12 pens of 4 pigs per pen. Pigs were weaned (about 21 d of age) and fed the experimental diets for 28 d, using a 3-phase feeding program (7, 7, and 14 d for feeding phases 1, 2, and 3, respectively). All diets were formulated to provide same amount of nutrients within feeding phase. Carbadox was added at 55 mg/kg of diet to all treatments. The PMD and FOS interacted on the ADG ($P < 0.05$) and G:F ($P < 0.01$). During the first 7 d, PMD increased ADG by 35 g/d in the absence of FOS, but decreased it by 25 g/d in the presence of FOS. Overall, PMD increased ADG by 37 g/d in the absence of FOS, but decreased it by 10 g/d in the presence of FOS. The same pattern of response was observed for G:F in both periods, but no effect was detected for ADFI (Table 1). No main effects of PMD or FOS were detected. These results were consistent with previous dose-response company studies, in which the inclusion of up to 0.2% of prebiotic in nursery diets improved pig performance, but then reduced performance with larger doses of prebiotic. In summary, the inclusion of PMD at 0.2% of the diet improved pig performance only in the absence of FOS.

Table 1. Effect of wheat dextrin (PMD) and fructooligosaccharide (FOS) on pig performance

Item	None	PMD	FOS	PMD+FOS	SEM
Initial BW, kg	5.84	5.85	5.86	5.88	0.02
Days 1-7					
ADG, g/d[a]	189	224	203	178	14
ADFI, g/d	173	198	179	182	12
G:F, g/kg[b]	1,091	1,134	1,129	969	35
Days 1-28					
ADG, g/d[a]	373	410	392	382	11
ADFI, g/d	457	490	474	477	13
G:F, g/kg[b]	817	836	829	802	8

[a]PMD × FOS interaction, $P < 0.05$; [b]PMD × FOS interaction, $P < 0.01$.

Key words: wheat dextrin, fructooligosaccharide, prebiotic

M218 Effects of ractopamine feeding duration on performance and carcass traits of finishing pigs. V. V. Almeida*[1], A. J. C. Nuñez[2], C. Andrade[1], J. C. C. Balieiro[2], and V. S. Miyada[1], *[1]USP/ESALQ, Piracicaba, SP, Brazil, [2]USP/FZEA, Pirassununga, SP, Brazil.*

The β adrenergic agonist ractopamine is increasingly used in the swine industry due to its ability to improve performance and carcass leanness by directing nutrients from adipose tissue toward skeletal muscle. However, the response may vary as a function of ractopamine treatment duration. Therefore, 80 barrows weighing 69.23 ± 7.74 kg BW were used to determine the effects of ractopamine feeding duration on performance and carcass traits of finishing pigs. A randomized complete block design experiment was carried out to evaluate 5 treatments with 8 replications per treatment and 2 pigs per experimental unit

(pen). Dietary treatments included control (without ractopamine for 28 d) and 10 ppm of ractopamine fed for 7, 14, 21 or 28 d before slaughter. Diets were based on corn-soybean meal, formulated to contain 0.88% of digestible lysine and 3.23 Mcal/kg ME. Feed intake and live body weight were recorded weekly to determine ADG, ADFI, and G:F. After 28 d on test, pigs were slaughtered at 101.94 ± 9.06 kg BW and carcass measurements made at 24 h postmortem. Treatment effects were assessed by ANOVA and regression analysis using the GLM procedure of SAS. G:F was quadratically improved (0.331, 0.352, 0.369, 0.377, and 0.367 ± 0.03; $P < 0.05$) as the duration of ractopamine feeding increased from 0 to 28 d; however, ADG and ADFI were not affected ($P > 0.05$) by treatments. Increasing ractopamine feeding duration from 0 to 28 d before slaughter resulted in linear increases on loin eye area (40.28, 42.24, 43.37, 45.03, and 48.86 ± 5.79 cm^2; $P < 0.01$) and loin depth (62.69, 63.69, 66.06, 65.69, and 70.19 ± 6.21 mm; $P < 0.01$). Ractopamine feeding duration did not affect ($P > 0.05$) carcass weight, carcass length, dressing percentage, backfat thickness and lean percentage. These results suggest that the maximum improvement in performance of finishing pigs is achieved within 21 d of ractopamine feeding, while the magnitude of carcass response seems to be directly dependent on ractopamine feeding duration.

Key words: beta-adrenergic agonist, carcass leanness, swine

M219 Effect of zilpaterol hydrochloride supplementation on growth performance in male Japanese Quails. M. Mohammadi*, A. Towhidi, H. Moravej, and A. Z. Shahneh, *Department of Animal Science, university of Tehran, Karj, Karaj, Alborz, Iran.*

Zilpaterol hydrochloride is a β-adrenergic agonist that has been shown to increase lean muscle and decrease fat deposition. In this study, 128 birds at 33 d of age were randomly assigned to 4 treatments. Each treatment consisted of 4 replicates of 8 birds. Diets were formulated based on corn and soybean meal for finishing period (24% CP and 2.9 Mcal/kg of ME) that were supplemented with 0, 0.2, 0.225, or 0.25 mg/kg of live weight d^{-1} of zilpaterol. Quails were fed the diets until d 47 and then slaughtered on d 50. Data were analyzed with using the GLM procedure of SAS. Results showed that during d 33–47, zilpaterol supplementation improved G:F ($P < 0.04$), and live weight gain in group 0.2 and 0.225 compared with control, but did not affect feed intake (Table 1). Birds fed zilpaterol had lower abdominal and subcutaneous fat percentage ($P < 0.05$). Dietary zilpaterol did not affect carcass, thigh, breast and liver weight. It was concluded that zilpaterol hydrochloride supplementation in japans quail improved growth performance and the optimal level of this β-agonist was 0.225 mg/kg of live weight d^{-1}.

Table 1. Effect of zilpaterol supplementation on growth responses in Japanese Quails

Item	T_1 0	T_2 0.2	T_3 0 .225	T_4 0 .25	SEM	*P*-value
Total weight gain(g)	64.31[a]	71.71[b]	75.28[b]	69.87[ab]	2.23	0.03
Feed intake(g)	363.34	369.4	372.87	357.06	6.77	0.4
gain:feed	0.176[a]	0.194[b]	0.202[b]	0.195[b]	0.005	0.041

[ab]Means in each row without a common superscript letter differ ($P < 0.05$).

$T_{1, 2, 3, 4}$: 0, 0.2, 0.225, 0.25 mg/kg of LW^{-1} d^{-1} zilpaterol, respectively.

Key words: zilpaterol hydrochloride, Japanese quail, growth performance

M220 Safety and efficacy of *Moringa oleifera* powder for growing poultry. J. O. Ashong* and D. L. Brown, *Cornell University, Ithaca, NY.*

Leaves from *Moringa oleifera* have been reported to have a remarkable range of qualities from superior nutritional composition, therapeutic applications and prophylactic uses for both humans and animals. Most of these claims are based on anecdotes or uncontrolled observations. The objective of the present study was to evaluate the safety and nutritional efficacy of *Moringa oleifera* leaf meal. At 7 d of age, 60 White-leghorn type chicks were randomly assigned to 4 isocaloric and isonitrogenous experimental diets formulated to contain 0% (control group), 10%, 20% and 30% moringa leaf powder. There were 5 chickens per cage with 3 replicates per diet. Daily feed intake and weekly BW were recorded for the duration of the 5 wk study. Chicks were observed for any signs of abnormal behavior and/or toxicity. Post-trial postmortem examination conducted included weighing of kidney, liver and heart and biochemical analyses such as, cholesterol, uric acid, thyroxine (T4), total protein and iron. There were no signs of abnormal behavior and/or toxicity and mortality during the entire period of the experiment. The control group had a higher feed intake ($P < 0.05$) with a corresponding higher weight gain ($P < 0.0001$) compared with the other treatment groups. Chicks fed with 10% moringa leaf meal, had the lowest feed intake although it did not correspond to the lowest weight gain. Heart, liver and kidney weights were heaviest in the control group even though the kidney weight was not significantly ($P > 0.05$) different from the kidney weights of chicks on the treatment diets. The heart weight decreased with increasing percentage of moringa leaf powder in the meal. The control group had significantly higher levels of cholesterol; triglyceride and uric acid. These results suggest that although incorporation of moringa leaf meal may reduce intake and rate of gain, this ingredient otherwise is not toxic to growing poultry and has some effects on blood lipids profiles that may be of interest to human nutritionists.

Key words: *Moringa oleifera*, safety, poultry

M221 Singular consumption of either *Lactobacillus plantarum* or inulin reduces manure odor from finishing pigs; however, this is negated when offered in combination. C. J. O'Shea, T. Sweeney, B. Bahar, M. Ryan, and J. V. O'Doherty*, *University College Dublin, Dublin, Ireland.*

A 2 × 2 factorial experiment was conducted to investigate the effects of inulin (0 vs. 12.5 g/kg) and/or *Lactobacillus plantarum* (LP) inclusion (0 vs. 0.5 g/kg) on nutrient digestibility, nitrogen excretion, distal gastrointestinal tract (dGIT) fermentation and manure ammonia and odor emissions from finishing pigs. Consumption of diets containing LP and inulin had no influence on apparent total tract nutrient digestibility when offered either singularly or in combination ($P > 0.05$). In the colon, pigs offered diets containing LP decreased concentrations of propionic acid ($P = 0.048$) and valeric acid ($P = 0.007$) when compared with unsupplemented diets. Consumption of inulin-supplemented diets decreased concentrations of isobutyric acid ($P = 0.050$) in the colon when compared with unsupplemented diets. Consumption of diets containing LP increased the *Lactobacillus* spp.:*Enterobacteriaceae* ratio (2.12 vs. 1.66; sem 0.14; $P = 0.034$) when compared with unsupplemented diets. Pigs offered diets containing inulin had decreased numbers of *Enterobacteriaceae* (5.85 vs. 6.66; sem 0.256; $P = 0.035$) compared with unsupplemented diets. There was an interaction between dietary inulin and LP supplementation on fecal *Clostridia* ($P = 0.004$). Singular consumption of either

inulin or LP had no effect on fecal *Clostridia*, however when offered in combination fecal *Clostridia* were increased when compared with the C diet. There was an interaction between dietary inulin and LP supplementation on manure odor at 72h. Consumption of diets supplemented with LP reduced manure odor ($P = 0.007$) when compared with the C diet, however there was no effect of LP when offered in combination with inulin on manure odor emissions. In summary, consumption of a LP-supplemented diet modified the distal gastrointestinal contents and increased the ratio of *Lactobacillus* spp. to *Enterobacteriaceae* in fecal matter. Consumption of LP singularly reduced manure odor, however when offered in combination with inulin this beneficial event was negated.

Key words: pig, odor, microbes

M222 Standardized total tract digestibility of P in Dried Fermentation Biomass, Peptone 50, and P.E.P. 2 Plus fed to weanling pigs. J. K. Mathai*[1], R. C. Sulabo[1], J. L. Usry[2], B. W. Ratliff[3], D. M. McKilligan[3], and H. H. Stein[1], *[1]University of Illinois, Urbana, [2]Ajinomoto Heartland, LLC, Chicago, IL, [3]TechMix, LLC, Stewart, MN.*

Forty barrows (BW: 12.4 ± 1.3 kg) were used to measure the apparent (ATTD) and standardized total tract digestibility (STTD) of P in Dried Fermentation Biomass (DFB), Peptone 50 (PEP50), and P.E.P. Two Plus (PEP2+) fed to weanling pigs and to compare these values to those in fish meal. The DFB product (Ajinomoto Heartland LLC) is a co-product from AA production and PEP50 and PEP2+ (TechMix LLC) are produced from hydrolyzed pig intestines. Pigs were housed individually in metabolism cages and were randomly allotted to 5 diets with 8 replicate pigs per diet. Four diets were formulated with DFB, PEP50, PEP2+, or fish meal as the sole source of P in the diet. A P-free diet was used to measure basal endogenous P losses (EPL). Feces were collected for 5 d based on the marker to marker approach after a 5-d adaptation period. Analyzed total P in DFB, PEP50, PEP2+, and fish meal were 0.88, 0.74, 0.80, and 3.25%, respectively. Daily P intake of pigs fed DFB, PEP50, and PEP2+ were less (0.80, 0.82, 0.96 g/d; $P < 0.01$) than in pigs fed fish meal (1.77 g/d). Fecal P concentration (0.41, 0.57, 1.12, 2.56%) and daily P output (0.08, 0.09, 0.27, 0.62 g/d) were less ($P < 0.01$) in pigs fed DFB and PEP2+ than in pigs fed PEP50 and fish meal. The amount of P absorbed was different ($P < 0.01$) between all treatments (0.56, 0.72, 0.87, and 1.15 g/d in PEP50, DFB, PEP2+, and fish meal, respectively). The ATTD of P was greater ($P < 0.01$; SEM = 1.8) in DFB (90.4%) and PEP2+ (90.6%) than in PEP50 and fish meal (68.0 and 65.5%, respectively). The basal EPL was measured at 148 ± 63 mg/kg DMI in pigs fed the P-free diet. The STTD of P in DFB (96.9%) and PEP2+ (97.6%) were greater ($P < 0.01$; SEM = 2.2) than in PEP50 and fish meal (76.2 and 68.5%, respectively). Likewise, PEP50 had greater ($P < 0.01$) STTD of P than in fish meal. Therefore, DFB, PEP50, and PEP2+ had greater STTD of P, but lower concentration of P, than fish meal.

Key words: alternative feedstuffs, phosphorus, pigs

M223 Digestibility of green banana flour (*Musa cavendishi*) in roosters. E. Toledo*[1], F. Martínez–Bustos[2], and A. G. Borbolla[1], *[1]Department of Swine Medicine and Production, School of Veterinary Medicine, Universidad Nacional Autónoma de México, Mexico City, Mexico, [2]CINVESTAV, IPN, Unidad Queretarétaro, Querétaro, Qro. Mexico.*

Banana flour can be used in swine and poultry, as an alternative energy source, when the fruit is locally available and cheaper than the cereals regularly fed to these species. The aim of this study was to evaluate the fecal digestibility of banana flour in roosters (Ross, 308). Green bananas were chopped in pieces (1cm thickness/10cm length), and heat dried in a convection oven (Yakomoto 900, YKN), at 55, 70, 80 and 90°C, for 48 h. The trial was conducted in 12 roosters, which were randomly assigned to 4 groups (3 roosters/group). Each treatment (temperature of dehydration), was changed every wk using a Latin Square Model. Digestibility of the flour was evaluated using the methodology described by Douglas et al. (1997), where each bird received 32 g of banana flour in one shot daily. Feces were collected after 48 h and dehydrated in a convection oven at 60°C for 48 h. The percentage of digestibility was determined using the following formula: {[(feed, g – feces, g) / feed, g] * 100}.The resulting data was analyzed using the statistical package SPSS 17.0. The amount of feces collected was higher ($P < 0.05$), for those animals that consumed the flour dehydrated at 80°C (19.97 g ± 2.05), than the other 3 treatments (55°C = 12.88 g ± 1.73; 70°C = 11.38 g ± 1.62 and 90°C = 13.83 g ± 1.37). Therefore, the digestibility of the flour dried at 80°C was lower ($P < 0.05$), than the values observed for the other drying temperatures (36.63% ± 6.41 vs.. 59.12% ± 5.32; 63.88% ± 5.02 and 56.14% ± 4.27; for 80, 55, 70 and 90°C, respectively). Banana flour dehydrated at 55 and 70°C showed the highest digestibility and the lowest amount of feces produced by roosters. According to these results, it can be concluded that roosters had a better use of the nutrients of the banana flour, when it is dried at low temperature (55 and 70°C). Banana flour might be considered a good source of energy for monogastric species such as swine and poultry.

Key words: banana flour, digestibility, rooster

M224 Effects of increasing levels of dietary turmeric on growth performance and immune response of nursery pigs. M. R. Bible*[1], S. D. Carter[1], H. J. Kim[1], T. M. Walraven[1], C. Houchen[2], S. Anant[3], and R. Ramanujum[4,5], *[1]Oklahoma State University, Stillwater, [2]University of Oklahoma Health Sciences Center, Oklahoma City, [3]University of Kansas Medical Center, Kansas City, KS, [4]Swaath Inc., Oklahoma City, OK, [5]ADNA Inc., Dublin, OH.*

Turmeric is a common dietary spice used in India and Southeast Asia that contains the active ingredient curcumin, a potent polyphenolic phytochemical. Curcumin and curcuminoids in turmeric are known to have anti-inflammatory and anti-microbial activities. Therefore, 32 crossbred (D x (L x Y)) barrows (7.5 kg; 20 d of age) were weaned and used to determine the effects of dietary turmeric on performance and immune response. Pigs were blocked by BW and ancestry, and allotted randomly to 4 dietary treatments in a randomized complete block design. Pigs were housed individually in metabolism crates in an environmentally-controlled building (8 pigs/trt). During a 3-d adjustment period to the crates, barrows consumed a standard, phase 1, nursery diet. After the adjustment period, the experimental diets were fed for 21 d. A corn-soybean meal-based diet (1.44% SID Lys) containing no antibiotics served as the control. The experimental diets contained increasing levels of turmeric at 2, 4, and 8 g/kg of diet, respectively. ADG, ADFI, and G:F were calculated weekly. Turmeric consumption per day (linear, $P < 0.0001$) was 0, 89, 181, and 354 mg/kg BW, respectively. Turmeric increased (quad, $P < 0.03$) final BW (14.8, 15.8, 16.3, 15.5 kg), ADG (350, 389, 417, 382 g), ADFI (458, 487, 508, 459 g), and G:F (0.762, 0.798, 0.820, 0.826; linear, $P < 0.03$). On d 20 of the experiment, a lipopolysaccharide (LPS) challenge was performed. Pigs were administered intraperitoneally saline-based *E. coli* O111:B4 LPS (25 μg/kg of BW). Rectal temperature was measured and blood was collected for the analysis of tumor necrosis factor-α (TNF-α) at 0

h, and 3, 6, 12, and 24 h post-injection. Turmeric decreased (quad, $P < 0.05$) rectal temperature at h 3 (41.0, 40.6, 40.8, 40.7°C) with a corresponding numerical decrease (quad, $P = 0.12$) in blood serum TNF-α (2509, 805, 1300, 1585 pg/mL). In general, there were no differences observed for TNF-α concentrations or rectal temperature at any other hour post-LPS. In conclusion, dietary turmeric increased performance and lowered the inflammatory cytokine, TNF-α, during an *E. coli* LPS challenge in weanling pigs.

Key words: pig, turmeric, performance

M225 Evaluation the effect of inositol monophosphate supplementation on growth performance, blood profiles and nutrient digestibility in weaning pigs. H. Y. Baek*, H. W. Cho, and I. H Kim, *Dankook University, Cheonan, Choongnam, South Korea.*

This study was conducted to evaluate the effect of inositol monophosphate (IMP) supplementation on growth performance, blood profiles and nutrient digestibility in weaning pigs. A total of 200 weaning pigs [(Yorkshire × Landrace) × Duroc] with an initial BW 6.21 ± 0.90 kg were randomly assigned to 5 dietary treatments as follows: 1) CON (basal diet), 2) IMP02 (basal diet + 0.2% IMP), 3) IMP04 (basal diet + 0.4% IMP), 4) IMP06 (basal diet + 0.6% IMP) and 5) IMP10 (basal diet + 1.0% IMP). There were 8 replicate pens per treatment and 5 pigs per pen. Average daily gain (ADG) was higher ($P < 0.05$) in IMP04 treatment than that in IMP10 treatment during the overall experiment. Dry matter digestibility was higher ($P < 0.05$) in IMP06 treatment compared with that in CON, IMP02 and IMP10 treatments and CON treatment was lower ($P < 0.05$) than that in IMP04 and IMP06 treatments on d14. Nitrogen digestibility was higher ($P < 0.05$) in IMP04 treatment than that in CON treatment. Also, energy digestibility was higher ($P < 0.05$) in IMP04 treatment compared with that in CON, IMP02 and IMP10 treatments. On d28, nitrogen digestibility was higher ($P < 0.05$) in IMP04 treatment compared with that in CON and IMP10 treatments. IgG concentration was higher ($P < 0.05$) in IMP04 treatment than that in CON, IMP02 and IMP06 treatment on 28d. However, total cholesterol, Red blood cell (RBC), White blood cell (WBC) and lymphocyte were not affected by dietary treatments during this experiment ($P > 0.05$). Jejunum crypt depth was lower ($P < 0.05$) in IMP04 treatment compared with that in CON treatment ($P > 0.05$). In conclusion, growth performance was enhanced by supplementation of 0.4% IMP, and nutrient digestibility was increased by 0.4 and 0.6% IMP, and IgG concentration was improved by the supplementation of 0.4 and 1.0% IMP, and villi and crypt statue of small intestine was improved by the supplementation of 0.4 and 1.0% IMP.

Key words: growth performance, pigs, nutrient digestibility

M226 Effects of probiotics and probiotics mix on growth performance and blood characteristics. J. M. Lee*, S. M. Hong, and I. H. Kim, *Dankook University, Cheonan, Choongnam, South Korea.*

A total of 150 weaned pigs with an average BW of 6.42 ± 0.91 kg were used in a 4 wk study to investigate the effects of *Bacillus subtilis* and *Bacillus licheniformi* mix (BBM) (1:1) and *Bacillus subtilis* (BS) on growth performance, blood characteristics and nutrient digestibility. Pigs were allocated to 1 of 6 dietary treatments with 5 replicate pens per treatment and 5 pigs per pen. Dietary treatments included: 1) NC (no antibiotics), 2) PC (antibiotics), 3) NBP (NC + 0.04% BBM), 4) PBP (PC + 0.04% BBM), 5) NCP (NC + 0.05% BS) and 6) PCP (PC + 0.05% BS). Data were subjected to the GLM procedures of SAS and Duncan multiple range test was used to compare the means of the treatments. On d 14, pigs fed NBP, PBP and PCP diets showed a higher ADG than pigs fed NC diet (286, 282, 282 vs. 228 g; $P < 0.05$). The ADFI was greater in NBP treatment than that in NCP treatment (345 vs. 271 g; $P < 0.05$). On d 28, pigs fed NBP and PCP diets showed a higher ADG than NC diet (604, 641 vs. 490 g; $P < 0.05$). The ADFI was greater in PC, NBP, BPB and PCP treatments than that in NCP treatment (779, 795, 792, 812 vs. 713 g; $P < 0.05$). G:F was greater in NCP treatments than NC treatment (0.812 vs. 0.652; $P < 0.05$). Overall the experiment, NBP, PBP and PCP diets had a higher ADG than NC diet (445, 435, 462 vs. 359 g; $P < 0.05$) and ADFI was greater in NBP and PCP treatments than NC and NCP treatments (570, 575 vs. 522, 492; $P < 0.05$). G:F was greater in NCP treatment than NC treatment (0.831 vs. 0.688; $P < 0.05$). On d 28, IgG was higher in PC and NCP treatments than that in NC, PBP and PCP treatments (434, 428 vs. 348, 357 mg/dl; $P < 0.05$). Dry matter digestibility was greater in PC treatment than that of NC treatment (82.18 vs. 78.39%; $P < 0.05$). Nitrogen digestibility was higher in PC treatment than that of NC and PCP treatments (74.18 va 67.85, 69.85%; $P < 0.05$). Energy digestibility was higher in PC, PBP and NCP treatments than that of NC and PCP treatments (81.51, 80.30, 80.46 vs. 77.65, 78.22%; $P < 0.05$). In conclusion, dietary supplementation of *Bacillus subtilis* and *Bacillus licheniformi* mix and *Bacillus subtilis* can be considered as an alternative to antibiotics.

Key words: growth performance, probiotics, weaned pig

Physiology and Endocrinology I

M227 ACTH-induced stress impairs the expression of genes involved in steroidogenesis and angiogenesis in dairy cow preovulatory follicles. D. Biran[1], R. Braw-Tal[2], Y. Lavon[1], and Z. Roth*[1], *[1]Department of Animal Sciences, The Robert H. Smith Faculty of Agriculture, Food and Environment, The Hebrew University, Rehovot, Israel, [2]Institute of Animal Science, Agricultural Research Organization, Bet Dagan, Israel.*

Ovulation failure, follicular persistence and follicular-cyst formation are known to impair dairy cow fertility. While the mechanism is not entirely clear, stress-induced alteration in adrenal hormone secretion can cause such ovarian pathologies. We examined changes in genes involved in steroidogenesis and angiogenesis upon ACTH-induced stress. Six synchronized lactating cows were scanned daily by ultrasound (Aloka SSD-900) and plasma samples were taken throughout the experiment. Treated cows (n = 3) were administered ACTH analog (Synacthen Depot; 1mg, s.c.) every 12h from d 15 to d 21 of the cycle. Control cows (n = 3) were administered $PGF_{2\alpha}$ (Estroplan) on d 6 of the cycle to induce development of a preovulatory follicle. Ovaries from both control and treated cows were collected at the slaughterhouse 40h after the last $PGF_{2\alpha}$ administration and on d 23 of the cycle, respectively. Follicular diameter was measured and follicular fluids were aspirated to determine steroid concentrations. Slices of the follicular wall were taken for total mRNA isolation and sqRT-PCR. Administration of ACTH increased ($P < 0.02$) cortisol concentration in the plasma and reduced ($P < 0.01$) milk production, indicating stress. Androstenedione and estradiol concentrations in the follicular fluids were lower ($P < 0.05$) in ACTH-treated follicles relative to controls. The expression of mRNA for LH receptor, 3Î²-HSD and P450arom was lower ($P < 0.02$) in the ACTH-treated group than in controls but P450scc, StAR protein and P450c17 mRNA levels did not differ between the groups. mRNA expression for angiopoietin-1 and angiopoietin-2 did not differ between the groups but that for VEGF120 and VEGF164 was higher ($P < 0.01$) in controls than in ACTH-treated follicles. Findings indicate that ACTH induced stress, and impaired follicular steroidogenesis and angiogenic capacity, characterized by reduced follicular-fluid steroid concentration and low expression of genes involved in these processes. Such alterations might explain, in part, the mechanism underlying ovulation failure and the formation of persistent or cystic follicles under stress.

Key words: persistent follicle, cyst

M228 Comparison of different staining methods on sperm from Holstein bulls. A. Ata, M. E. Inanc, O. Kankavi, O. Yildiz Gulay*, and M. S. Gulay, *Mehmet Akif Ersoy University, Faculty of Veterinery Medicine, Burdur, Turkiye.*

The aim of the current study was to compare effectiveness of various semen staining methods in frozen-thawed and epididymal cattle semen. Frozen semen (American Breeder Service and Ege-Vet) were placed in a water bath first at 37°C for 30 s and thawed. Epididymal semen from cauda epidiymis was obtained from slaughter house (Güç-Birligi, Burdur, Turkiye) and diluted with phosphate buffer solution (PBS). After preliminary examination under the microscope, frozen-thawed and epididymal semen samples were smeared on glass microscope slides using another glass slide and air-dried. Sperm on the slides were stained with Coomassie Blue, Silver nitrate, May–Grünwald+Giemsa, Ponceau-S, Naphthol yellow-S+Eritrosin-B, Ponceau-S+Naphthol yellow-S+Eritrosin-B, Trypan Blue+Giemsa, Eosin+Coomassie Blue and modified Wright′s stain. Stained froty samples were examined under bright field microscopy (Nikon E-600). From all froties at least 100 spermatozoa were investigated. Different staining methods were compared by one way ANOVA. Differences between epididymal and frozen-thawed samples were analyzed by *t*-test procedure. Equatorial region of intact spermatozoa was well defined and acrosomal region was stained differently than other regions by some staining methods (Coomassie Blue, May-Grünwald+ Giemsa, Ponceau-S, Naphthol yellow-S+Eritrosin-B, Eosin+Coomassie Blue; $P < 0.05$). Equatorial regions of spermatozoa with corrapted acrosomes were not stained well. Epidiymal spermatozoa were stained better than frozen-thawed spermatozoa in all staining methods investigated in the present study ($P < 0.05$). This could be because of the substances used in frozen semen as cryoprotectans (proteins of animal origin, etc.). In conclusion, our results demonstrated that Eosin+Coomassie Blue staining method is simple, inexpensive, and reliable method for staining semen from Holstein bulls. The method works quickly, needs fewer methodological steps, and does not require complex laboratory conditions for assessment of establishing live-dead spermatozoa and acrosomal/morphological status in frozen-thawed and epididymal semen obtained from Holstein bulls

Key words: cattle, spermatozoa, staining

M229 Insulin sensitivity correlates with parameters of hepatic lipid metabolism, and is lower in older dairy cows. H. A. van Dorland[1], M. Graber[1,2], S. Kohler[2], T. Kaufmann[3], and R. M. Bruckmaier*[1], *[1]Veterinary Physiology, Vetsuisse Faculty, University of Bern, Bern, Bern, Switzerland, [2]Department of Animal Science, Swiss College of Agriculture, Zollikofen, Bern, Switzerland, [3]Clinic for Ruminants, Vetsuisse Faculty, University of Bern, Bern, Bern, Switzerland.*

Insulin sensitivity may be estimated by the “Revised Quantitative Insulin Sensitivity Check Index” (RQUICKI), which is based on plasma concentrations of insulin, glucose, and free fatty acids (NEFA). It was indicated before that RQUICKI might be used to identify lactating cows with disturbed insulin function. In the present study, data from a field study were used to investigate the association between RQUICKI and the parity of the dairy cows, and of parameters involved in hepatic metabolism. Blood and liver samples were obtained from 185 dairy cows in wk 3 ante partum (-wk3) and in wk 4 (+4wk) and 13 postpartum (+13wk). Blood plasma was assayed for concentrations of NEFA, glucose, and insulin. Liver was analyzed for mRNA expression levels by qRT-PCR encoding 27 enzymes and nuclear receptors related to carbohydrate and lipid metabolism. The results show that cows of >3 parities have a significant lower RQUICKI across sampling points than cows with <3 parities ($P < 0.001$). In addition, RQUICKI was lower in +4wk than in −3wk and +13wk ($P < 0.001$). Significant ($P < 0.01$) Spearman Rank Correlation Coefficients were observed between RQUICKI and mRNA abundance of liver X receptor α (LXRα), sterol regulatory element binding factor 1 (SREBF1), ATP citrate lyase, fatty acid synthase (FASN), Glycerol-3-phophate acyltransferase (GPAM), 3-hydroxy-3-methylglutaryl-coenzyme A reductase (HMGCR), which may illustrate the pathological changes in the liver through infiltration of fat as observed to be associated with disturbed insulin function in man.

Key words: insulin resistance, metabolism, liver

M230 Intrauterine position and adjacent fetal sex status influences fetal and placental growth but not embryonic viability under crowded uterine conditions in pigs. B. A. Freking* and C. A. Lents, *USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE.*

Intrauterine position and sex of adjacent fetuses in litter bearing species have been implicated in physiological and behavioral differences in males and females. Our objective was to quantify influences of uterine position and sex status of flanking fetuses under crowded uterine conditions and test the impact on fetal and placental growth rate. Gilts were subjected to unilateral-hysterectomy-ovariectomy surgery at 160 d of age and mated at approximately 280-d of age. Gilts were assigned to be harvested at d 45, 65, 85, or 105 of gestation. A total of 297 pregnancies were evaluated in 4 contemporary groups. Position in the uterus relative to the cervix, fetal status (alive, dead, mummy), fetal weight, and placental weight were recorded at harvest. Data were coded to test when each fetus was adjacent to 0, 1, or 2 opposite sex fetuses. Data were analyzed by mixed-model ANOVA procedures fitting contemporary group, line, and flanking fetal sex code as fixed effects and sire as a random effect. Nonlinear functions were fitted to the fetal and placental weight data to establish unique growth curves for each flanking sex status code. When considering only observations that had an opportunity to be flanked by 2 adjacent fetuses, the fraction of live fetuses represented by each classification (0, 1, 2) were 26.4%, 50.1%, and 23.4%, respectively, indicating no impact on fetal survival. Fetal weight was not influenced by flanking sex status code at d 45, but was significant ($P < 0.05$) by d 65, and became highly significant ($P < 0.001$) by d 105. Least squares means at d 105 were 800.0 ± 20.3, 748.5 ± 17.8, and 672.7 ± 25.2 g, respectively for flanking sex status codes 0, 1, 2. Placental weight was also similarly influenced by flanking sex status code, but only apparent ($P < 0.01$) by d 105. Fetal growth development in pigs is influenced by sex status of adjacent fetuses, and could be a potential source of variation in behavioral and reproductive differences later in life.

Key words: fetal growth, pigs, survival

M231 The effect of teasing rams with a ewe stimulus prior to semen collection. A. G. Fahey*[1], P. Duffy[1], and S. Fair[2], *[1]University College Dublin, Belfield, Dublin 4, Ireland, [2]University of Limerick, Limerick, Ireland.*

The objective of this study was to determine if exposing rams to a ewe stimulus for 1 h before semen collection could improve the rams' libido and/or semen quality. The experiment was carried out during the breeding season. Rams (European breeds; 1.5 to 4 years of age) were allocated to one of 3 treatments according to breed and age: Treatment 1 (Control); rams (n = 5) were exposed to a ewe not in estrus for 1 h and were subsequently allowed to mount another ewe in estrus for semen collection. Treatment 2 (Non novel ewe); rams (n = 6) were exposed to a ewe in estrus for 1 h after which the same ewe was restrained on a ramp for semen collection. Treatment 3 (Novel ewe); rams (n = 6) were exposed to a ewe in estrus for 1 h after which the rams were allowed to mount a different ewe in estrus for semen collection. Rams did not have tactile contact with the teaser ewe during the 1 h exposure time and the experiment was repeated on each of 5 consecutive days. Libido was measured by the rams' reaction time (time from first foot on the ramp to when ejaculation into the artificial vagina had occurred) and the number of mounts taken before ejaculation. Each ejaculate was assessed for volume, concentration, wave motion and progressive linear motion after 1 h. Data were analyzed using ANOVA with repeated measures using the MIXED procedure of SAS. There were no significant effects of treatment, day or their interaction on reaction time, the number of mounts or on wave motion or progressive linear motion of sperm. There was no significant effect of treatment on semen volume, however, there was a significant effect of day ($P < 0.05$) and a treatment × day interaction ($P < 0.05$). Semen concentration and total sperm number were significantly affected by treatment ($P < 0.05$) and day ($P < 0.01$), however, there was no treatment × day interaction. Exposing rams to an estrus ewe before semen collection does not improve ram libido but does assist in improving the sperm number in the ejaculate.

Key words: ram, libido, semen

M232 Effects of supplemental progesterone and timing of initiation of resynchronization on fertility in lactating dairy cows. T. R. Bilby*[1], R. G. S. Bruno[1], K. J. Lager[1], R. C. Chebel[2], J. G. N. Moraes[2], P. M. Fricke[3], G. Lopes[3], J. O. Giordano[3], J. E. P. Santos[4], F. S. Lima[4], J. S. Stevenson[5], and S. L. Pulley[5], *[1]Texas AgriLife Research and Extension, Texas A&M System, Stephenville, [2]Department of Veterinary Population Medicine, University of Minnesota, St. Paul, [3]Department of Dairy Science, University of Wisconsin, Madison, [4]Department of Animal Sciences, University of Florida, Gainesville, [5]Department of Animal Sciences and Industry, Kansas State University, Manhattan.*

Our objective was to determine the effect of exogenous progesterone (P_4) within a timed artificial insemination (TAI) protocol initiated at 2 different times post-AI on pregnancies per AI (P/AI) in lactating dairy cows. Lactating cows (n = 1,982) from 5 commercial dairy herds were assigned randomly at 31 ± 3 d post-AI, at non-pregnancy diagnosis, in a 2 × 2 factorial arrangement of 4 resynchronization treatments initiated early (EP; 31 ± 3 d) or late (LP; 39 ± 3 d) post-AI. Cows were either treated with a CIDR (C) insert or not (NC) as part of an Ovsynch-56 protocol (GnRH, 7 d later $PGF_{2\alpha}$, 56 h GnRH, 16 h TAI). Therefore, the 4 treatments were: 1) EPNC (n = 509), open cows at 31 ± 3 d post-AI and not receiving a CIDR; 2) EPC (n = 501), open cows at 31 ± 3 d post-AI and receiving a CIDR; 3) LPNC (n = 485), open cows at 39 ± 3 d post-AI and not receiving a CIDR; and 4) LPC (n = 487), open cows at 39 ± 3 d post-AI and receiving a CIDR. Cows were inseminated if observed in estrus before TAI. Pregnancies per AI were determined 31 and 60 d after TAI. In a subgroup of cows (n = 1,101), blood samples were collected and ovarian structures were examined at first GnRH (G1) and $PGF_{2\alpha}$ of the Ovsynch-56 protocol. Percentage of cows with CL at G1 was not affected by treatment but percentage of cows with CL at $PGF_{2\alpha}$ was greater ($P < 0.01$) for EP vs.. LP cows (87.9 vs.. 79.4%). In addition, percentage of cows with P_4 concentration > 1 ng/mL at G1 was not affected by treatment but was increased ($P < 0.01$) for EP vs.. LP cows at $PGF_{2\alpha}$ (86.5 vs.. 74.3%). Treatment did not affect ovulation to G1 and P/AI 31 d after resynchronized TAI (EPNC = 30.1, EPC = 28.8, LPNC = 27.5, LPC = 30.5%). An interaction was detected ($P < 0.04$) between timing of initiation of resynchronization and supplemental P_4 at d 60 with the CIDR tending ($P = 0.11$) to increase P/AI in late (LPNC = 23.7 vs.. LPC = 28.0%), but not in early (EPNC = 26.9 and EPC = 24.2%) cows. Embryo loss was unaffected by treatment. In conclusion, addition of a CIDR insert within the Ovsynch-56 protocol initiated late (d 39 ± 3) but not early (d 31 ± 3) post-AI improved P/AI.

Key words: dairy cows, resynchronization, CIDR

M233 Effect of circulating progesterone (P4) and two different GnRH doses on LH secretion in lactating dairy cows. J. O. Gior-

dano*, P. M. Fricke, J. N. Guenther, G. Lopes, M. M. Herlihy, and M. C. Wiltbank, *Department of Dairy Science, University of Wisconsin-Madison, Madison.*

Our objectives were: 1) to determine the effect of circulating P4 (high P4; HP4 vs.. low P4; LP4), and 2) increasing the GnRH dose from 100 (LD) to 200 (HD) μg on LH secretion in HP4 and LP4 in lactating cows (n = 24). Double-Ovsynch (Presynchronization; GnRH-7d-PGF-3d-GnRH; 7d later Breeding-Ovsynch; GnRH-7d-PGF-48h-GnRH-16h-TAI) was used to create the HP4 and LP4 environments. At the 1st GnRH of Breeding-Ovsynch (HP4) all cows having a CL ≥20 mm received either a LD or HD of GnRH. At the 2nd GnRH of Breeding-Ovsynch (LP4) cows randomly received a LD or HD of GnRH. Blood samples (BS) were collected every 15 min from −15 to 180 min after GnRH, and then hourly until 5 h after GnRH. As expected, mean P4 in HP4 was greater than LP4 (2.8 vs. 0.2 ng/mL; $P < 0.01$). Mean LH for LD cows (n = 12) was affected by P4 (1.7 vs. 7.4 ng/mL for HP4 and LP4; $P < 0.01$), time ($P < 0.01$) and treatment by time ($P < 0.01$). Circulating P4 in LD cows also affected the LH peak (3.4 vs. 17.7 ng/mL for HP4 and LP4; $P < 0.01$) and area under the curve (AUC; 488.0 vs. 2346.9 ng for HP4 and LP4 ng; $P < 0.01$). Mean LH for HD cows (n = 10) was also affected by P4 (3.5 vs. 9.6 ng/mL for HP4 and LP4; $P < 0.01$), time ($P < 0.01$) and treatment by time ($P = 0.04$). Circulating P4 in HD cows decreased LH peak (7.9 vs. 21.3 ng/mL for HP4 and LP4; $P = 0.02$) and AUC (1065.9 vs. 2933.3 ng for HP4 and LP4 ng; $P = 0.01$). In HP4 (n = 24), mean LH was affected by GnRH dose (1.7 vs. 3.7 ng/mL for LD and HD; $P < 0.01$), time ($P < 0.01$), and treatment by time ($P < 0.01$). Dose of GnRH affected LH peak (3.3 vs. 8.5 ng/mL for LD and HD; $P < 0.01$), time to LH peak (1.3 vs. 1.8 h for LD and HD; $P = 0.04$), and AUC (501.0 vs. 1177.8 ng for LD and HD; $P < 0.01$). In LP4 (n = 22), mean LH was affected by GnRH dose (6.9 vs. 10.7 ng/mL for LD and HD; $P < 0.01$), time ($P < 0.01$), and treatment by time ($P < 0.01$). Likewise, GnRH dose affected LH peak (15.7 vs. 23.6 ng/mL for LD and HD; $P = 0.01$) and AUC (2186.4 vs. 3443.2 ng for LD and HD; $P < 0.01$). We conclude that circulating P4 reduces GnRH-induced LH secretion, and a higher dose of GnRH can increase LH secretion both in a high and low P4 environment. Supported by Hatch project WIS01171.

Key words: LH secretion, progesterone, GnRH

M234 Assessment of an accelerometer system (Heatime) for detection of estrus and timing of insemination in lactating dairy cows. A. Valenza, G. Lopes*, J. O. Giordano, J. N. Guenther, and P. M. Fricke, *Department of Dairy Science University of Wisconsin-Madison, Madison.*

Two experiments were conducted on a commercial dairy in Wisconsin to evaluate an accelerometer system (Heatime) to manage reproduction. In the first experiment, lactating Holstein cows (n = 54) received an i.m. injection of GnRH (100 μg) from 35 to 49 DIM followed 7 d later by an i.m. injection of PGF2α (PGF; 25 mg). Beginning 48 h after PGF, blood samples were collected for progesterone (P4) analysis and ovaries were monitored using ultrasound at 8 h intervals for 120 h. Ovulatory response to GnRH treatment was greater ($P = 0.027$) for cows with <0.5 ng/mL P4 (96.2%, 25/26) than for cows with ≥0.5 ng/mL P4 (66.7%, 16/24). Cows were removed from the analysis if they were detected in estrus by the system before PGF (n = 6) or if they did not regress their CL after PGF (n = 6). For the 42 cows included in the analysis, 26% (11/42) underwent luteal regression but did not ovulate (5% were detected in estrus by Heatime; 21% were not), whereas 74% (31/42) regressed their CL and ovulated (67% were detected in estrus by Heatime; 7% were not). Peak accelerometer activity occurred 67.1 ± 2.5 h after PGF, and cows were inseminated 9.9 ± 2.3 h after peak activity. Ovulation occurred 85.9 ± 2.4 h after PGF, 20.9 ± 3.1h after peak activity and 10.7 ± 2.5 h after AI. In the second experiment, cows (n = 426) were assigned by odd or even ID number to receive an i.m. injection of GnRH (G, 100 μg) at AI detected by the Heatime system (n = 401 AI) or no treatment (control, C; n = 482 AI). Pregnancy diagnosis was performed by the herd veterinarian 30 d after AI using ultrasonography. Based on logistical regression analysis, pregnancies per AI (P/AI) was affected ($P < 0.001$) by parity (35.2 vs.. 22.3% for primiparous vs.. multiparous cows) and season (34.7 vs.. 22.6% for cool vs.. warm seasons); however, treatment with GnRH at AI did not affect P/AI (29.8 vs.. 26.8% for C vs.. G cows, respectively). We conclude that the Heatime system determined the correct timing of AI for most of the cows that displayed estrus and that treatment with GnRH at the time of AI determined by the Heatime system did not affect fertility in lactating dairy cows.

Key words: estrous detection, GnRH, Heatime

M235 Presynchronization with double-Ovsynch improves conception at first postpartum AI in primiparous lactating dairy cows. M. M. Herlihy*[2,3], J. O. Giordano[1], A. H. Souza[1], A. Keskin[1], A. B. Nascimento[1], J. N. Guenther[1], M. A. Crowe[3], S. T. Butler[2], and M. C. Wiltbank[1], *[1]Department of Dairy Science, University of Wisconsin-Madison, Madison, [2]Animal and Bioscience Research Department, Teagasc, Moorepark, Cork, Ireland, [3]School of Agriculture, Food Science and Veterinary Medicine, University College Dublin, Ireland.*

Lactating dairy cows (n = 739; 341 primiparous, 398 multiparous) were enrolled in a study to test the hypothesis that improved pregnancies per AI (P/AI) following Ovsynch can be achieved in first service, first parity cows through the use of Double-Ovsynch for presynchronization compared with Presynch-Ovsynch. Cows were randomly assigned to: Double-Ovsynch (DO, n = 366; GnRH-7d-PGF-3d-GnRH-7d-Ovsynch-56[GnRH-7d-PGF-56h-GnRH-16hTAI]) or Presynch-Ovsynch (PS, n = 373; PGF-14d-PGF-12d-Ovsynch-56). Progesterone (P4) was determined at GnRH1 of Ovsynch-56. Pregnancy was diagnosed by palpation per rectum at 39 d and late embryo loss rate was determined at 74 d. Treatment effects were analyzed by logistic regression using the GLIMMIX Procedure of SAS. Explanatory variables in the statistical model included treatment, parity (1, ≥ 2), body condition score (BCS) (low ≤2.50; high >2.50), treatment*parity and treatment*BCS interactions. Presynchronization with DO tended ($P = 0.06$) to improve P/AI (DO = 46.6%, 171/366 vs.. PS = 41.5%, 155/373). One-tailed contrasts revealed improved ($P = 0.04$) P/AI for first parity cows treated with DO (DO = 56.3%, 95/168 vs.. PS = 47.4%, 82/173), with no improvement ($P > 0.05$) observed for older animals (DO = 38.1%, 75/198 vs.. PS = 36.3%, 73/200). There was no effect ($P > 0.05$) of presynchronization treatment on incidence of late embryo loss after first service (9.1 vs.. 6.1%). Presynchronization at first service had no effect ($P > 0.05$) on P/AI at second service (33.1 vs.. 34.9%). DO increased the percentage of cows with P4 ≥ 0.5 ng/mL at GnRH1 of Ovsynch (DO = 93.7%, 343/366 vs.. PS = 75.3%, 281/373; $P < 0.001$) with similar effects in all parities. A treatment by BCS interaction ($P < 0.05$) was observed for serum P4 at GnRH1, with low BCS cows having greater P4 if assigned to DO than PS (1.90 vs.. 2.44ng/mL; $P < 0.05$). Thus, presynchronization with Double-Ovsynch induced cyclicity in cows of all parities; however, Double-Ovsynch increased fertility only in first parity cows and not older cows. The physiology underlying this parity difference is not yet clear.

Key words: presynchronization, Ovsynch, dairy cow

M236 Effect of GnRH and double AI (24h apart) on fertility of high-producing cows detected in estrus by professional tail chalk service. D. Cunningham[1], A. Fisher[1], A. H. Souza*[2,1], H. Rivera[1], A. Skidmore[3], and M. C. Wiltbank[2], *[1]Accelerated Genetics, Baraboo, WI, [2]Department of Dairy Science, University of Wisconsin, Madison, [3]Intervet/Schering-Plough Animal Health, Summit, NJ.*

The objective of this study was to evaluate the effects of double AI and supplemental GnRH given at AI in Holstein cows detected in estrus by daily tail chalk. Lactating cows from 2 commercial herds in WI (n = 1,101), DIM = 166 ± 3, in their 1st to 14th postpartum breedings were randomly assigned in a 2 × 2 factorial design as follows: SAI) Single AI when tail chalk was rubbed off at 0h (standard tail chalk procedure); DAI) Double AI (at 0h and 24h) with second AI done regardless of chalk been rubbed off again after 1st AI; SAI+GnRH) Single AI at 0h plus supplemental GnRH treatment simultaneously to AI at 0h; DAI+GnRH) Double-AI (at 0h and 24h) plus GnRH at 0h second AI performed regardless of further chalk reading after 1st AI. Estrus detection based on daily tail chalk reading was performed by 2 experienced technicians. Pregnancy was diagnosed by ultrasound at 30 ± 3d after AI. Factorial design comparison was analyzed with procedure Glimmix of SAS, with cow treated as a random effect and interaction between number of AI and GnRH forced into the statistical model. In addition, final model also took into account main effects and the interactions for farm, parity, DIM at AI, and month of breeding. There was no interaction ($P > 0.10$) between number of AIs and GnRH treatment on pregnancies per AI (P/AI). Similarly, main effects of number of AIs (SAI = 30%; DAI = 32%) and GnRH treatment (no-GnRH 31%; yes-GnRH = 30%) did not alter P/AI. Further analysis using only hard breeders (cows not conceiving until 200DIM; n = 239) also showed no significant interaction between treatments; or effect of number of AI (SAI = 23%; DAI = 22%) and GnRH at 1st AI (no-GnRH = 22%; yes-GnRH = 23%). In conclusion, blanket use of double breeding and/or GnRH at the time of AI failed to enhance fertility in lactating Holstein cows detected in estrus by professional AI technicians doing AI service based on tail chalk removal.

Key words: artificial insemination, GnRH, dairy cow

M237 Paraoxonase expression and activity in bovine granulosa cells and follicular fluid. A. Schneider[1,2], V. A. Absalon-Medina[2], G. Esposito[3,2], M. N. Corrêa[1], and W. R. Butler*[2], *[1]Universidade Federal de Pelotas, Pelotas, RS, Brazil, [2]Cornell University, Ithaca, NY, [3]University of Naples Federico II, Naples, Italy.*

The aim of this work was to evaluate expression of paraoxonase (PON) 1, 2 and 3 in bovine granulosa cells and activity in follicular fluid (FFL). The PON enzyme family possesses anti-oxidant and anti-inflammatory effects and is highly expressed in liver. In plasma PON1 is bound to HDL and is reduced during pathophysiological challenges during the peripartum transition period. Ovaries were collected from cows during slaughter and follicles were used for expression analysis (7 estrogen-active follicles [EAF] and 7 atretic follicles [ATF]) and enzyme activity in FFL (10 EAF and 21 ATF). Follicles were dissected from the stroma, FFL was aspirated and the follicle walls immersed in RNALater. To recover granulosa cells, follicular walls were removed from the RNALater, halved, scraped and washed with cold saline into a Petri dish. Granulosa cells were recovered by centrifugation at 2000 x g for 3 min. Total RNA was isolated and real-time PCR used to evaluate PON 1, 2 and 3 mRNA expression according to the ΔΔCt method. Estradiol (E2), progesterone (P4), HDL, LDL, cholesterol and PON1 were evaluated in FFL. Additionally, FFL from 15 EAF was aspirated in Holstein cows to compare PON1 activity in FFL and plasma. In granulosa cells PON2 and 3 mRNA expression was not different between EAF and ATF, PON1 being undetectable. In EAF and ATF, FFL E2 concentration was 133 ± 33 and 12 ± 3 ng/mL, with E2/P4 ratio of 2 and 0.2, respectively. PON1 activity was higher ($P < 0.05$) in EAF (83 ± 8 kU/L) than ATF (62 ± 5 kU/L), as well as HDL, LDL and cholesterol concentrations ($P < 0.05$). E2 concentration in FFL was correlated to PON3 expression ($r = 0.59$, $P < 0.05$) and PON1 activity ($r = 0.50$, $P < 0.01$). PON1 activity in FFL (61 ± 5 kU/L) was lower ($P < 0.01$) than in plasma (123 ± 11 kU/L), but correlated ($r = 0.69$, $P < 0.01$). In summary, although PON1 activity in FFL increases with E2 concentration, its origin appears to be from plasma since it is not expressed in granulosa cells. Moreover, increased PON1 activity in FFL in association with increased concentration of HDL and cholesterol indicates that this is due to a higher transfer rate of the protein from plasma in EAF.

Key words: granulosa cells, PON, HDL

M238 Development of a lentiviral RNA interference (RNAi) system for interleukin–1 beta (IL1B) expressed in elongating porcine embryos. D. J. Mathew*, E. M. Newsom, R. D. Geisert, and M. C. Lucy, *University of Missouri, Columbia.*

Most embryonic loss in pigs occurs during conceptus elongation and attachment. During this time, pig conceptuses increase expression of IL1B but the function of this molecule in embryonic development is unknown. There appear to be at least 2 IL1B genes – the prototypical IL1B cytokine (secreted by macrophages and other immune cells) and an embryonic IL1B (IL1BE) expressed by the pig conceptus. Our ultimate objective is to assess the function of IL1BE by developing an in vivo RNAi lentivirus-based system that specifically knocks down IL1BE in porcine embryos. As a first step, we screened oligonucleotides for their capacity to knock down IL1BE but not IL1B in vitro. Full-length cDNA for IL1B and IL1BE were cloned into an expression vector that contained a luciferase reporter for monitoring RNAi (psi–CHECK1; Promega, Madison, WI). We then identified 8 19 bp oligonucleotides that were complimentary to IL1BE but not IL1B mRNA using the siRNA Target Designer program (Promega). Based on these original sequences, longer oligonucleotides that were designed to form short hairpin RNA (shRNA) were annealed to their complimentary oligonucleotides and inserted into the pGeneClip U1 expression vector (Promega). Baby Hamster Kidney (BHK–21) cells were simultaneously transfected with the psi–CHECK1 vector containing either IL1B or IL1BE and one of 8 shRNA vectors. After 48 h, cells were lysed and assayed for luciferace activity. In cells transfected with the IL1BE, 7 of 8 shRNA decreased ($P < 0.01$) luciferase activity compared with the positive control. Two of the shRNA that knocked down IL1BE did not knockdown IL1B (i.e., they were specific for IL1BE). Luciferase activity was reduced by >90% ($P < 0.001$) by the 2 shRNA specific for IL1BE. Luciferase activity in cells transfected with IL1BE and a vector containing scrambled shRNA was not different ($P > 0.10$) from the positive control. We conclude that IL1BE can be specifically knocked down in vitro by using RNAi. This project was supported by National Research Initiative Competitive Grant no. 2007–35203–17836 from the USDA National Institute of Food and Agriculture.

Key words: embryo, pig, expression

M239 Differential gene expression in liver of lactating (L) and non-lactating (NL) primiparous Holstein cows during early pregnancy. J. Green*, E. Newsom, C. Okamura, and M. Lucy, *University of Missouri, Division of Animal Science, Columbia.*

The objective was to determine the physiological effect of lactation on hepatic mRNA expression in primiparous Holstein cows during early pregnancy. Liver was collected from cows that were either L (n = 22) or NL (n = 18) and were either d 28 (n = 6 L and 6 NL), d 35 (n = 8 L and 6 NL), or d 42 (n = 8 L and 6 NL) of gestation. Hepatic RNA was submitted to the University of Missouri DNA core for microarray analysis (Bovine Genechip; Affymetrix, Santa Clara, CA). Data were analyzed by using JMP Genomics 4.1 (SAS Inst., Cary NC). Data Analyses identified 299 targets that were differentially expressed ($P < 0.001$) between L and NL. Gene lists were analyzed for functional significance by using the iPATH software (Letunic et al. 2008, Trends Biochem Sci. 33:101–3). The L cows had greater hepatic mRNA expression for enzymes involved in gluconeogenesis, cholesterol synthesis, lipid synthesis, and cholesterol metabolism compared with NL cows. Quantitative real time reverse transcription PCR (qRTPCR) assays were used to confirm microarray results. The qRTPCR assays were validated by DNA sequencing of the amplified product and by performing serial dilutions of a single sample to assess efficiency. Based on qRTPCR, there was an effect of lactation because L cows had greater expression of ATP citrate lyase (Acly; $P < 0.02$), acyl-CoA synthetase long-chain family member 1 (Acsl1; $P < 0.06$), acyl-CoA synthetase short-chain family member 2 (Acss2; $P < 0.03$), apolipoprotein A-1 (Apoa1; $P < 0.003$), cytochrome P450scc (Cyp11a1; $P < 0.05$), fatty acid synthase (Fasn; $P < 0.05$), HMG-CoA reductase (Hmgcr; $P < 0.002$), pyruvate carboxylase (Pc; $P < 0.08$), phosphoenolpyruvate carboxykinase 1 (Pck1; $P < 0.001$), stearoyl-CoA desaturase-1 (Scd; $P < 0.01$), and suppressor of cytokine signaling 2 (Socs2; $P < 0.001$) while NL cows had greater mRNA transcript levels of protein phosphatase 1 regulatory subunit 3C (Ppp1r3c; $P < 0.001$). There was no effect of lactation for cyclophilin (housekeeping gene). There were no effects of d of pregnancy on gene expression. In conclusion, lactation had a large effect on gene expression in liver that was not affected by d of pregnancy.

Key words: lactation, metabolism, Holstein

M240 Immunohistochemical evidence for the presence of G protein-coupled receptor 43 in cattle rumen epithelium but not in the pancreatic islets of Langerhans. A. Wang[1], R. M. Akers[2], and H. Jiang*[1], *[1]Department of Animal and Poultry Sciences, Virginia Tech, Blacksburg, [2]Department of Dairy Science, Virginia Tech, Blacksburg.*

Volatile fatty acids (VFAs) are the major products of microbial fermentation in the rumen. Besides serving as substrates for energy generation, VFAs are also known to stimulate rumen development, increase serum insulin and glucagon concentrations, and regulate gene expression in cattle and sheep. The mechanisms underlying these regulatory effects of VFAs are unknown, but recent discovery that VFAs can bind to G protein-coupled receptor 43 (GPR43) and 41 (GPR41) suggests that the regulatory effects of VFAs may be mediated by these receptors in VFA target tissues. As a step toward testing this possibility, we determined whether GPR43 was expressed in bovine rumen wall and the pancreatic islets of Langerhans. Rabbit antiserum against a bovine GPR43 peptide was generated. The specificity of the antiserum for binding to GPR43 was confirmed by Western blotting analysis of recombinant bovine GPR43 protein. Immunohistochemical analyses using this antiserum revealed the presence of GPR43-immunoreactive cells in the epithelium of both adult and newborn cattle rumen, but not in the mucosa, submucosa, or muscle layer. The same immunohistochemical analyses did not reveal any GPR43-immunoreactive cells in the bovine islets of Langerhans or the surrounding exocrine tissue. These data suggest that the effect of VFAs on rumen development in cattle may be mediated by GPR43 in the rumen epithelial cells and that the effects of VFAs on serum insulin and glucagon concentrations, however, unlikely involve binding to GPR43 in the pancreas.

Key words: receptor, rumen, VFA

M241 Effects of protein supplementation during heifer development on reproductive characteristics and success in beef heifers. A. S. Summers*[1], R. A. Cushman[2], S. P. Weber[1], M. L. Spangler[1], and A. S. Cupp[1], *[1]University of Nebraska-Lincoln, Lincoln, [2]USDA-ARS Roman L. Hruska U.S. Meat Animal Research Center, Clay Center, NE.*

A 2-yr study was conducted to determine the effects of feeding different protein supplements during heifer development on reproductive traits and performance. Our hypothesis was that protein supplementation would enhance reproductive performance in heifers with below average reproductive characteristics. Heifers from 2 herds at the University of Nebraska Animal Development and Research Center were used with heifers (Angus and Angus x Simmental hybrids) from the teaching herd (n = 56) being fed a modified dried distillers grain (MOD) supplement at 1.36 kg/d from weaning (mid September) through May. Heifers (MARC III x Red Angus) from the physiology herd (n = 173) were randomly assigned to groups and fed dried distillers grain-based (DDG) or corn gluten feed-based supplement (CFG) offered at 0.59% and 0.78% BW, respectively, from mid-November through May. Supplements were formulated to be isocaloric but differed in undegradable protein. All heifers were fed ad libitum meadow hay through winter while grazing dormant pasture. Prior to breeding, heifers were transrectally ultrasounded to determine antral follicle count (AFC), uterine horn diameter (UHD), ovarian size, presence of a CL, and to determine reproductive tract score (RTS). Heifers developed on MOD diet were 23 d older ($P < 0.01$) and had greater ($P < 0.01$) ovarian area, total AFC, and percent of CL present compared with other groups. However, MOD heifers had lower ($P < 0.01$) UHD compared with other groups. There was no difference ($P = 0.19$) in proportions of heifers bred to A.I.; however, overall pregnancy rates were lower ($P < 0.01$) for MOD compared with other groups. There was a positive effect of small follicle counts on RTS [RTS = 3.9 + 0.01(small follicles); $P < 0.01$, r2 = 0.04] and AFC [AFC = 4.9 + 0.8(small follicles); $P < 0.01$, r2 = 0.86]. Although MOD and DDG diets were similar, results from these groups varied, suggesting that age led to some variation in response to these supplements. We also conclude that RTS and AFC are influenced by small follicle counts. USDA is an equal opportunity provider and employer.

Key words: antral follicle counts, beef cattle, reproduction

M242 Effect of parity on thermal response and energy balance (EB) of sows housed at 24-27°C during lactation. W. R. Martin*, T. J. Safranski, D. E. Spiers, and M. C. Lucy, *University of Missouri, Columbia.*

An earlier study showed that parity 1 sows (P1) were more sensitive to heat stress compared with greater parity sows as indicated by rectal temperature (RT) and respiration rate (RR). To confirm this relationship, a second trial was designed to measure RT and RR of P1 (n =

7), parity 2 (P2; n = 4) and parity 6 (P6; n = 2) sows in one farrowing room. Sows entered 1wk before farrowing and remained until 4 d after weaning. Ear temperature (ET), shoulder temperature (ST), RT and RR were measured daily at 1400 h. Room temp was 24–27°C. Pregnant sows housed in the room served as a non-farrowed control group. Sow BW and litter wt were measured weekly. Feed offered and refused (kg) were recorded. EB (Mcal ME) was estimated from BW, litter wt, and feed consumed. There were effects of parity ($P < 0.05$) and d of lactation (DOL; $P < 0.001$) on RT. The RT increased after farrowing (38.2 ± 0.1°C on d −1 to 39.1 ± 0.1°C on d 0) and remained elevated during lactation (38.8 ± 0.1 to 39.3 ± 0.1°C). Before farrowing, RT was unaffected by parity ($P > 0.1$; 38.3 ± 0.1°C) but during lactation, RT was greatest in P1 sows (39.4 ± 0.1, 39.0 ± 0.1, 38.8 ± 0.2°C for P1, P2, and P6). Despite greater RT during lactation, P1 sows did not have greater RR (50 ± 1 breaths per min; BPM) or ET (37.3 ± 0.1°C), but ST was greater (36.5 ± 0.1, 36.2 ± 0.1, and 36.2 ± 0.2°C for P1, P2, and P6; $P < 0.05$). Control sows (pregnant, not lactating) had lesser RT (38.3 ± 0.1°C; $P < 0.001$), RR (41 ± 2 BPM; $P < 0.005$), ET (35.9 ± 0.1°C; $P < 0.001$), and ST (34.8 ± 0.2°C; $P < 0.001$) compared with lactating sows. There was an effect of DOL on EB during lactation, but parity had no effect. Sow EB increased from d 0 (−8.5 ± 1.2 Mcal ME) to d 5 (−1.9 ± 1.2 Mcal ME), but then decreased to d 9 (−3.8 ± 1.2 Mcal ME) and then achieved neutrality by d 11. Previous trial results showing greater RT in younger sows were confirmed. Greater RT in younger sows may be due to thermal insensitivity as result of metabolic heat production for growth. This may partially explain summertime infertility in P1 sows. This project was supported by National Research Initiative Competitive Grant no. 2007–55203–18261 from the USDA National Institute of Food and Agriculture.

Key words: sow, heat stress, parity

M243 Effects of progesterone concentrations at the end of a fixed-time AI protocol and time of administration of PGF2α in fixed-time AI and ET protocols in lactating dairy cows. M. Pereira[1], A. Rodrigues[1], T. Martins[1], F. Aono[1], P. Borges[2], T. Guzella[1], C. Sanchez[1], M. Veras[2], F. Aragon[2], and J. L. M. Vasconcelos*[1], *[1]FMVZ-UNESP, Botucatu, SP, Brazil, [2]Pioneiros Veterinary Clinic, Carambei, PR, Brazil.*

Two experiments were performed in lactating Holstein cows. Experiment 1 (n = 565) evaluated the influence of progesterone (P4) concentrations at removal of the P4 intravaginal device (CIDR) on pregnancy rates of cows assigned to the following estrous synchronization protocol + fixed-time AI: d 0 – 2 mg of estradiol benzoate and insertion of a new or used CIDR (previously used once or twice, originally containing 1.9 g of P4); d 7 – 25 mg PGF2α injection; d 8 - removal of the CIDR and administration of 1 mg of estradiol cypionate; d 10 – fixed-time AI. Blood samples were collected concurrently with CIDR removal for P4 analysis. Experiment 2 (n = 610) evaluated if administration of PGF2α at d 7 (PG7) or d 8 (PG8) of the same protocol utilized in Exp. 1 affects pregnancy rates in cows submitted to fixed-time AI or ET. Data from Exp. 1 and 2 were analyzed with the PROC LOGISTIC of SAS. In Exp. 1, the number of the CIDR use did not affect ($P > 0.05$) P4 concentrations at CIDR removal (1.47, 1.29 and 1.16 ng/mL of P4 for new, used once, or used twice CIDR) or pregnancy rates (27, 26, and 32% of pregnant cows/total cows for new, used once, or used twice CIDR). There was no effect ($P > 0.05$) of P4 concentration on d 8, independently of CIDR usage, on subsequent pregnancy rates (P4 < 1.0 ng/mL = 27% pregnant cows/total cows; P4 between 1.0 and 2.0 ng/mL = 28% pregnant cows/total cows; and P4 > 2.0 ng/mL = 32% pregnant cows/total cows). In Exp. 2, PG7 cows had greater ($P < 0.05$) pregnancy and conception rates to fixed-time AI and ET, respectively, compared with PG8 cows (35 vs.. 25% pregnant cows/total cows at fixed-time AI, respectively; 54 vs.. 46% pregnant cows/transplanted cows at fixed-time ET, respectively). In conclusion, in synchronization protocols where age of follicles are similar, the interval between beginning of circulating P4 decrease and ovulation may affect pregnancy rates in lactating dairy cows.

Key words: progesterone, prostaglandin, dairy cows

M244 Period of dominance of the ovulatory follicle influences conception rates in Nelore pubertal heifers detected in estrus. T. Martins[1], A. Rodrigues[1], F. Aono[1], M. Pereira[1], R. Peres[2], H. Graff[2], E. Carvalho[2], and J. L.M. Vasconcelos*[1], *[1]FMVZ-UNESP, Botucatu, SP, Brazil, [2]Agropecuaria Fazenda Brasil, Nova Xavantina, MT, Brazil.*

Length of dominance of the ovulatory follicle and exposure to estradiol during proestrus can affect fertility in beef females. The aim of this study was to compare intravaginal progesterone devices (CIDR; containing 1.9 g of progesterone) non-previously (CIDR1) or previously used for 18 d (CIDR3) during estrous synchronization, as well as effects of timing of CIDR removal on conception rates of pubertal Nelore heifers. Cycling Nelore heifers (n = 705) were randomly assigned to receive on d 0 either CIDR1 or CIDR3 and 2 mg of estradiol benzoate. On d 7 all heifers received 12.5 mg of PGF2α and were assigned within CIDR1 and CIDR3 to CIDR removal on d 7 (D7; n = 335) or d 9 (D9; n = 370). Estrus detection was performed twice daily after CIDR removal and heifers were inseminated 12 h after being detected in estrus. At insemination, the largest follicle was measured by transrectal ultrasonography. Pregnancy diagnosis was performed on d 61 also via transrectal ultrasonography. Data were analyzed with PROC LOGISTIC and PROC MIXED of SAS. Conception rates were not affected by CIDR use ($P > 0.05$) but were affected ($P < 0.05$) by timing of CIDR removal (57.8 vs.. 66.5% of pregnant heifers/inseminated heifers for D7 and D9, respectively). Estrus detection rate was 60.9% for D7 and 67.0% for D9 ($P < 0.10$). Follicle diameter at AI was affected ($P < 0.01$) by CIDR use (11.4 vs.. 12.0 mm for CIDR 1 and CIDR3, respectively). Further, follicle diameter was greater for cows assigned to CIDR3 and removal on d 9 ($P < 0.05$) compared with all other treatment combinations. Interval between CIDR removal and heat detection was also affected ($P < 0.01$) by CIDR use (3.62 vs.. 2.92 d for CIDR1 and CIDR3, respectively) and timing of CIDR removal (3.71 vs.. 2.83 d for D7 and D9, respectively). According to these results, variation in the period of dominance of the ovulatory follicle influences fertility of heifers inseminated after estrus detection.

Key words: conception rates, Nelore heifers, progesterone

M245 Impacts of L-arginine on ovarian function and reproductive performance at the time of maternal recognition of pregnancy in ewes. C. Schauer*[1], C. Saevre[1,2], A. Meyer[2], M. VanEmon[1,2], J. Kirsch[2], M. Kapphahn[2], J. Luther[3], J. Caton[2], and D. Redmer[2], *[1]Hettinger Research Extension Center, North Dakota State University, Hettinger, [2]Department of Animal Sciences, North Dakota State University, Fargo, [3]Department of Animal and Food Science, University of Wisconsin-River Falls, River Falls.*

Objectives were to determine if arginine supplementation surrounding the time of maternal recognition of pregnancy enhances ovarian function and minimizes early reproductive losses. Ewes received L-arginine HCL (equivalent to 27 mg of L-arginine/kg of BW; ARG; n = 47) or saline (CON; n = 47) i.v. once daily from d 9 to d 14 following

estrus (d 0). Daily blood samples were obtained from a subset of 10 ewes/group to assess progesterone (P4) concentrations and at −0.5, 0, 0.5, 1, 2, 4, 6, and 8 h following treatment on d 10 to determine serum amino acid concentrations. Reproductive losses were determined with B–mode ultrasonography on d 25, 45, and 65 of gestation. On d 10, serum concentrations of arginine (nmol/mL) were elevated in ARG vs.. CON ewes at 0, 0.5, 1, 2, and 4 h ($P < 0.001$), but were similar ($P \geq 0.70$) at −0.5, 6, and 8 h. Despite similarities in the number of corpora lutea (CL) per ewe (ARG, 1.69 ± 0.12 and CON, 1.67 ± 0.16; $P > 0.05$), serum progesterone concentration (ng/mL) was greater in this subset of CON compared with ARG ewes on d 9 ($P < 0.02$) and 10 ($P < 0.005$), but similar for the remaining treatment period ($P \geq 0.06$). On d 12, there were no differences in pulsatility index and resistance index in those ewes treated with arginine in the ovarian hilus or the CL ($P > 0.05$). Treatment with arginine increased overall pregnancy rate at d 25 (ARG, 55% and CON, 30%). Pregnant ewes were similar in CL number per ewe (ARG, 1.69 ± 0.12 vs.. CON, 1.67 ± 0.13; $P > 0.05$) and embryo number (ARG, 1.62 ± 0.12 vs.. CON, 1.53 ± 0.13; $P > 0.05$) at d 25 of gestation. As pregnancy progressed to d 45, similar ($P > 0.05$) number of embryos per ewe were observed in pregnant ARG ewes (1.45 ± 0.14) vs.. pregnant CON (1.50 ± 0.15) with overall pregnancy rate remaining greater ($P \leq 0.02$) in ARG (47%) compared with CON (26%). In summary, treatment with arginine surrounding the time of maternal recognition of pregnancy may have prevented pregnancy loss, but did not enhance ovarian hemodynamics or progesterone concentration.

Key words: L-arginine, ovarian hemodynamics, sheep

M246 Failure of differences in prepubertal dietary intake to affect ovarian development in pubertal beef heifers. S. E. Echternkamp*, D. R. Eborn, and R. A. Cushman, *USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE.*

Developing replacement heifers on lower energy diets to a lighter body weight at first breeding can reduce input costs but may impede follicular development and onset of puberty. The objective was to determine whether lower dietary intake prepubertally impedes ovarian development in purebred or crossbred heifers. In 2009 and 2010, 8-mo-old Angus and composite MARC II heifers were assigned equally by body weight and genetic line (n = 120 / line) to receive either a low- (LE) or high- (HE) energy diet to achieve an ADG of 0.45 or 0.9 kg/d for 180 d or 55 vs.. 65% of mature BW at 14 mo of age. At 14 mo, heifers were monitored twice daily for estrus behavior for 21 d. Total number of antral follicles (AFC), ovarian length and height, and preovulatory follicle diam. were measured by transrectal ultrasonography at about 12 h after estrus; corpus luteum (CL) diam. was measured 7 to 14 d later. Uterine horn diam. was only measured in 2010. Data were analyzed by ANOVA with diet, line, and year as independent variables and their 2-way interactions. At 14 mo, HE heifers were heavier (419.4 vs.. 364.9 ± 7.1 kg) and fatter (6.8 vs.. 5.5 ± 0.1 BCS) than LE heifers ($P < 0.01$); LE heifers were 11% heavier in 2010 than 2009 (diet x year; $P < 0.01$). Puberty occurred in 94.6% of heifers by 14 mo of age. Size of preovulatory follicle (13.8 ± 0.2 mm), AFC (22.2 ± 0.6), ovary (length = 26.5 ± 0.3 mm; height = 15.1 ± 0.2 mm), CL (19.3 ± 0. Three mm), and uterine horn diam. (11.6 ± 0.2 mm) did not differ between HE and LE, but follicle diam. (14.3 vs.. 13.2 ± 0. Two mm; $P < 0.01$) and ovarian length (26.4 vs.. 25.3 ± 0.4 mm; $P = 0.07$) were greater for MARC II vs.. Angus heifers. AFC was correlated with ovarian length ($r = 0.56$; $P < 0.01$), and CL diam. was correlated with preovulatory follicle diam. ($r = 0.34$; $P < 0.01$). Results indicate that AFC and ovarian size in pubertal heifers are not influenced by differences in prepubertal growth and body condition associated with diet. USDA is an equal opportunity provider and employer.

Key words: beef heifers, diet, ovarian follicles

M247 Follicular fluid composition of the preovulatory follicle in beef cows grazing different forage allowances of native pastures. M. Carriquiry*[1], P. Soca[1], A. C. Espasandín[1], A. Meikle[2], and C. Viñoles[3], *[1]School of Agronomy, UdelaR, Montevideo, Uruguay, [2]School of Veterinary Sciences, UdelaR, Montevideo, Uruguay, [3]National Research Institute for Agriculture, Tacuarembó, Uruguay.*

The follicular microenvironment has been shown to play a critical role in determining follicular fate. To evaluate the effect of long-term nutrition on metabolite follicular fluid composition in beef cows on grazing conditions, multiparous cows (Angus, Hereford and F1 crossbred, n = 32) at 2 forage allowances of native pastures throughout the year (6 vs.. 10 kgDM/100kgBW/d; LO vs.. HI) were used in a complete randomized block design. At the end of the third year, at 178 ± 15 d postpartum, cows were synchronized with 2 prostaglandin (PG) injections 11 d apart and slaughtered 32 ± 1 h after the last PG injection. Cows were classified as cyclic or in anestrus based on the presence of a corpus luteum on the ovaries. Ovaries of cyclic cows were collected (n = 16 and n = 12 for HI and LO, respectively) and largest follicle present on the ovarian surface was dissected, and follicular fluid was aspirated for metabolite analyses. At slaughter, cow BCS did not differ ($P = 0.32$) between groups and averaged 3.9 ± 0.08. The preovulatory follicle was larger for HI than LO cows (13.1 ± 0.8 vs.. 10.3 ± 1.3 mm; $P < 0.05$). Glucose (23.1 vs.. 25.9 ± 5.4 mg/dL), NEFA (0.79 vs.. 0.57 ± 0.11 mmol/L) and urea (19.6 vs..19.1 ± 2.4 mg/dL) concentrations in follicular fluid did not differ ($P > 0.74$) due to forage allowance. However, follicular fluid cholesterol concentrations were greater in LO than HI cows (112 vs.. 79 ± 8 mg/dL, $P = 0.01$). Glucose and cholesterol concentrations increased ($P < 0.02$) with size of the preovulatory follicle (3.3 ± 1.3 mg/dL of glucose and 6.4 ± 1.8 mg/dL of cholesterol for each mm of increase in follicle size). Results showed minor effects of long-term nutrition in follicle fluid composition of the preovulatory follicle of beef cows grazing different forage allowances of native pastures.

Key words: cattle, grazing, ovary

M248 Longitudinal assessment of the somatotropic axis in free-ranging, juvenile Steller sea lions. K. D. Hebert*[1], J. P. Richmond[1,2], L. D. Rea[3], and S. A. Zinn[1], *[1]University of Connecticut, Storrs, CT, USA, [2]University of North Florida, Jacksonville, FL, USA, [3]Alaska Department of Fish and Game, Fairbanks, AK, USA.*

The decline of the Western population (144 degrees west longitude) of Steller sea lions is hypothesized to be the result of impaired nutritional status and decline of growth rate, especially in juveniles, and subsequent natality. Because changes in components of the somatotropic axis can be predictive of nutritional status and growth rate in this species, 2 groups of free-ranging juvenile Steller sea lions were captured in Prince William Sound, AK. Group 1 (n = 30) was initially captured at 5 mo and recaptured at 10 mo of age, whereas group 2 (n = 9) was captured at 7 and 8 mo of age. At capture, animals were anesthetized, age estimated, and blood and BW collected. Concentrations of GH and IGF-I were quantified (ng/mL) using RIA and IGFBP-2 and −3 were quantified [Arbitrary Units, (AU)] using Western ligand blots. Data were analyzed using the Mixed Procedure in SAS. Mass of Steller sea lions increased ($P < 0.01$) with age from 69 ± 1.3 kg at 5 mo to 100

± 2.8 kg at 10 mo (group 1) and 93 ± 5.8 kg at 7 mo to 101 ± 5.7 kg at 8 mo (group 2). Concentrations of IGFBP-2 decreased with age from first to second capture (group 1; 37.8 ± 2.5 vs.. 36.0 ± 2.5; group 2; 43.7 ± 4.8 vs.. 39.8 ± 4.4 AU; $P < 0.01$) and across all animals GH, IGF-I and IGFBP-3 averaged 1.6 ± 0.1 ng/mL, 165.7 ± 10.4 ng/mL, 304.0 ± 13.4 AU respectively, but there was no effect ($P > 0.1$) of age on concentrations of these hormones. Greater concentrations of IGFBP-3 were positively associated with greater growth rate ($P = 0.06$) across all animals. In group 2, the increase in IGF-I concentrations between captures was positively correlated with growth rate ($P < 0.05$), indicating that changes in IGF-I and IGFBP-3 may be useful indicators of growth rate in juvenile Steller sea lions. These data provide a more detailed description of the changes in the components of the somatotropic axis and their relationship with growth rate in juvenile Steller sea lions, and may provide insight into survival and the continued decline of the Western population.

Key words: somatotropic axis, Steller sea lions, insulin-like growth factor binding proteins

M249 Analysis of bovine liver transcriptomics data due to level of prepartal dietary energy using two bioinformatics approaches. K. Shahzad*, M. Bionaz, and J. J. Loor, *University of Illinois, Urbana.*

We used a newly-developed approach (dynamic impact analysis, DIA) that allows visualizing the dynamic adaptations of pathways, and the well-established enrichment analysis using DAVID to evaluate at the transcriptomic level the impact of prepartal plane of energy intake [overfed (OF) or restricted (RE)] on biological pathways in liver. Both approaches rely on freely-available pathway databases from the KEGG database. Analysis of variance with a false discovery rate (FDR) correction resulted in 4,111 genes with a time × diet interaction (FDR <0.05, DEG). For the DIA analysis the whole data set with Entrez gene IDs, FDR, fold-change, and post-hoc *P*-value between the 2 treatments at each time point were uploaded. For the DAVID analysis a list of up-and downregulated genes with Entrez Gene ID was uploaded. A cut-off of FDR = 0.05 and *P* -value = 0.05 was applied in both approaches. Among DEG between OF vs. RE, DAVID analysis uncovered oxidative phosphorylation as the most significantly-enriched (FDR < 0.05) pathway followed by ribosome and proteasome. Without multiple correction (i.e., simple *P*-value < 0.05) other enriched pathways included fatty acid metabolism, glycan biosynthesis, lysosome, and complement, which were more induced in RE vs. OF; whereas, base excision repair, ubiquitination, and ECM receptor were more induced in OF vs. RE. The DIA approach revealed that RE vs. OF led to a higher utilization of glucose, amino acids (AA), and fatty acids (FA) to produce energy (e.g., more impacted/induced TCA cycle, oxidative phosphorylation, and FA metabolism together with degradation of most of AA). Dietary OF vs. RE resulted in large induction of cell cycle, protein turnover, glycan metabolism, with larger ECM receptor activity (e.g., glycan degradation, ubiquitin, Wnt and Notch signaling pathways). Overall, results from the 2 bioinformatics approaches indicated that OF vs. RE prepartum increased liver proliferation and ECM components while reducing utilization of energy and protein synthesis. This adaptation might partly explain the greater liver lipid accumulation due to OF vs. RE postpartum.

Key words: systems biology, pathway analysis, transition cow

M250 Follicle-stimulating hormone induces the canonical WNT/beta-catenin pathway in bovine granulosa cells. B. I. Castañon*, A. D. Stapp, L. J. Spicer, C. A. Gifford, and J. A. Hernandez Gifford, *Oklahoma State University, Stillwater.*

The WNTs are a family of secreted glycoproteins that evoke a response by interacting with specific 7 transmembrane frizzled (FZD) receptors. In the canonical WNT/β-catenin pathway, WNT binding to a FZD receptor leads to inactivation of the β-catenin (CTNNB1) degradation complex. Disruption of the destruction complex allows CTNNB1 to accumulate in the cytoplasm and translocate to the nucleus where it activates transcription by contact with T-cell factor and lymphoid enhancer-binding factor. Several WNT and FZD transcripts are expressed at defined stages of follicular development in the adult ovary. However, the role of the WNT/CTNNB1 pathway in folliculogenesis remains to be elucidated. This study evaluates FSH regulation of the WNT signaling pathway components that contribute to steroid production in bovine granulosa cells. Granulosa cells were isolated from small ovarian follicles (1–5 mm) and plated ($2.3–4 \times 10^5$ cells/35 mm dish) in DMEM/F12 medium. At 48 h after plating, cells were incubated in the presence or absence of 100 ng/ml FSH for 24 or 48 h (n = 6). Expression of *WNT2* mRNA was induced 3.75 (±0.68) fold after 24 h of FSH stimulation compared with controls (0.12 ± 1.09; $P < 0.05$). Likewise, at 48 h *WNT2* tended to be induced (3.14 vs. 1.00 ± 1.03; $P < 0.06$) with FSH treatment. Analysis of other members of the WNT/CTNNB1 signaling pathways did not demonstrate hormone-regulated expression. Granulosa cells and follicular fluid were collected from large mid-luteal antral follicles (8–22 mm) and classified as estrogen active (n = 8) (>25 pg/mL) or estrogen inactive (n = 5). Nuclear and cytoplasmic protein fractions were enriched and CTNNB1 was analyzed using Western blot. Preliminary evidence indicates estrogen active follicles have greater amounts of nuclear CTNNB1 compared with estrogen inactive follicles. Together, these data demonstrate FSH regulates WNT signaling pathway components which are important in granulosa cell steroidogenesis.

Key words: WNT, beta-catenin, follicle-stimulating hormone

M251 Effects of organic versus inorganic trace mineral supplementation on bull semen quality before and after freezing. M. P. Rowe*, C. L. Williams, R. J. Page, T. D. Lester, C. F. Rosenkrans, E. B. Kegley, J. G. Powell, and R. W. Rorie, *University of Arkansas, Fayetteville.*

Limited information is available on the effects of organic trace mineral supplementation on bull fertility. The objective of this study was to evaluate the effect of trace mineral supplementation on bull semen quality before and after freezing, as measured by computer-assisted sperm analysis (CASA). Angus and Balancer bulls were assigned to inorganic (n = 9) and organic (n = 10) trace mineral treatments, based on semen quality, breed, body weight, and age. The bulls were maintained in a dry lot pen and fed mixed grass hay. Three times a week bulls were individually fed a grain supplement that served as the carrier for treatments containing trace mineral for 123 d (May to September). Treatments were supplemental Zn (450 mg/d), Cu (150 mg/d), Co (12 mg/d), Mn (300 mg/d), Se (3 mg/d), and I (5 mg/d) as either inorganic or as a portion of the same levels as organic sources. Starting on d 60, semen was collected by electro-ejaculation on wk 1, 4, and 8. Semen was evaluated by CASA for percent motile and progressive sperm within 5 min of each collection. Sperm was extended, slowly cooled to 4°C, loaded into 0.5 mL straws, and frozen in liquid nitrogen. After thawing, semen was washed to remove extender and then re-suspended in TALP media. Semen was then evaluated using CASA at 0 and 2 h post-thaw. Data was analyzed by treatment, week and their

interaction, using PROC GLM. Week and treatment by week were not significant ($P > 0.05$), so they were dropped from the analysis. At collection, motile (69.1 vs. 55.2%) and progressive (50.3 vs. 38.5%) sperm were greater ($P < 0.05$) for bulls in the organic than the inorganic groups. After thawing, motile (16.3 vs. 7.9%) and progressive (8.9 vs. 4.1%) sperm were also higher ($P < 0.05$) for semen from bulls in the organic vs. inorganic treatments, respectively. At 2 h post-thaw, motile sperm remained higher (8.5 vs. 3.7% $P < 0.05$) but progressive sperm (4.2 vs. 1.7%) was similar ($P > 0.05$) for the organic and inorganic groups, respectively. Although post-thaw motility was low for both treatments, results suggest organic trace mineral supplementation may improve bull semen quality.

Key words: fertility, bulls, trace minerals

M252 Exposure of beef females to the biostimulatory effects of bulls prior to AI. K. E. Pfeiffer*[1], J. A. Binversie[1], J. D. Rhinehart[2], and J. E. Larson[1], *[1]Mississippi State University, Mississippi State, [2]University of Tennessee, Nashville.*

The objective of this study was to evaluate the biostimulatory effect of bull exposure on the expression of estrus and pregnancy rate to AI in cattle. Beef heifers (n = 86) and cows (n = 193) during 2 consecutive yr were allocated to one of 3 treatments: 1) no bull exposure (CON; n = 95), 2) exposure to a bull with a surgically deviated penis for 21 d before AI (SB; n = 88), or 3) exposure to a vasectomized bull for 21 d before AI (VB; n = 96). The SB treatment provided the physical presence of the bull but prevented intromission whereas the VB treatment allowed for intromission and deposition of seminal plasma but not spermatozoa. The estrous cycles of all females were synchronized using the Hybrid-Synch+CIDR protocol ($GnRH^{+}$CIDR insertion-7 d-CIDR removal+$PGF_{2\alpha}$, visual detection of estrus 3 × daily with AI 12 h later for 82 h, and clean-up TAI+GnRH at 82 h). Blood samples were collected on d −17 and −7 relative to the initial injection of GnRH and analyzed for concentrations of progesterone to determine cyclicity status at the initiation of the experiment (at least one sample ≥1 ng/mL). Pregnancy was detected by transrectal ultrasonography on d 35 post-AI. At the onset of the experiment, 75.7% of heifers and 86.1% of cows were cycling. The percentages of females that displayed estrus after CIDR removal were increased ($P < 0.001$) in Year 1 (52.3%) compared with Year 2 (23.1%) as well as increased ($P < 0.05$) in nulliparous (52.3%) compared with primiparous and multiparous females (26.0 and 31.5%, respectively). The percentages of females that displayed estrus were similar ($P = 0.15$) among treatments (31.6, 39.8, and 39.6% for CON, SB, and VB, respectively). Pregnancy rates were increased ($P < 0.01$) in Year 2 (55.8%) compared with Year 1 (42.4%) and were increased ($P < 0.05$) in females treated with CON and SB (49.5 and 59.1%, respectively) compared with females treated with VB (40.6%). In conclusion, a similar percentage of females among treatments displayed estrus during the 82 h detection period but pregnancy rates were decreased in females exposed to a vasectomized bull compared with those exposed to either no bull or a bull presence only.

Key words: beef cattle, biostimulatory effects, bull exposure

M253 Effect of selenium and a glucogenic precursor on fertility in Creole Rodeo cows synchronized with CIDR, PGF2α, eCG, and GnRH. C. Sanchez-Arcineiga*, J. A. Ramirez-Godinez, D. Dominguez-Diaz, A. Flores-Mariñelarena, E. Santellano-Estrada, J. A. Grado-Ahuir, G. Corral-Flores, and L. A. Borunda-Pacot, *Universidad Autonoma de Chihuahua, Chihuahua, Chihuahua, Mexico.*

The objective was to evaluate the effect of calcium propionate (CaP) and sodium selenium (Se) on average daily gain (ADG), backfat thickness (BF), body condition (BCS) and pregnancy rate (PR) in Creole Rodeo cows (CC) supplemented for 60 d with 2 Kg of a concentrate (29 ± 1.6% CP) every other day. Forty-five dry CC were randomly assigned to T1 (n = 11), concentrate only; T2 (n = 11), concentrate + 10.95 mg of Se/50 Kg BW; T3 (n = 11), concentrate + 100 g of CaP and T4 (n = 12), 10.95 mg of Se/50 Kg of BW + concentrate + 100 g of CaP. Cows selected across treatments based on the presence of a palpable corpus luteum (n = 34, 9 from T1, 7 from T2, 9 from T3, and 9 from T4) received a 8 d CIDR. Later, 25 mg of Lutalyse were injected at CIDR removal, and 18 cows (5 from T1, 3 from T2, 6 from T3, and 4 from T4) were treated with 400 IU of eCG. All CC received 100 mg of GnRH 56h after CIDR removal, and fixed-time AI (TAI). Data were analyzed under a 2x2 factorial design with repeated measures. For PR a chi-squared test was used to analyze the effect of eCG. BCS was similar ($P > 0.05$) between treatments, CaP supplementation had a negative effect ($P < 0.0001$) on ADG over time (T) and the interaction CaP*T was significant ($P = 0.0192$). BF was similar between treatments ($P > 0.05$). The use of Se had no effect on BCS, ADG and BFT. Supplementing Se or CaP had no effect ($P > 0.05$) on PR; similarly, the use of eCG at CIDR removal did not improved fertility (44.1% and 55.8%, $P > 0.05$, respectively) in GnRH treated CC at TAI.

Key words: Creole cattle cow, calcium propionate, eCG

M254 Effects of heat stress on skeletal muscle insulin responsiveness in lactating Holstein cows. L. C. Cole[1], M. V. Skrzypek[1], S. R. Sanders[1], M. R. Waldron[3], L. H. Baumgard[2], and R. P. Rhoads*[1], *[1]University of Arizona, Tucson, [2]Iowa State University, Ames, [3]University of Missouri, Columbia.*

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. Cows were subjected to 2 experimental periods (P): 1) thermoneutral (TN) conditions (18°C, 20% humidity) with ad libitum intake for 9d and 2) either heat-stress (HS) conditions (cyclical temperature 31.1–38.9°C, 20% humidity: min THI = 73, max THI = 80.5) fed for ad libitum intake (n = 6), or TN conditions, pair-fed (PF) with a HS animal (n = 6) for 9d. Rectal temperature (Tre) and respiration rate (RR) were measured thrice daily at 0430, 1200 and 1630h. To evaluate skeletal muscle insulin responsiveness, biopsies were obtained immediately before and after an insulin tolerance test (ITT). Insulin receptor (IR), insulin receptor substrate (IRS), Akt/protein kinase B (AKT) and phosphorylated AKT (P-AKT) were measured by Western blot analyses. During P2, HS cows had ($P < 0.01$) a 1.48°C increase in Tre 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 during P2. The ITT caused a greater glucose disposal in P1 compared with P2 ($P < 0.05$), but did not differ between environments in P2. Protein abundance of the IR, IRS and AKT remained stable between periods and environments. Insulin increased P-AKT in each period ($P < 0.05$), but this response tended to decline in P2 for PF animals ($P = 0.10$), but not during HS. These results indicate that mild insulin resistance during HS may be related to reduced nutrient intake. Moreover, a reduction in skeletal muscle insulin responsiveness may stem from a post-receptor signaling defect.

Key words: heat stress, lactation, insulin

M255 Withdrawn

M256 Effects of heat-stress and fresh or frozen semen on reproductive efficiency in dairy cows treated with rbST throughout lactation. E. Sepúlveda*[1], O. Ange-García[1], CA Meza-Herrera[2], FG Veliz[1], and M. Mellado[1], *[1]Universidad Autonoma Agraria Antonio Narro, Torreón, Coahuila, México, [2]Universidad Autonoma Chapingo, Bermejillo, Durango, México.*

The objective of this study was to assess the effect of high ambient temperature and the use of fresh or frozen semen on reproduction performance of dairy cows in a hot arid environment. Reproductive variables (n = 18,037 services) of a large Holstein dairy herd in northern Mexico were evaluated with respect to the average temperature-humidity index [(ITH = (0.8 x temperature + (relative humidity/100) x (temperature - 14.4) + 46)] of the 1 and 3 d before breeding, the day of breeding, and 1 and 3 d following breeding. Increased ITH from < 70 to > 95 was associated with a decrease in pregnancy rate from 47% to 26%. Pregnancy rates for cows serviced on days with an ITH 85–90 but cooler temperatures before breeding were 6 percent points higher than cows exposed to higher ITH before breeding. Pregnancy rates for cows serviced on days with an ITH 80-85 but cooler temperatures before breeding were 3-4 percent points higher than cows exposed to higher ITH before insemination. Pregnancy rates for cows serviced on days with an ITH 75-80 but cooler temperatures before breeding did not differ compared to cows exposed to higher ITH before insemination. With ITH cooler the days after insemination pregnancy rates were also higher for all ITH classes the day of breeding. Pregnancy rates were higher ($P < 0.05$) from January to March compared with all other months of the year. On the other hand, the average number of inseminations per pregnancy was higher from May to July (3.0-3.4) than from all other months of the year (2.1 to 3.0). Pregnancy rate was higher (36 vs. 28%) with insemination with fresh semen (natural mating) than frozen semen, although this difference was noted only during the warmest period of the year. It was concluded that the climatic conditions of the site where this dairy operation is located, drastically hampers the reproductive performance of Holstein cows subjected to three milking and treated with somatotropin throughout lactation. This data also show that natural service markedly increases pregnancy rate during the warm months of the year, compared to AI with frozen semen.

Key words: heat stress, pregnancy rate, natural service

M257 Expression patterns of eNOS in 13 different tissues shows a new isoform in bovine brain stem. M. De Donato*[1], M. A. Adefenwa[1,2], and I. G. Imumorin[1], *[1]Dept of Animal Science, Cornell University, Ithaca, NY, [2]Dept of Cell Biology and Genetics, University of Lagos, Lagos, Nigeria.*

Endothelial nitric oxide synthase (eNOS), along with inducible nitric oxide synthase (iNOS) and neuronal nitric oxide synthase (nNOS), catalyze the generation of nitric oxide, a reactive free radical which acts as a biologic mediator in several processes, including neurotransmission and antimicrobial and antitumoral activities. Expression of eNOS mRNA is restricted to the endothelial cell layer of arterial blood vessels, and is a critical mediator of cardiovascular homeostasis through regulation of the diameter of blood vessels and maintenance of an antiproliferative and antiapoptotic environment in the vasculature. Here we report the expression pattern of eNOS in 13 different bovine tissues as a first step to study possible association of different isoforms with animal performance and health. We used semiquantitative PCR to assess expression with specific primers that amplified exons 5 and 6, with GAPDH as control. Similar expression was detected in cerebellum, cerebral cortex, heart, skeletal muscle, lung, kidney, spleen, liver, pancreas, stomach, placenta and ovary. However, in brain stem tissue, a larger fragment, which represents the unspliced section of exon 5, intron 5 and exon 6, was the major expressed isoform, with low expression of the smaller isoform. Small amounts of this larger isoform were also seen in the cerebral cortex, skeletal muscle, kidney, placenta and ovary. The presence of this isoform as a major protein product in the brain stem could indicate a more specialized function of the gene in this tissue. Further studies will be needed to confirm this observation and compare differences in the function of this protein.

Key words: eNOS, bovine, brain stem

M258 Analysis of bovine adipose transcriptomics data during the transition from pregnancy to early lactation using two bioinformatics approaches. K. Shahzad*[1], J. Sumner-Thomson[2], J. P. McNamara[2], and J. J. Loor[1], *[1]University of Illinois, Urbana, [2]Washington State University, Pullman.*

We used a newly-developed approach (dynamic impact analysis, DIA) that allows visualizing the dynamic adaptations of pathways, and the well-established enrichment analysis using DAVID to evaluate the impact of change in physiological state on biological pathways in adipose tissue of Holstein dairy cattle. Both approaches rely on freely available pathway information from the KEGG database. RNA was hybridized to Affymetrix Bovine Gene Array containing 14,200 elements. Analysis of variance with a false discovery rate (FDR) correction resulted in 1,692 genes with a time effect (FDR <0.10, DEG). For the DIA analysis the whole data set (encompassing −21, −7, 7, and 28 d relative to parturition) with Entrez gene IDs, FDR, fold-change, and post-hoc P value between time points was uploaded. For the DAVID analysis a list of up-and downregulated genes with Entrez Gene ID was uploaded. A cut-off of FDR = 0.05 and P-value = 0.05 was applied in both approaches. Among DEG between time points, DAVID analysis uncovered that fatty acid biosynthesis, linoleic acid metabolism, biotin metabolism, and glycerolipid metabolism were markedly inhibited postpartum than prepartum; whereas, complement and coagulation cascades and riboflavin metabolism were the only pathways with sustained induction postpartum than prepartum. The DIA approach revealed that the onset of lactation resulted in a gradual decrease in the utilization (metabolism) of glucose, lactate, and acetate to produce energy (e.g., most impacted pathways included TCA cycle, Pyruvate metabolism). Furthermore, fatty acid biosynthesis, desaturation, elongation, and PPAR signaling were markedly inhibited during lactation. Overall, the combined results from both bioinformatics approaches indicated that the adipogenic capacity of adipose tissue is quite robust during late pregnancy while the innate immune response of the tissue becomes predominant during early lactation. The latter may be a response of the tissue to stressors including cytokines/hepatokines, NEFA, and/or pathogens. Alternatively, it may represent a mechanism associated with tissue remodeling.

Key words: systems biology, transition cow

M259 Reproduction of dairy cows receiving 1 vs. 3 timed AI (TAI) when not observed for estrus and subjected to natural service (NS). F. S. Lima*[1], R. S. Bisinotto[1], E. S. Ribeiro[1], H. Ayres[1], L. F. Greco[1], C. A. Risco[2], W. W. Thatcher[1], and J. E. P. Santos[1], *[1]Animal Sciences Department, University of Florida, Gainesville, [2]Large Animal Clinical Sciences, University of Florida, Gainesville.*

Objectives were to determine the effects 1 vs. 3 TAI followed by NS on time to pregnancy of lactating dairy cows not observed for estrus. Holstein cows, 1,050 received the double Ovsynch TAI program (d −27 GnRH, d −20 PGF2a, d −17 GnRH, d −10 GnRH, d −3 PGF2a, d −1 GnRH, and d 0 AI) for first AI. On the day of first AI, cows were blocked by parity and randomly assigned to receive one (1TAI, n = 533) or 3 TAI (3TAI, n = 517) before subjected to NS. Cows were moved to NS 7 d after the first or third AI according to treatment. Pregnancy was evaluated 32 d after TAI and each 28 d during NS. Nonpregnant cows in 3TAI were resynchronized with the Ovsynch program starting on d 32 after the previous insemination, such that the re-insemination interval was 42 d. Pregnant cows were re-evaluated for pregnancy 28 d after the initial diagnosis. Cows were scored for body condition 32 d after the first AI. All cows had a period of 231 d after the first AI to become pregnant, and non- pregnant cows were censored. Data were analyzed with the Cox's proportional hazard model or by Logistic regression using SAS. Models included the effects of treatment, parity, body condition and season. As expected, pregnancy at the first TAI did not differ between 1TAI and 3TAI on d 60 after insemination (30.9 vs. 33.4%). Cows receiving 3TAI had greater ($P = 0.04$) rate of pregnancy than those in 1TAI (AHR = 1.15; 95% CI = 1.01–1.31). This resulted in median d open of 142 (95% CI = 130–150) and 123 (95% CI = 121–144) for 1TAI and 3TAI, respectively. Primiparous cows had greater ($P < 0.01$) pregnancy rate than multiparous cows (AHR = 1.44; 95% CI = 1.16–178). Cows receiving the first TAI in the cool season had greater ($P < 0.01$) pregnancy rate than cows exposed to heat stress (AHR = 1.77; 95% CI = 1.53–2.05). Finally, cows with BCS > 2.75 had greater ($P < 0.01$) pregnancy rate than those with BCS < 3.0 (AHR = 1.59; 95% CI = 1.38–1.84). In conclusion, in spite of the long re-insemination interval, cows receiving 3TAI had improved reproductive performance than those receiving 1TAI.

Key words: dairy cow, natural service, timed AI

M260 Effect of intravaginal progesterone insert on GnRH-induced GnRH-induced LH release, follicle growth, and plasma progesterone, estradiol, and inhibin concentrations. L. G. D. Mendonça*[1], M. Amstalden[2], and R. C. Chebel[1], *[1]Department of Veterinary Population Medicine, University of Minnesota, St. Paul, [2]Department of Animal Science, Texas A&M, College Station.*

The objectives of this experiment were to evaluate the effect of treatment with a controlled internal drug release (CIDR) insert containing 1.38 g of progesterone (P4) at the time of GnRH injection on GnRH-induced GnRH-induced LH release, follicular growth and plasma concentrations of P4, estradiol and inhibin. Non-pregnant lactating Holstein cows were randomly assigned to one of 3 treatments after balancing for parity, body condition score and 305-d projected milk yield. The treatments were control (CON, n = 7), 1GP4 (n = 10) and 2GP4 (n = 10). All cows were presynchronized with a CIDR insert for 5 d, one day before and upon CIDR removal cows received a 25mg PGF injection, and 2 d later a 100µg GnRH injection. The day of the GnRH injection was considered d0 of the estrous cycle. On d6, CON cows received 100µg of GnRH, 1GP4 cows received 100µg GnRH injection and a CIDR insert, and 2GP4 cows received 200µg of GnRH and a CIDR insert. Ovaries were scanned 0, 10, and 20h after the GnRH given on d6. Blood was sampled at 0, 15, 30, 60, 120, 240, 345, 600, and 1200 min after the GnRH given on d6. Data were analyzed by ANOVA for repeated measures. Although LH concentration from 0 to 345 min was greater ($P < 0.01$) for 2GP4 cows (3.1 ± 0.2ng/ml) than CON (2.1 ± 0.3ng/ml) and 1GP4 cows (2.2 ± 0.2ng/ml), that was mainly because at 60 (CON = 2.6 ± 0.4, 1GP4 = 2.7 ± 0.3, 2GP4 = 3.7 ± 0.3ng/ml) and 120 (CON = 4.6 ± 0.8, 1GP4 = 5.1 ± 0.6, 2GP4 = 7.6 ± 0.6ng/ml) min LH concentrations were ($P < 0.01$) greatest for 2GP4 cows. Progesterone concentrations were smaller ($P < 0.01$) for CON cows (1.9 ± 0.3ng/ml) than 1GP4 (3.3 ± 0.2ng/ml) and 2GP4 (3.4 ± 0.2ng/ml) cows, but there were no ($P = 0.82$) differences between 1GP4 and 2GP4 cows. There were no differences ($P = 0.75$) among treatments in size of the dominant follicle at 10 and 20 h after the GnRH injection given on d6. Treating cows with intra-vaginal P4 concurrently with GnRH does not decrease LH concentration or peak, but treatment with 200µg of GnRH results in earlier rise in LH and greater LH peak concentration than treatment with 100 µg of GnRH.

Key words: dairy cow, CIDR, LH

M261 Environmental effects on semen quality of beef bulls used for artificial insemination. D. O. Stepp*, K. J. Stutts, M. M. Beverly, and S. F. Kelley, *Sam Houston State University, Huntsville, TX.*

Semen quality, like other phenotypic expressions, consists of a genetic component, an environmental component, and a variety of interactions between the 2. The objective of this study was to evaluate environmental effects on semen quality of beef bulls used for artificial insemination. Angus and Brangus bulls (n = 76) that were housed at a commercial collection facility in southeast Texas were used in this study. Bulls were collected twice per week with 2 collections attempted on each collection day. Following collection, volume, concentration, and motility of the sample were evaluated. The sample was then cooled, extended, and frozen in liquid nitrogen following standard protocol of the collection facility. A post-thaw analysis of the sample was performed the following day. Data collected on each sample included: motility immediately after thawing (MOT0), motility 3 h post-thaw (MOT3), and the number of primary, secondary, and tertiary morphological abnormalities. Mean ambient temperature and relative humidity were recorded for the time of collection and the preceding 60 d. ANOVA was performed using Minitab15.1. All main effects and all 2-way interactions were included in the model. There was a significant effect of season on MOT0, MOT3, and number of primary, secondary, tertiary, and total abnormalities. MOT0 was higher ($P < 0.05$) in the winter (34.2%) and spring (33.6%) than in the fall (32.2%). MOT3 was higher ($P < 0.01$) in the spring (31.60%) than in the winter (29.77%) and fall (29.61%). Total abnormalities were highest ($P < 0.03$) in the summer (28.05%), followed by the fall (25.47%), spring (23.74%) and winter (23.35%). Season also had significant effects on ejaculate volume and concentration. Ejaculate volume was higher ($P < 0.01$) in the fall than in the winter, and sperm cell concentration was highest ($P < 0.01$) in the spring. These results indicate that environmental factors have a negative effect on semen characteristics of beef bulls. Semen quality is most degraded in the summer and fall seasons after exposure to a combination of high ambient temperatures and high relative humidity in southeast Texas.

Key words: beef bulls, semen quality, environment

M262 Plasma progesterone concentration and follicle dynamics of lactating Jersey cows treated with 1 or 2 intra-vaginal progesterone insert. J. G. N. Moraes*, P. R. B. Silva, N. Bortoletto, A. L. A. Scanavez, and R. C. Chebel, *Department of Veterinary Population Medicine, University of Minnesota, St. Paul.*

The objectives of the current study were to determine the progesterone (P4) concentration and the follicle dynamics of lactating Jersey cows treated with 1 or 2 intra-vaginal P4 insert. Cows were enrolled in the study at 34 ± 3 DIM and were paired by parity, BCS (3.1 ± 0.1), body weight (421.7 ± 5.2kg), and milk yield (28.8 ± 0.6kg/d). All cows were presynchronized with an injection of GnRH concurrent with controlled internal drug release (CIDR) insert containing 1.38 g of P4 and 5 and 6 d later all cows received a PGF2α injection. The day of the first PGF2α injection was determined d −2 of the study. Cows assigned to the 1CIDR treatment received a CIDR insert from d 0 to 8, cows assigned to the 2CIDR treatment received 2 CIDR inserts from d 0 to 8, and control cows did not receive further treatment. Cows were examined by ultrasound and ovarian structures were measured and mapped on d −2 and daily from d 0 to 8. Blood samples were collected for determination of P4 on d −2 and daily from d 0 to 8 and blood samples were collected for determination of estradiol concentration from d 0 to 8. Average P4 concentration from d 0 to 8 was ($P < 0.01$) smallest for control cows (0.73 ± 0.17 ng/ml) followed by 1CIDR (1.37 ± 0.10ng/ml) and 2CIDR (2.21 ± 0.09ng/ml) cows, respectively. Diameter of the largest follicle on d 0 (16.2 ± 0.6mm) was not different ($P = 0.14$) among treatments, but percentage of cows that developed codominant follicles was smallest for 1CIDR cows (1CIDR = 8.0, 2CIDR = 30.8, control = 50%; $P = 0.02$). Percentage of cows ovulating the dominant follicle identified on d 0 was greatest for control cows (1CIDR = 0, 2CIDR = 3.9, control = 80%; $P < 0.01$) and the interval to ovulation was 96 h from d −2 for the 2CIDR cow and averaged 123.0 ± 12.4 h from d −2 for control cows. Control cows were more likely to develop a new dominant follicle from study d 0 to 8 (1CIDR = 12, 2CIDR = 7.7, control = 60%; $P < 0.01$), but there was no ($P = 0.65$) difference in interval to identification of the new dominant follicle (106.9 ± 9.9h from d −2). Treatment with CIDR insert results in increase in P4 similar to those described for Holstein cows.

Key words: progesterone, Jersey cow, follicle

M263 Effect of a rumen-protected niacin product on lactation performance by dairy cows during summer in Wisconsin. K. Yuan*, R. Shaver, M. Espineira, and S. Bertics, *Department of Dairy Science, University of Wisconsin-Madison, Madison.*

Research suggests that supplemental dietary niacin may improve the ability of lactating dairy cows for coping with heat stress. However, niacin is extensively degraded in the rumen. With advances in vitamin encapsulation technology, a niacin product, NiaShure, was developed to protect niacin from rumen degradation (Balchem Corp., New Hampton, NY). The objective of this study was to evaluate the effect of this rumen-protected niacin product on lactation performance by dairy cows during the summer in Wisconsin. Eighty lactating cows (63 ± 29 DIM) were used in a 10-wk lactation trial (a 2-wk pretreatment covariate period followed by an 8-wk treatment period). Cows were stratified by breed, parity and DIM, and randomly assigned to 10 pens of 8 cows each. Pens were assigned randomly either to control (C) or 12 g/d per cow rumen-protected niacin (RPN) TMR group. Ambient temperature and humidity were monitored weekly to calculate temperature-humidity index (THI) and individual cow rectal temperatures were measured weekly, to characterize heat stress conditions during the experiment. Data were analyzed as a completely randomized design with a covariate using SAS Proc Mixed. Milk yield (48.6 vs. 48.4 kg/d), milk fat percent (3.41 vs. 3.35%), milk protein percent (2.90 vs. 2.92%), milk fat yield (1.66 vs. 1.62 kg/d), milk protein yield (1.41 vs. 1.41 kg/d), milk lactose percent (4.89 vs. 4.87%), dry matter intake (27.2 vs. 27.3 kg/d), body weight (714 vs. 717 kg), body condition score (2.81 vs. 2.78) and rectal temperature (38.4 vs. 38.4°C) were not different ($P > 0.05$) between RPN and C. In summary, under summer conditions in Wisconsin, dietary supplementation with 12g/d per cow RPN did not affect lactation performance or body temperature of dairy cows.

Key words: dairy cow, heat stress, rumen-protected niacin

M264 Body condition score at calving affected milk yield and blood metabolites in Holstein dairy cows. Y. Moharrami[1], G. R. Ghorbani[1], H. R. Rahmani[1], S. M. Nasrollahi[1], and C. Li*[2], *[1]Department of Animal Sciences, Isfahan University of Technology, Isfahan, Iran, [2]Agriculture and Agri-Food Canada, Research Centre, Lethbridge, AB, Canada.*

A study was conducted to evaluate the effect of body condition score (BCS) on milk yield and blood metabolites in Holstein dairy cows. Three hundred and 12 multiparous Holstein dairy cows from 2 commercial dairy farms were scored for body condition beginning at one month before dry-off. Cows were scored monthly before calving and bi-weekly after calving until 120 DIM. Body condition score were assigned by 2 independent individuals ranging from 1 (thin) to 5 (obese) using the visual technique. The experiment was designed as a 2 × 2 factorial arrangement of treatment included farm (1 and 2), and BCS (<3.5; low and ≥ 3.5; high). Milk yield and fat were recorded for individual cows. Plasma glucose, insulin, leptin, triglyceride, NEFA and BHBA were determined a week before and a week after parturition. Data were analyzed using the PROC MIXED in SAS. The effects of farm, BCS and the interaction were considered as fixed effects and cow was considered as random effect in the model. There were no interactions between farm and BCS, and no differences were observed between the 2 farms on milk production and blood metabolites. Cows calving with high BCS produced more milk (high vs. low BCS; 41.3 vs. 40.0 kg/d; $P < 0.07$) with higher milk fat content (high vs. low BCS; 3.43 vs. 3.18%; $P < 0.01$); consequently produced more 4%FCM (high vs. low BCS; 37.6 vs. 35.5 kg/d; $P < 0.01$) compared with the low BCS group. Plasma glucose was higher (high vs. low BCS; 59 vs. 55 mg/dl; $P < 0.03$) but other blood metabolites were not different between the low and high BCS groups. The results indicated that managing adequate BCS during the dry period or early lactation improved milk production and milk fat content. Calving with BCS ≥3.5 may be suitable for more milk fat production.

Key words: BCS, milk yield and milk fat content, dairy cows

M265 Body condition score at calving affected reproductive performance and metabolic disorders in Holstein dairy cows. Y. Moharami[1], G. Ghorbani[1], H. Rahmani[1], S. M. Nasrollahi[1], and C. Li*[2], *[1]Department of Animal Sciences, Isfahan University of Technology, Isfahan, Iran, [2]Agriculture and Agri-Food Canada, Research Centre, Lethbridge, AB, Canada.*

A study was conducted to investigate whether body condition score (BCS) at calving affect reproduction performance and metabolic disorders in high producing dairy cows. Three hundred and 12 multiparous Holstein dairy cows from 2 commercial dairy farms were used. The experiment was designed as a 2 × 2 factorial arrangement of treatment included farm (1 and 2), and BCS (<3.5; low and ≥3.5; high). Reproduction performance including conception at first service, days from calving to first insemination, open days, services per conception and conception rate were recorded. Metabolic disorders including dystocia, retained placenta, LDA, laminitis and mastitis were recorded within 120 DIM. Metabolic disorder and conception data were analyzed using the GENMOD procedure of SAS. Other data were analyzed using the mixed model procedure of SAS to account for farm, BCS and the interaction as fixed effects and cows as random effect. There were no interactions between farm and BCS, and no differences were observed between the 2 farms. Days from calving to the first insemination was reduced ($P < 0.02$) by 7 d with high versus low BCS. Similarly, cows with high BCS at calving had less ($P < 0.05$) open days (90 d) compared with low BCS (103 d). Conception at first service, services per conception and conception rate were not different between high and low BCS groups. BCS of 3.5 or higher at calving were associated with an increased (56%; $P < 0.02$) risk for laminitis which could be due to heavier BW on the legs. Incidence of dystocia, retained placenta, LDA and mastitis were not different between the low and high BCS groups. Results suggest that the adequate BCS may reduce interval between calving and first insemination and open days, but had limited influence on metabolic disorders. The calving BCS at 3.5 point or slightly higher may be suitable for transition period management.

Key words: BCS, reproduction performance, dairy cows

M266 Effects of bovine somatotropin (rbST) at 250 mg or 500 mg administered to crossbred cows (*Bos taurus* x *Bos indicus*). B. G. Campos*[1,2], S. G. Coelho[1], A. M. Q. Lana[1], E. Rabelo[3], E. A. Alvarenga[1], and B. F. Silper[1], *[1]Escola de Veterinária da Universidade Federal de Minas Gerais, Belo Horizonte, Minas Gerais, Brasil, [2]Fundação de Amparo à Pesquisa do Estado de Minas Gerais, Belo Horizonte, Minas Gerais, Brasil, [3]Recursos Humanos no Agronegócio, Belo Horizonte, Minas Gerais, Brasil.*

Numerous studies been conducted to determine the effects of rbST in *Bos taurus* dairy cows, however, there are a few studies evaluating the rbST response in crossbred cows ((*Bos taurus* × *Bos indicus*). Since the Brazilian herd is compound mostly by crossbred cows (*Bos taurus* × *Bos indicus*), the objective of this study was to evaluate the effects of the 250 or 500 mg rbST on milk production and milk composition, body weight and body condition score of crossbred cows of 3/4 and 7/8 (*Bos taurus* × *Bos indicus*). The 57 animals were assigned to 3 treatments: T0- control (7 primiparous and 12 multiparous), without administration of rbST; T250- 250 mg rbST (5 primiparous and 12 multiparous and T500- 500 mg rrbST (21 cows (8 primiparous and 13 multiparous). Cows received 16 consecutive rbST injections of 500 mg or 250 mg, respectively (BOOSTIN 500 mg or HILAC-250 250 mg - Schering-Plough/Intervet), starting at 63+3.5 d of lactation, administered at 14-d intervals. Milk production was measured twice weekly and milk composition every 15 d; BW and body condition scores were evaluated monthly. All animals were under the same nutritional management with confinement in the winter and rotational grazing in the summer and milked twice daily. The study was conducted as a completely randomized design. To test differences between means of milk yield, milk composition and body weight, the Dunnett test ($P < 0.05$) was used. Regression analysis was used for the evaluation times. For the analysis of body condition scores the Friedman and Kruskal-Wallis test ($P < 0.05$) were used for groups and days evaluation respectively. Milk production was higher for T500 (21.8 ± 7.0 kg/day) compared with T0 (20.0 ± 5,8 kg/day) and T250 (19.2 ± 7.1 kg/day) treatment ($P < 0.05$). All treatments had the same rate of decrease in production of 0.043 kg milk / day ($P > 0.05$). There were no differences between treatments for milk composition, body weight and body condition scores at different times evaluated ($P > 0.05$). Research supported by FAPEMIG - APQ 01005/08.

Key words: crossbred, milk composition, milk production

M267 Effect of pen change on daily milk yield of dairy cows. A. Zwald* and R. D. Shaver, *University of Wisconsin-Madison, Madison.*

The objective of this experiment was to determine the effect of pen change on daily milk yield by dairy cows over the first 10 d after changing pens in a commercial setting. The study was conducted during fall of 2010 in a 4,000 cow Jersey and Holstein x Jersey crossbred herd. Study cows were stratified by parity (multi- or primiparous). Two pens of 420 animals under the same management were evaluated. Animals were either Jerseys or Holstein x Jersey crossbreds. Pens were stocked at 100 percent. Animals were evaluated by days in milk (DIM) and cows between 65 and 170 DIM were eligible for enrollment. Ten percent of the pen was enrolled to the non-move (NM) group and 10 percent of the pen was enrolled to the move (M) group. The day of the move, the 42 animals enrolled to the M group in pen one switched places with the M group of pen 2. New cows were enrolled and this procedure was repeated once, 4 weeks after the initial move. Weights were taken from each milking in the parlor from the Boumatic meter system and downloaded to DairyComp 305. If a milking was missing, the weekly average weight was used. Animals were removed from the trial if more than 5 full days on either side of the move were missing. Data were analyzed using Proc Mixed of SAS with starting pen, parity, treatment, day, and treatment*day interaction as fixed effects and cow within treatment as a random effect. The least squares means for the average daily milk yield for the NM group were 32.5, 31.5, 32.3 kg/cow for the 5 d prior, day of, and 5 d after pen change, respectively. Least squares means for average daily milk yield for the M group were 32.0, 31.3, and 32.0 kg/cow for the same time periods. The least squares means for average daily milk yield for the 5 d before and 5 d after regrouping were not different ($P > 0.10$). The least squares means for the M and the NM groups were not different ($P > 0.10$) during any period. Changing pens with large groups of animals does not appear to have a detrimental effect on production.

Key words: grouping, milk yield, dairy cow

M268 Milking management of crossbred Holstein x Gyr (F1) cows without calf on production performance. L. H. Oliveira[1], J. M. S. Filho[1], F. L. B. Toral[1], and R. B. Reis*[1,2], *[1]Federal University of Minas Gerais (UFMG), Belo Horizonte, Minas Gerais, Brazil, [2]FAPEMIG, Belo Horizonte, Minas Gerais, Brazil.*

Crossbred Holstein (*Bos taurus*) × Gyr (*Bos indicus*) cows for milk and calf production is very popular in Brazil because production and adaptation in tropical conditions. However, these animals have strong link with their offspring turning them susceptible to lactation failure if milked in absence of their calf. Exogenous oxytocin injection has been used to stimulate milk ejection without calf presence during the milking. The objective of this research was to compare the effect of exogenous oxytocin injection or calf presence during milking on milk production and composition, lactation persistency of crossbred Holstein × Gyr (F1) cows. Seventy 4 multiparous cows were randomly assigned to 1 of 2 experimental groups. Group (BP) cows were milked in the presence of their calf and suckled post-milking for 30 min (n = 36). The cows in group (OT) were milked in the absence of the calf and injected in the mammary vein with 2.0 IU of oxytocin (Postipofisin, Hertape Calier), immediately before milking (n = 38). Cows were weekly checked for milk yield and milk samples were collected for milk composition and Somatic Cell Count (SCC). The adjustment of the lactation curve was performed using incomplete gamma function proposed by Wood (1967) and the parameters of each function estimated by the NLIN procedure of SAS. Accumulated milk yield at 30, 60, 90 120 and 150 d, initial milk yield, milk production at peak, protein, lactose, total solids % and SCC did not differ between groups ($P > 0.05$). The group OT did not have the milk production reduced due to absence of their calf. The peak of lactation occurred at 24.3 DIM. Group OT had a higher lactation persistency (K = 0.00383 vs. K = 0.00480; $P = 0,01$) and higher fat content at 90 DIM (2.40+0.35 vs. 3.77+0.19; $P < 0.05$) and 120 DIM (2.78+0.27 vs. 3.45+0.17; $P < 0.05$). The cows receiving oxytocin injection showed better performance, indicating that this practice is a valuable management tool for milking Holstein × Gyr F1 cows in the absence of calf.

Key words: oxytocin, milk production, crossbred cows

M269 Risk management practices by Idaho dairy producers. R. J. Norell*[1], C. W. Gray[2], and M. Chahine[2], *[1]University of Idaho, Idaho Falls, [2]University of Idaho, Twin Falls.*

A mail-in survey was conducted to evaluate risk management strategies and practices on Idaho dairies. The survey was mailed to every dairy producer registered in the state of Idaho (n = 489) and 140 surveys were returned (28.6% response rate). Survey data were compared with Proc GLM and Proc Freq in SAS (SAS Inst. Inc., Cary, NC). Dairies were categorized as small (n < 250 cows, 45.7%), medium (n = 250 to 749 cows, 25.7%) or large (n > 749 cows, 28.5%). Eighty percent of dairies have utilized one or more risk management strategies with 41 ± 4% using 1 to 3 strategies and 39 ± 4% using 4 or more. Large dairies utilized more strategies at a higher frequency of use ($P < 0.0001$) than small dairies with medium dairies intermediate.

Overall use of risk management practices were: feed contracts (70 ± 4%), milk contracts (63 ± 4%), hedge milk (42 ± 4%), hedge corn (38 ± 4%), hedge soybean meal (27 ± 4%), put options (26 ± 4%), put + call options (22 ± 4%) and Livestock Gross Margin (12 ± 3%). Eighty 2 percent have a current lender and 36 ± 5% are encouraged by their lender to use risk management strategies. Producers utilized on average 4.7 ± 0.2 sources of market information and the number of sources did not differ between herd size groups ($P > 0.25$). Market information sources included: Chicago Mercantile Exchange (87 ± 3%), magazines (86 ± 3%), processors (81 ± 3%), extension newsletters (67 ± 4%), commercial newsletters (64 ± 4%), newspaper (53 ± 4%), and broker (35 ± 4%). Respondents were interested in 4 educational programs: how to hedge (70 ± 4%), how to use options (71 ± 4%), how to protect dairy margins (80 ± 3%), and Dairy Livestock Gross Margin program (76 ± 4%). Small operations were less interested in hedging and options education than large and medium operations ($P < 0.05$). Producers preferred educational training methods in the following order: producer meetings (80 ± 3%), one on one (66 ± 4%), newsletters (56 ± 4%), magazine articles (48 ± 4%), web based materials (46 ± 4%), and webinars (29 ± 4%). Preference for educational method did not differ between herd size categories ($P > 0.25$). We conclude that risk management strategies are an important management tool for Idaho dairy producers and further risk management training is desired by the industry.

Key words: risk management, educational methods

M270 High diurnal fluctuations of ambient temperature do not improve the adaptation of dairy cows to heat stress. H. Khelil[1,2], P. Faverdin[1,2], and A. Boudon*[1,2], *[1]INRA, UMR1080 Production du Lait, Saint-Gilles, France, [2]Agrocampus Ouest, UMR1080 Production du Lait, Rennes, France.*

Climate change should increase the frequency of heat stress periods in temperate conditions. This study was designed to compare the effects of 2 types of heat stress (constant or variable within day) to thermoneutral conditions, on 8 cows either in early (73 d in milk) or mid (155 d in milk) lactation. The patterns of ambient temperature were a constant temperature of 18.0°C (thermoneutrality, TN), a constant temperature of 29.0°C (High Temperature Constant, HTConst), a variable temperature of 32.2°C between 6:00 and 17:00 and 21.5°C between 18:00 and 4:00 with a daily average of 28.4°C (High Temperature Variable, HTVar). Patterns were compared according to a crossover design, with 2 climatic rooms containing each, 2 early and 2 mid lactation cows during 3 periods of 15 d. Recovery periods of 15 d at a constant temperature of 18°C were included between measurement periods. Daily average of temperature-humidity index (THI) was 63 for TN, 75 for HTConst and 76 for HTVar with THI exceeding 78 between 6:00 and 17:00. Between 6:00 and 17:00, cows increased their respiration rate from 29.0 respirations/s at TN to 53.5 at HTConst and 66.5 at HTVar ($P < 0.001$) and their vaginal temperature from 38.5°C at TN to 39.2°C at HTConst and 39.5°C at HTVar ($P < 0.001$). Daily average of vaginal temperature increased from 38.6 to 39.3 C° from TN to HT ($P < 0.001$) with no differences between HTConst and HTVar. Dry matter intake decreased from 21.8 kg at TN to 18.4 kg at HT ($P < 0.01$). Daily milk yield averaged 28.6 kg and was not significantly affected by the temperature pattern even though morning milk yield decreased from 18.7 kg at TN to 16.3 kg at HT ($P < 0.05$). Milk fat and protein contents decreased from 42.2 and 30.5 g/kg respectively at TN to 40.0 and 28.7 g/kg at HT ($P < 0.001$) with no significant differences between HTConst and HTVar. Proportion of eating time between 6:00 and 17:00 decreased at HTVar compared with TN and HT Const (0.41 vs. 0.55, $P < 0.001$). In conclusion, high diurnal fluctuations of ambient temperature did not improve cow performance compared with a constant temperature with a similar daily average.

Key words: heat stress, temperature-humidity index, dairy cow

M271 Assessment of long-term nitrogen runoff reduction from dairy pastures. R. White* and J. L. Capper, *Washington State University, Pullman.*

A 20-yr assessment was run simulating a pasture on a dairy to determine the effect of various harvesting techniques on Nitrogen (N) removal from the system. The aim was to identify a treatment that resulted in the greatest uptake of N by plant matter thereby diminishing N loss through runoff. Grass, shrubs and trees were modeled to function as they would in a riparian system, grass diffused water to allow absorption by soil, whereas shrubs and trees functioned to absorb nutrients. The pasture was located next to a dairy from which runoff inputs were given as N, Carbon and water sources. Other inputs to the system were historical data for monthly rainfall, temperature and soil attributes. The output was expressed as N runoff from the soil profile. The model was run over 20 yrs to view the long-term consequences of treatments. Mowing, grazing and planting were hypothesized to stimulate a grass density increase inhibiting water flow from the system while pruning and burning plants were thought to stimulate growth and increase nutrient uptake from the soil. These hypotheses were tested via 5 treatments: mowing grass to a stubble height of 0.1 m^2, pruning 1 m^2 from trees and 0.5 m^2 from shrubs, planting 90 kg of grass/acre, grazing of 450 kg of cattle/acre, and burning 70% of the biomass. A total of 4.335 kg N per acre was calculated to runoff during the 20-yr time period. Annual planting in October, burning before yr 5 and pruning after yr 3 were all found to significantly decrease N runoff. When grazing during the spring N runoff increased to 5.16 kg; however, during the winter, runoff did not significantly increase. Mowing did not change N runoff. The most effective reduction resulted from annual fires in the first 5 yrs, pruning annually in August starting in yr 7, grazing cattle annually starting in yr 6 and annual planting of grass in October. This combination of treatments resulted in a runoff reduction to 1.09 kg N, nearly a 75% decrease. This reduction shows that good riparian area management, including use by cattle, can reduce N runoff from dairy pastures.

Key words: nitrogen, runoff, dairy

M272 Milk, fat, and protein production in relationship to herd linear somatic cell score in Minnesota. R. F. Leuer* and J. K. Reneau, *University of Minnesota, St. Paul.*

The impact of herd average udder heath on production is significant. It has long been recognized that herds with low somatic cell counts also excel in other aspects of herd management that contribute to overall herd productivity. Linear somatic cell score (LSCS) has been shown to be highly related to milk and other yield characteristics of individuals within a herd. The objective of this study was to evaluate the relationship between herd test day average LSCS and rolling herd average milk production (RHAM), rolling herd average fat production (RHAF), and rolling herd average protein production (RHAP). Minnesota DHIA monthly average herd records were collected from January 2007 to November 2010. Monthly tests with fewer than 30 cows and without SCC, milk, fat, and protein information were removed. Herds averaging less than 10 tests per year over the collection period were also removed. Monthly records (n = 62,582) were analyzed using PROC REG. The equation for rolling herd averages are: RHAM =

12,449.5 Kg – 916*LSCS, RHAF = 419 Kg – 28.8*LSCS, RHAP = 372.7 Kg – 24.9*LSCS. The R2 for the regressions were RHAM = 0.13, RHAF = 0.11, RHAP = 0.11. Herds with a lower LSCS produced a greater volume of milk, fat, and protein. Herd linear somatic cell score gives insight to overall management level and production ability.

Key words: linear somatic cell score, milk quality

M273 Effects of water total dissolved solids on milk-fed calves weight gain, feed intake and weaning age in winter. R. Ramezankhani[1], A. Alizadeh[1], A. Nasserian[2], M. Chehrazi[3], and B. Saremi*[4], *[1]Department of Animal Science, Islamic Azad University, Saveh Branch, Saveh, Iran, [2]Department of Animal Science (Excellent Center of Animal Nutrition), Faculty of Agriculture, Ferdowsi University of Mashhad, Mashhad, Iran, [3]Epidemiology and Reproductive Health Department, Royan Institute for Reproductive Biomedicine, ACECR, Tehran, Iran, [4]Institute of Animal Science, Physiology and Hygiene unit, University of Bonn, Bonn, Germany.*

In some areas of Iran dairy farms use drinking water that containing elevated total dissolved solids (TDS). Reliable information concerning water TDS on calves' performance is limited, especially in winter. The aim of this study was to compare 3 water TDS groups ; High TDS (HTDS) ≈3000 ppm, Medium (MTDS) ≈1100 ppm and Low (LTDS) ≈160 ppm used as calf drinking water. Holstein calves (n = 21) were randomly assigned to 3 groups in a commercial dairy farm (Laban, Qom, Iran) during winter. Calves were subjected to different treatments from 3 d after birth up to 30 ± 2 d old (0.5 L per day). Thereafter, ad libitum access to drinking treatments was available until weaning. Dairy calves were weaned after they reached 1kg starter intake for 3 consecutive days. Data were analyzed by SPSS 17. Mean ambient temperature during the experiment was 12°C. Calves in the HTDS group had highest water consumption (Table1), although this group had the lowest starter intake. Body weight of calves for the MTDS group was highest on d 60. Weaning weight did not differ among treatments. Weaning day was affected by water TDS and calves in the MTDS group weaned earlier than HTDS. Urine pH decreased linearly as TDS increased. Body temperature, height, and body length were similar among treatments. This study indicated that water TDS can increase feed intake with a reduction in water intake. Decreased milk feeding period was a consequence of increased feed intake. TDS values at 160ppm are recommended in winter.

Table 1. Performance, feed and water consumption and urine pH of dairy calves receiving several water TDS contents

Item	LTDS	MTDS	HTDS	SE
Water consumption (L/d)	1.95 ^{b}	2.05 ^{ab}	2.24 ^{a}	0.19
Feed intake(g/d)	540 ^{a}	545 ^{a}	525 ^{b}	7.6
Body weight- 60 d (kg)	63.7 ^{b}	65.6 ^{a}	61.7 ^{b}	1.24
Weaning day(d)	69.8 ^{ab}	68.7 ^{b}	73.7 ^{a}	0.9
Urine pH	6.55 ^{a}	6.52 ^{b}	6.49 ^{c}	0.006

$^{a-c}$Values with differing letters within the same row are significantly different ($P < 0.05$).

Key words: water total dissolved solids, calf, winter

M274 Occurrence of milk unstable protein in dairy farms from southeastern region of Brazil. L. C. Roma Junior*[1], A. C. O. Rodrigues[2], T. G. R. Amaral[2], F. Cardoso[2,3], and P. F. Machado[2], *[1]APTA Centro Leste, Ribeirao Preto, Sao Paulo, Brazil, [2]Clinica do Leite/ESALQ/USP, Piracicaba, Sao Paulo, Brazil, [3]Department of Animal Science, University of Illinois, Urbana.*

Milk quality is important to achieve good dairy industrialized products. The stability of milk protein is one of the most important factors. During the industrialization process thermal treatment (heat) is applied to milk. Milk characterized as unstable protein (UP) is affected by thermal treatment and has negative impacts on dairy farmers, industry and consumers. UP is defined as low casein stability resulting in precipitation during the alcohol test without the presence of acidity on milk. The present study had the objective of evaluating the quality of milk protein regarding its thermal stability in the Brazilian Southeastern Region. This evaluation was carried through by quantification of the problem of UP and the analysis of the factors related to the occurrence. During the years 2005/2006, 2,970 bulk tank milk samples from individual farms were processed. In this period, samples were classified by identifying and quantifying the UP occurrence. Finally, the characteristics of both the facilities and factors which would affect the occurrence of the problem were verified. As a result, 7% of the total volume of produced milk, throughout one year, showed the UP problem, without any kind of geographic influence. However the season of the year had an influence on this occurrence ($P < 0.05$), being identified the beginning of the Autumn and the end of the Winter as the periods with higher numbers of occurrence. Reduction of lactose level ($P < 0.05$) was present in samples with UP that also presented a reduction of its the thermal stability, without presenting any kinds of raised acidity. This problem was related to animals, which were in advanced periods of lactation or presented a reduction of their corporal score due to the low consumption of dry matter, specifically for diets with low energy levels, resulting in the reduction of lactose in milk.

Key words: milk quality, thermal stability, dairy nutrition

M275 Alternative cooling of dairy cows by wetting the udder. J. A. Binversie*[1], J. D. Davis[1], K. G. Gebremedhin[2], C. N. Lee[3], and J. E. Larson[1], *[1]Mississippi State University, Mississippi State, [2]Cornell University, Ithaca, NY, [3]University of Hawaii, Honolulu.*

Heat stress is a major inhibitor of production in livestock operations, causing severe economic loss. The objective of this study was to determine whether spraying the udder with water, with or without fans blowing air onto the udder, cools the body as effectively as spraying water on the back of the animal with or without fans blowing air on the back. Twelve pregnant, lactating Holstein cows were used over 4 d with 4 applications of each treatment each d. Treatments included wetting of the back with a fan (B+F, n = 24), and without a fan (B+NF, n = 72) blowing air on the back; wetting of the udder, with a fan (U+F, n = 24) or without a fan (U+NF, n = 72) blowing air on the udder. The back or udder of each animal was sprayed with water for 1 min, and in appropriate treatment groups, air from identical fans was blown on the wetted area for the duration of the treatment and measurement time periods. Rectal temperature, respiration rate, and surface skin temperature of the back and udder were collected 10 min after treatment application. Data were analyzed using the Mixed Procedure of SAS with the replication during each day analyzed as a repeated measurement and Black globe humidity index (BGHI) used as a covariate. Mean BGHI and Temperature Humidity Index for the period were 80.3 ± 0.3 and 81 ± 0.3, respectively. Rectal temperatures and respiration rates were not different ($P > 0.05$) among treatments. The LSMeans and SEM of rectal temperatures were 39.8 ± 0.1, 39.6 ± 0.2, 39.6 ± 0.1, and 39.6 ± 0.2°C and the respiration rates were 110.6 ± 1.6, 106.1 ± 2.9, 109.0

± 2.9 and 109.0 ± 1.6 breaths/min for cows treated with B+NF, B+F, U+NF, and U+F treatments, respectively. Skin surface temperatures of the back were similar among treatments. Interestingly, cows that received B+F had a cooler udder surface temperature (38.1 ± 0.3°C; $P \geq 0.05$) compared with all other treatments: 38.5 ± 0.2, 38.7 ± 0.3, and 38.5 ± 0.2°C for cows receiving U+NF, U+F, and B+NF, respectively. In conclusion, efforts to abate heat stress by spraying the udder with water either with or without a fan is as effective as spraying the back with water.

Key words: dairy cows, heat stress, wetting

M276 Effect of essential oils on production and reproduction in early lactating cows during heat exposure. U. Serbester[1], M. Çmar[1], A. Ceyhan[1], H. Erdem[2], M. Görgülü[3], H. R. Kutlu[3], L. Baykal Çelik[3], Ö. Yücelt[4], P. W. Cardozo*[5], and M. Blanch[5], *[1]Bor Vocational School, University of Nigde, Turkiye, [2]Department of Obstetrics and Gynecology, Faculty of Veterinary Medicine, University of Selcuk, Turkiye, [3]Department of Animal Science, Faculty of Agricultural, University of Cukurova, Turkiye, [4]Ekol Company, Turkiye, [5]Novus International Inc., St. Charles, MO.*

Twenty-five Holstein cows (8 primiparous and 17 multiparous, DIM 37.4 ± 3.1 d; milk yield 29.8 ± 1.23 kg/d) were used for 78 d to evaluate the effect of essential oil compound mixture (EOCM; containing cinnamaldehyde and diallyl disulfide; Novus International, Inc.) on productive performance and pregnancy rate during heat exposure. The early lactation dairy cows were subjected to presynch-ovsynch protocol 12 d apart and inseminated to timed AI (TAI). Cows were individually fed a total mixed ration comprising (DM basis) 60% concentrate and 40% silage of common vetch with triticale. The concentrate differed only in the addition of EOCM as 25 mg/kg concentrate (as fed). Ambient temperature and relative humidity were recorded, and temperature-humidity index (THI) was calculated throughout the study. Dry matter intake, milk production were measured daily, milk samples were taken twice a week, blood samples were collected weekly, and ultrasonography was performed at 29 and 42 d post-TAI to determine conception rate. Results were analyzed using PROC MIXED for repeated measures and conception rates were analyzed utilizing GENMOD procedure of SAS. Differences were declared at $P < 0.05$. Average of ambient temperature, relative humidity and THI were 25.9°C, 73.4% and 76.8%, respectively. Even with addition of EOCM, body weight, DMI, milk yield, milk composition, serum glucose, IGF-I, progesterone concentrations and conception rate were not affected ($P > 0.05$); however, EOCM supplementation increased ($P < 0.01$) insulin concentration, and tended to decrease ($P = 0.07$) serum total cholesterol concentrations, and increase ($P = 0.10$) NEFA concentrations. Results indicate that at the level offered, EOCM did not affect milk production and conception rate of early lactating dairy cows during heat stress. The increase of insulin and reduction of total cholesterol observed in EOCM group needs to be confirmed with further research.

Key words: essential oils, dairy cows, conception rate

M277 The relationship between milk urea nitrogen with milk yield and protein percentage categories for Iranian Holstein cows. F. Fatehi*[1], M. Honarvar[2], M. Dehghan-Banadaky[1], A. Zali[1], and A. Young[3], *[1]1Department of Animal Science, Campus of Agriculture and Natural Resource, University of Tehran, Karaj, Iran, [2]Islamic Azad University, Shahriar_Shahr_e_Qods Branch, Shahriar, Iran, [3]Department of Animal, Dairy, and Veterinary Sciences, Utah State, Logan.*

Considerable interest has developed in using MUN as a monitor of the efficiency of nitrogen utilization by dairy cows. However, the association between MUN and both nutritional management and performance should be determined under field conditions using commercial testing procedures. To investigate these associations, a measure of the Production Variables factors affecting MUN is needed. The objectives of this study were to determine the relationships among MUN, milk yield, and milk protein in Iranian Holstein cows. Milk production was grouped by increments of 9.1 kg/d with the upper grouping of 63.6 kg and greater for Holstein cows. Also for milk protein the categories were less than 3.0%, 3.01 to 3.2%, and >3.2% milk protein. Multivariate mixed linear regression models using the Proc Mixed procedure in SAS (SAS, 2004) was used to determine the association between MUN (dependent variable) and milk yield and protein categories (independent variables). Multiple comparisons were made with P-values adjusted using Tukeys procedure. In Iranian Holstein cows, MUN was lower when milk protein was > 3.2% (vs. < 3.0% or 3.01 to 3.2%). Also, MUN was lower for cows with milk protein 3.01 to 3.2% than the group of <3.0% milk protein for all milk yields (Table 1). Because of these relationships, milk protein percentage should be considered in addition to MUN concentration as a management tool to determine if rations are properly balanced.

Table 1. Least squares means and SE of MUN concentration by milk yield and protein percentage categories for Iranian Holstein cows

	≤ 3.0%		3.01-3.2%		> 3.2%	
Milk Category, kg	MUN	SE	MUN	SE	MUN	SE
9.0-18.2	16.1[a]	0.18	15.0[b]	0.05	14.3[c]	0.1
18.2-27.3	17.1[a]	0.08	15.1[b]	0.05	14.8[b]	0.04
27.3-36.4	17.5[a]	0.04	15.6[b]	0.05	15.2[c]	0.03
36.4-45.5	17.5[a]	0.06	15.9[b]	0.04	15.4[c]	0.04
45.5-54.5	17.8[a]	0.04	16.1[b]	0.07	15.7[c]	0.07
54.5-63.6	17.9[a]	1.03	16.4[b]	0.03	15.9[c]	1.07

[abc]Least squares means within the same row with different superscripts differ at $P \leq 0.05$.

Key words: milk urea nitrogen, milk yield and milk protein, Iranian Holstein cows

M278 Stage of lactation is associated with differences in the metabolic profiles and innate immunity in dairy cows transitioning to an organic management system. J. F. Odhiambo*, Q. Zebeli, S. Iqbal, D. A. Mansmann, U. Farooq, S. Sharma, S. M. Dunn, and B. N. Ametaj, *University of Alberta, Edmonton, AB, Canada.*

Negative energy balance during early lactation is a major concern in organic dairy herds due to restrained use of concentrates. Metabolic profiles and plasma haptoglobin (Hp) in dairy cows transitioning from conventional to organic management system were evaluated during the following periods: dry period (DP), 0–30, 30–60, and 60–90 DIM (n = 7 cows per period). Blood samples were obtained from cows by tail venipuncture once during the period and utilized for metabolite analysis by colorimetric methods. Data were evaluated by the mixed procedures of SAS. Concentrations of NEFA were elevated ($P < 0.01$) between 0 to 30 DIM, but did not differ between 30 to 60 and 60 to 90 DIM, and DP (259.9 ± 19.9, 201.6 ± 21.7, 210.4 ± 23.2 and 186.3 ± 19.8 μEq/L, respectively). Concentrations of BHBA in the serum were also

greater ($P < 0.001$) between 0 to 30 DIM, intermediate between 30 to 60 and 60 to 90 DIM, and were lower in the DP (1037.7 ± 45.7, 908.6 ± 50.1, 860.9 ± 53.2 and 775.0 ± 45.5 μmol/L, respectively). Serum concentrations of cholesterol increased ($P < 0.001$) with increasing DIM and returned to nadir levels during DP (153.8 ± 6.9, 194.9 ± 7.4, 217.8 ± 7.7, and 146.9 ± 6.9 mmol/L, for 0–30, 30–60, 60–90 DIM, and DP, respectively). Low glucose concentrations were observed 0 to 30 DIM, levels were intermediate during 30 to 60 and 60 to 90 DIM, and peaked during DP (51.6 ± 1.3, 55.5 ± 1.4, 57.3 ± 1.5, and 61.9 ± 1.3 mg/dL, respectively, $P < 0.001$). Concentrations of lactate tended ($P = 0.08$) to be higher during the DP but remained unchanged from 0 to 90 DIM. Serum concentrations of Hp were elevated during the DP; reached peak levels during 0 to 30 DIM and decreased gradually with increasing days postpartum (344.9 ± 32.3, 415.2 ± 32.4, 333.8 ± 35.6, and 267.6 μg/mL, for dry, 0–30, 30–60, 60–90 DIM, respectively, $P < 0.001$). Taken together, these data indicate that metabolic changes associated with initiation of lactation are preceded by an acute phase response in dairy cows under an organic management system.

Key words: stage of lactation, metabolic profile, organic dairy cows

M279 Delayed effect of heat stress on dry matter intake and milk yield in dairy cows. A. S. Atzori* and A. Cannas, *Dipartimento di Scienze Zootecniche, Università di Sassari, Sassari 07100, Italy.*

During summer, dairy cows in Sardinia (Italy) have marked declines of milk production even if the area in which most farms are located is considered at medium risk of heat stress. Thus, this work studied the main meteorological variables involved in the cow response to heat stress. From June to September 2009 the data related to daily herd consistency, feed supplied and refused, and milk yield (MY) were obtained from a farm management software (Ecostalla, J-Service, Arborea, Italy) currently used in one farm of Arborea (OR, Sardinia, Italy). During the same period, mean air temperature (T_m) and relative humidity (RH) were recorded, 2 m above the feed bunk, every 2 h, and the temperature-humidity index (THI) was calculated (Kliber, 1964). The daily mean values of recorded variables (range within parenthesis) were: number of lactating cows 161 ± 0.5; DMI 20.2 ± 0.1 (18.3–22.5) kg/cow per d; MY 26.2 ± 0.1 (23.9–28.0) L/cow per d; T_m 24.9 ± 2.0 (20.7–31.7) °C; RH 67.1 ± 7.6% (38.6–77.8); THI 73.3 ± 2.8 (67.7–78.6) °F. DMI was negatively correlated with T_m (−0.38; $P < 0.001$) and THI (−0.44; $P < 0.001$). MY was poorly associated with the same day weather variables. Correlations were higher when DMI or MY were associated to previous days T_m and THI. The highest correlation were observed with a delay of 3 d for DMI (r = −0.56 and −0.61 with T_m and THI, respectively; $P < 0.001$), and with a delay of 5 d for MY (r = −0.58 and −0.63; for T_m and THI respectively; $P < 0.001$). Estimated delayed stress was equal to −0.23 kg of DMI/cow per d and −0.174 kg of MY/cow per d per increased unit of THI above the threshold of 70°F (21°C). The RH was significant only combined with T_m in the THI. The MY on a certain day was best predicted as MY (L/cow per d) = 25.2 - 0.095 × THI_{-5} (°F) + 0.391 × SSI_{-2} (kg/cow per d) ($r^2 = 52.6$), where the subscripts −5 and −2 indicate the days before MY. This study suggest that delayed MY losses due to heat stress can be minimized if appropriate actions are taken as soon as THI increases above the threshold.

Key words: temperature humidity index, threshold, short-time stress

M280 Effect of feed-line soaking and Niashure (NI) on heat–stressed lactating Holsteins housed in an evaporative tunnel ventilated barn in Thailand. S. Rungruang*, J. Collier, and R. Collier, *University of Arizona, Tucson.*

Total of 86 lactating Holstein cows (28.2 ± 4.6kg/d) were assigned to a completely randomized design to evaluate the impact of feed-line soaking in conjunction with 12 g/d Niashure (NI) supplementation on body temperature indices, feed intake and production parameters. All cows were housed in an evaporative tunnel ventilated barn for 21 d Jul–Aug 2010 in Nakhon Ratchasima, Thailand. The Temperature Humidity Index (THI) values inside the barn ranged from 72 – 82 and average humidity values were more than 90%. Cows had access to feed-line soaking from 12:00 to 06:00 each day and were randomly assigned to one of 2 groups, control or NI supplement. Groups were balanced for parity, days in milk and milk yield. Rectal, skin and vaginal temperatures were recorded on a subset of 10 cows per group.NI doses were split and top–dressed on ration by feeding 6 g at 06:00 and 6 g at 13:00. Feeding NI with soaking significantly reduced skin temperature but not rectal and core body temperature during peak THI periods. Dietary NI decreased shaved (30.9 vs. 32.8°C, $P < 0.01$) and unshaved shoulder (30.6 vs. 31.9°C, $P < 0.02$) skin temperature and also decreased shaved rump skin temperature (32.0 vs. 33.3°C, $P < 0.03$) at 14:00. Milk yield in NI group was lower than controls (26.2 vs. 28.5 kg/d, $P < 0.04$). We did not detect an effect of feeding NI on dry matter intake (DMI) or milk composition. Feeding NI did not lower mean core body temperature but soaking reduced body temperature and respiratory rate. Soaking decreased average rectal temperatures and respiratory rates of both groups to lowest values at 14:00 compared with 08:00, 11:00 and 16:00 (38.9°C, $P < 0.02$ and 59 breath/min $P < 0.03$). Use of NI with soaking numerically reduced average rectal temperature to the lowest values at 14:00 compared with other time points and lower when compared with control group. Results indicate that the effect of feed–line soaking reduced body temperature indices while NI supplementation in addition to soaking did not further reduce core temperatures of lactating dairy cows.

Key words: heat-stressed, niacin, soaking

M281 Economic assessment of postpartum milking frequencies on dairy farms. F. Soberon*, D. M. Galton, and T. R. Overton, *Cornell University, Ithaca, NY.*

The additional milk yield associated with increased milking frequency (IMF) during lactation has been well-documented, but implementation of this management technique depends upon the balance between potential revenue and cost. We compared the marginal profitability of cows milked 4x for 21 d followed by 2x for the remainder of the lactation (4x-2x) and cows milked 3x throughout the entire lactation (3x) to cows milked 2x throughout the entire lactation (2x). Energy-corrected milk (ECM; 3.5% fat and 3.2% true protein) increases were assumed to be 1.5 and 3.0 kg/d of ECM for 4x-2x and 3x, respectively, compared with 2x and were determined according to results from a large study on commercial farms focused on 4x-2x milking and literature reports for 3x milking. The model analysis included marginal feed cost, farm size (number of cows), parlor size (cows per hour), parlor efficiency (worker equivalents per hour of milking time), energy usage ($20.00 per hour of milking) and other milking supplies ($0.15/cow per milking). For an example smaller farm with 200 milking cows, an assumption of 2.5 workers per hour, a milking capacity of 50 cows per hour, 3x milking is more profitable than 2x milking at all milk prices greater than $15.70/45.4 kg; however, 4x-2x milking is more profitable than 2x milking at all milk prices greater than $8.35/45.4 kg. When milk prices are higher than $23.40/45.4 kg 3x milking is more profitable

than 4x-2x milking. For an example larger farm of 1,000 milking cows and 5 workers per hour with a milking capacity of 200 cows per hour, 3x milking is more profitable than 2x when milk prices are above $9.35/45.4 kg and 4x-2x milking is more profitable than 2x at milk prices above $5.90/45.4 kg. A 3x milking scheme on larger farms was more profitable than 4x-2x milking at milk prices above $13.00/45.4 kg. We conclude that management decisions regarding milking frequency on any given farm should consider herd size, parlor efficiency, current milk prices along with other facility- and management-related factors that are beyond the scope of this analysis.

Key words: milking frequency, economics

M282 Milk fat and protein:fat ratio in California dairies. N. Silva-del-Río*[1], A. Lago[2], B. Verboort[3], and H. Selvaraj[3], *[1]University of California Cooperative Extension, Tulare, [2]APC Inc., Ankeny, IA, [3]AgriTech Analytics, Visalia, CA.*

The aim of this study was to report the prevalence of herds: a) with low milk fat, and b) at risk of ketosis in California dairies. Dairy Herd Improvement Association records were obtained from AgriTech Analytics (Visalia, CA). Information included milk composition at herd level [51 Jersey (JE) and 534 Holstein (HO) herds], and at cow level (2,321,563 observations from 138 HO herds) from Nov-09 to Oct-10. Milk fat (MF) depression was evaluated based on herd averages below 3.2% (HO) and 4.2% (JE), and on the proportion of cows below 2.5% of MF at any given test. The risk of ketosis was evaluated based on the proportion of cows within a herd that at first test had protein:fat ratio (P/F) less than 0.75. During the study period, 39.2% (n = 51) of the JE herds and 22.0% (n = 534) of the HO herds had at least one MF test below 4.2% and 3.2%, respectively. The proportion of JE and HO herds that had more than 25% of the tests with MF below 4.2% and 3.2% was 14.5% and 7%, respectively. The percentile distribution of cows within herd with MF <2.5% was Q1 = 2.8%, Q2 = 4.3%, Q3 = 5.8% of the cows. In 6.3% of all the tests conducted more than 10.0% (up to 27.1%) of the cows had MF <2.5%. A total of 26.1% of the herds had at least one monthly test where more than 10% of the cows tested had MF content below 2.5%. Eleven herds (8.0%) had more than 25% of their tests with at least 10% of the cows with MF <2.5%. The percentage of herds with more than 10% of the cows with MF <2.5% ranged from 3.3% in Apr and 9.5% in Nov. The risk of ketosis was evaluated and 79.0% of the herds had at least one test where cows with P/F < 0.75 at first test represented more than 40% of the herd. A large proportion of herds (25.0%) had 75% to 100% of their tests with more than 40% of the cows having P/F < 0.75. The percentage of herds with more than 40% of the cows with P/F < 0.75 ranged by month from 25.9% in Aug to 52.0% in Feb. At a given test, herds were identified where all the cows at first test had a P/F <0.75 (4 herds) or P/F > 0.75 (5 herds). This information suggests that milk fat depression and subclinical ketosis need further evaluation in California dairy herds.

Key words: milk fat, protein fat ratio, DHIA records

M283 Performance of post-weaned Holstein heifers fed a grain mix with free choice hay or a total mixed ration (TMR) containing sweet corn cannery waste, hay and dried distillers grains. D. Schimek*[1], D. Ziegler[2], B. Ziegler[1], H. Chester-Jones[2], M. Raeth-Knight[3], and G. Golombeski[3], *[1]Hubbard Feeds Inc., Mankato, MN, [2]University of Minnesota Southern Research and Outreach Center, Waseca, [3]University of Minnesota, St. Paul.*

Two consecutive studies were conducted to evaluate post-weaned heifer performance when fed TMR diets containing sweet corn cannery waste (SCCW), hay and dried distillers grains (DDGS). In study 1, 112 4-mo old Holstein heifers (av.136.5 ± 1.03 kg) were assigned to 1 of 8 pens (7 heifers/pen) and 1 of 2 treatments for 56 d. Treatments included: 1) Control 16% CP grain mix fed at 2.27 kg/hd daily with free choice (FC) hay; 2) Free choice ensiled TMR (33% SCCW, 33% hay, 33% DDGS, DM basis) top-dressed with 0.75 kg protein pellet at feeding. Heifers fed the TMR had higher ($P < 0.05$) ADG (1.2 vs. 0.98 kg/d), hip height gain (+1.22 cm), body condition score change (+0.44), and gain/feed (0.23 vs. 0.17 kg BW/kg DMI) compared with those fed the control diet. For study 2, dietary composition of the TMR was modified to reduce heifer gain to approximately 1 kg/d and 126 3-mo old Holstein heifers (av. 114.3 ± 0.93 kg) were assigned to 1 of 6 pens (7 heifers/pen) and 1 of 3 treatments for 84 d. Treatments included: 1) Control 16% CP grain mix fed at 2.27 kg/hd daily with FC hay; 2) Free choice ensiled TMR (40% SCCW, 28% hay, 32% DDGS, DM basis) top-dressed with 0.14 kg mineral mix at feeding; 3) Ensiled SCCW mixed daily with hay and distillers grains (40% SCCW, 28% hay, 32% DDGS, DM basis) top-dressed with 0.14 kg mineral mix at feeding. Heifers fed the TMR diets had higher ($P < 0.05$) ADG (1.05 vs.0.93 kg/d), hip height gain (14.1 vs. 13.1 cm), BCS change (+0.87 vs. +0.77) and gain/feed (0.28 vs. 0.22 kg BW/kg DMI) than those fed the control diet. Heifers fed the TMR diets performed similarly but a higher refusal rate was evident when the TMR was mixed daily. Under the conditions of these studies preparing a complete SCCW, hay and DDGS ensiled TMR or mixing a TMR daily with individual ingredients offers a lower cost alternative feed for post weaned heifers from 3 to 6 months of age compared to limit feeding a grain mix with FC hay.

Key words: Holstein heifers, performance, total mixed rations

M284 Effect of feeding duration on growth of group fed dairy calves during transition to an organic production system. B. J. Heins*, D. G. Johnson, and E. A. Bjorklund, *University of Minnesota, St. Paul.*

Heifer calves (n = 61) were used to evaluate the effect of early life feeding duration in a group management system on body weight and hip height. Calves were assigned to feeding groups of 10 in super hutches by birth order, and were born at the University of Minnesota West Central Research and Outreach Center, Morris, Minnesota from March to June 2010. Breed groups of calves were: Holsteins (n = 9) selected for high production (HO), Holsteins (n = 14) maintained at 1964 breed average level (H64), crossbreds (n = 28) including combinations HO, Montbeliarde, and Swedish Red selected for high production (HMS), and crossbreds (n = 10) including combinations of HO, Jersey, and Swedish Red selected for durability (HJS). Early weaning (EW) groups were fed 1.5% of birth weight 13% total solids organic milk once daily until the youngest calf in the group was 4 weeks old, reduced to 0.75% of birth weight for 1 week, and then weaned when the group consumption averaged 0.91 kg starter/calf/day. Late weaning (LW) groups were fed 1.5% of birth weight of organic milk once daily, and then weaned when the group consumed 0.91 kg of starter/calf/day, and the youngest calf in the groups was 9 weeks old. Body weight and hip height were recorded at birth, weaning, and d 90 and 120. Independent variables for statistical analysis were the fixed effects of weaning group (EW or LW) and breed group. Weaning group performance was weaning age (days), EW (44.6) vs. LW (63.6) ($P < 0.01$); gain per day (kg), EW (0.42) vs. LW (0.59) ($P < 0.01$); weaning weight (kg), EW (56.4) vs. LW (73.5), ($P < 0.01$); weaning hip height (cm), EW (83.3) vs. LW (90.4) ($P < 0.01$); 90-d weight (kg), EW (91.1) vs. LW (99.7)

($P < 0.05$); and 120-d weight (kg), EW (113.3) vs. LW (118.5) ($P > 0.25$). The HO (0.51; 67.2), H64 (0.44; 60.8), HMS (0.54; 69.4), and HJS (0.53; 62.3) calves were not significantly different for gain per day (kg) or weaning weight (kg), respectively. In summary, EW calves had less body weight and hip height compared with LW calves during organic transition.

Key words: organic, crossbreeding, calf

M285 Pre- and post-weaning performance and health of dairy heifer calves fed calf starters and grain mixes with glycerol as a replacement for corn. D. Ziegler*[1], H. Chester-Jones[1], A. Doering[2], D. Timmerman[2], M. Raeth-Knight[3], and G. Golombeski[3], *[1]University of Minnesota Southern Research and Outreach Center, Waseca, [2]Agricultural Utilization Research Institute, Waseca, MN, [3]Unversity of Minnesota, St. Paul.*

In phase 1, 120 (2–4 d old) individually fed Holstein heifer calves (40.3 ± 0.08 kg BW) were randomly assigned to 1 of 4 treatments for 56-d. Our objective was to evaluate the use of glycerol as a replacement for corn in calf starters (CS) by evaluating its impact on performance and health pre-(d 1–42) and post-weaning (d 43–56). Treatments were: 1) Complete texturized 18% CP control CS (CON); 2) Complete pellet 18% CP control CS (CONP); 3) 18% CP pelleted CS containing 3% glycerol (27.3 kg/ton; 3%GLY) and 4)18% CP pelleted CS containing 6% glycerol (54.6 kg/ton; 6%GLY). All calves were fed a 20:20 (CP:fat) milk replacer at 0.28 kg/d powder in 2 L water 2 X daily d 1 to 35 and once daily d 36 to 42 weaning. There were no treatment differences ($P > 0.05$) in pre- and post weaning calf performance. Average daily gain and feed/gain for the nursery phase were 0.61kg/d and 1.88 kg feed/kg BW for d 1 to 56, respectively. Health treatment costs were highest ($P < 0.05$) for calves on 6%GLY. Calves were transitioned to group pens and fed the CON CS for 7 d. One-hundred-36 calves (av. 84.7 ± 0.71 kg) were assigned to 6 replicate pens (7 calves/pen) each of 3 limit-fed grain mixes with free choice hay for a 112-d study. Treatments included: 1) 16% CP corn and pellet grain mix fed at 2.73 kg/hd daily for 56 d and 2.27 kg/hd daily from 57 to 84 d; 2) 16% CP corn and pellet mix with 3% added glycerol fed as in 1; and 3), 16% CP corn and pellet mix with 6% added glycerol fed as in 1 and 2. From d 85 to 112 all group pens were fed a common 16% CP grain mix at 2.27 kg/hd daily with free choice hay. There were no overall treatment effects on calf ADG or feed/gain ($P > 0.05$) averaging 1.04 kg/d and 4.39 kg feed/kg BW respectively. Hay intake was lowest ($P = 0.02$) for calves fed the grain mixes with glycerol. Under conditions of this study, glycerol was an effective alternative energy source when partially replacing corn in CS or grain mix formulations.

Key words: calf performance, glycerol, feed formulations

M286 Effect of lactation number, year and season of initiation of lactation on milk yield of rbST-treated cows hormonally induced into lactation. M. Mellado*[1], E. Antonio-Chirino[2], C. Meza-Herrera[3], F. G. Veliz[2], and J. R. Arevalo[4], *[1]Autonomous Agrarian University Antonio Narro, Department of Animal Nutrition, Saltillo, México, [2]Autonomous Agrarian University Antonio Narro, Faculty of Veterinary Medicine, Torreon, Mexico, [3]Universidad Autónoma Chapingo, Unidad Regional Universitaria de Zonas Áridas, Bermejillo, México, [4]University of La Laguna, Department of Parasitology, Ecology and Genetics, La Laguna, Spain.*

Records representing 1,500 barren Holstein cows from a dairy farm in northern Mexico were used to determine the effects of lactation number and season and year of initiation of lactation on milk yield of cows induced hormonally into lactation and treated with rbST throughout lactation. Peak and 305-d milk yield were also assessed as predictors of total milk yield in cows. Variables related with milk yield were analyzed using the MIXED procedure of SAS. Treatment means were separated using the PDIFF option of SAS. Regression analyses were applied to discern relationships between peak milk yield and total milk yield. A significant quadratic relationship was found between 305-d milk yield and number of lactation (7,607 ± 145 and 9,548 ± 181kg for first and ≥ 6 lactation cows, respectively; mean ± SEM) with the highest production occurring in the 5th lactation. Total milk yields of cows with ≤ 2 lactations were approximately 4,500 kg less than milk yields of adult cows (the overall average ± SD milk yield was 13,544 ± 5491 kg per lactation and the average lactation length was 454 ± 154 d). 305-d milk production was depressed ($P < 0.01$) in cows induced into lactation in spring (8,804 ± 153 kg; mean ± SEM) and summer (8,724 ± 163 kg) than in fall (9,079 ± 151 kg) and winter (9,085 ± 143 kg). Partial regression coefficients for 305- milk yield and peak milk yield indicated an increment of 157 kg of milk per lactation per every kg increase in peak milk yield ($r^2 = 0.69$). Neither peak milk yield ($r^2 = 0.18$) or 305-d milk yield ($r^2 = 0.29$) were accurate for predicting total milk yield per lactation. It was concluded that year, parity, and season effects are significant influences on milk yield of cows induced into lactation and treated with rbST throughout lactation, and that peak milk yield can assist in the prediction of 305-d milk yield, but not total milk yield. This study also shows that hormonal induction of lactation is a reliable, practical and affordable technique in countries where rbST treatment and prolonged steroid administration of dairy cows is legally permitted.

Key words: lactation induction, extended lactation, somatotropin

M287 Impact of corn processing method and soy glycerin on fecal shedding from cattle inoculated with *Escherichia coli* O157:H7. D. Paulus*, R. Fink, F. Diez-Gonzalez, J. Jaderborg, G. Crawford, and A. DiCostanzo, *University of Minnesota, St. Paul.*

An experiment was conducted comparing the effects of soy glycerin (GLY), dry rolled corn (DRC), and steam flaked corn (SFC) on *Escherichia coli* O157:H7 shedding in cattle. Twenty-eight Holstein steer calves (160 ± 18 kg) were assigned randomly to one of 4 dietary treatment resulting from a 2 × 2 factorial arrangement (DRC vs. SFC and GLY vs. no GLY) of treatments in a completely randomized design. Diets contained (DM basis): 35% modified distillers grains with solubles, 8% grass hay, 9% supplement, and either 0 or 10% soy glycerin, with the balance of the diet made up of either SFC or DRC. Soy glycerin replaced corn in the 10% soy glycerin treatments. Cattle were inoculated with a dose of 10^{11} cfu per calf with a cocktail of 4 *E. coli* O157:H7 strains resistant to 2 specific antibiotics (nalidixic acid and rifampin) at the start of the 20-d experiment. Individual fecal samples from each animal were collected 3 times weekly over the course of the experiment. Concentrations of *E. coli* O157:H7 in fecal samples were determined through enumeration on selective medium and reported in cfu/g. Data were analyzed using the Proc Mixed procedure of SAS. No significant differences ($P \geq 0.05$) in *E. coli* O157:H7 concentrations were found between the treatments. Overall average fecal counts of *E. coli* O157:H7 decreased ($P \leq 0.05$) over time from 4.5 to less than 1.0 log cfu/g 20 d after inoculation. Results from this experiment indicate that neither soy glycerin inclusion nor corn processing method stimulated the shedding of artificially inoculated of *E. coli* O157:H7. Therefore, under the conditions of our experiment, we conclude that feeding soy glycerin and processed corn had little impact on the colonization of cattle by *E. coli* O157:H7.

Key words: cattle, *Escherichia coli*, glycerin

M288 Different levels of urea in concentrate supplementation of grazing cattle during the transition period of dry to rainy seasons under tropical conditions. A. G. Silva[1], H. J. Fernandes*[2], L. O. Tedeschi[3], M. F. Paulino[1], S. A. Lopes[1], and A. A. Rocha[1], *[1]Federal University of Viçosa, Viçosa, MG, Brazil, [2]State University of Mato Grosso do Sul, Aquidauana, MS, Brazil, [3]Texas A&M University, College Station.*

The objectives of this study were to evaluate the effect of concentrate supplementation and of levels of urea in this concentrate on the nutrient intake and nutrient digestibility of grazing animals during the transition period of dry to rainy seasons. Five young bulls with average BW of 286 ± 21 kg were used in a 4 × 4 Latin square design, with an extra animal. The animals were housed in *Brachiaria decumbens* stapf. pasture and received one of the following supplements during each period: ad libitum mineral (control) or 1.5 kg/d of concentrated supplements (32% of CP) formulated with corn, soybean meal, and 0, 4, or 8% of urea. Each experimental period had 9 d for adaptation and 3 d for consumption and digestibility evaluation. A commercial isolated, purified, and enriched lignin product (LIPE©) was used as the fecal excretion marker and the indigestible NDF was used as an indicator of intake. The concentrate DMI was measured directly. The pastures were hand sampled. The feces samples were collected during 3 d at different times. The effect of the concentrate supplementation and the linear and quadratic effects of the urea levels were evaluated by orthogonal contrasts. The concentrate supplementation reduced the pasture DM and the NDF intakes and increased the CP intake without affect the total DMI. These results showed a substitution effect of the concentrate consumption, reducing the pasture consumption. The digestibility was not affected by the concentrate supplementation. The urea level did not affect the intake or the digestibility of any nutrient.

Table 1. Intake and digestibility in animals supplemented with concentrate with different urea levels

	Supplements				CV (%)	*P*-value		
		Urea level in concentrate						
	Control	0%	4%	8%		Concentrate effect	Linear effect of urea	Quadratic effect of urea
Intake, kg/d								
DM	6.45	6.67	6.52	6.75	9.24	0.562	0.852	0.588
Pasture DM	6.45	5.27	5.13	5.39	11.0	0.005	0.758	0.564
CP	1.08	1.37	1.33	1.39	12.7	0.009	0.839	0.606
NDF	3.76	3.30	3.20	3.34	8.57	0.016	0.856	0.362
Digestibility, %								
OM	65.3	68.8	68.0	69.7	5.82	0.126	0.723	0.591
NDF	63.9	67.4	66.8	67.5	4.97	0.708	0.959	0.709

Key words: grazing animals, supplementation

M289 Effects of monensin on rumen metabolism of steers fed 60% dried distillers grains diets. T. L. Felix*[1], N. A. Pyatt[2], and S. C. Loerch[1], *[1]The Ohio State University, Wooster, [2]Elanco Animal Health, Greenfield, IN.*

The S in dried distillers grains with solubles (DDGS) may cause sulfide toxicosis either by inhalation of hydrogen sulfide gas (H_2S) or absorption of sulfides across the rumen wall. Inhalation of H_2S causes S-induced polioencephalomalacia (PEM). Therefore, methods of mitigating H_2S production are needed. Monensin affects acetogenic bacteria by reducing acetate and hydrogen ions. Reduction in hydrogen ions may decrease H_2S formation. Results are conflicting regarding the role of ionophores on H_2S production in vitro. The objectives of this study were to determine the effects of monensin on ruminal pH, H_2S, and organic acids. Eight ruminally fistulated steers (BW = 610 ± 56 kg) were used in a replicated 4 × 4 Latin Square design and assigned to 1 of 4 treatments: 1) 0 mg monensin/kg diet, 2) 22 mg monensin/kg diet, 3) 33 mg monensin/kg diet, and 4) 44 mg monensin/kg diet. The diet was 60% DDGS, 10% corn silage, 15% supplement, and 15% corn on a DM basis and was offered once per day. Calculated dietary S concentration was 0.48%. Periods were 14 d for diet adjustment and 1 d for sample collections (0, 1.5, 3, 6, 9, 12 and 18 h post-feeding). There was no effect ($P = 0.99$) of monensin on DM intake. There was no effect ($P = 0.40$) of monensin on ruminal H_2S concentration. Ruminal H_2S increased from an average of 1913 ppm at 0 h to 4682 ppm within 1.5 h after feeding and remained elevated up to 12 h after feeding for all treatments. Rumen pH was not affected by treatment; however, mean rumen pH dropped from 6.04 to 5.09 within 1.5 h after feeding and was below 5.0 for all treatments up to 12 h after feeding. Despite the low rumen pH and high H_2S concentrations, steers did not suffer clinical symptoms of acidosis or PEM. Rumen liquid sulfide was not affected by time or treatment (range: 14.0 to 38.7 ppm). Rumen concentrations of acetate (A), propionate (P), and A:P were not affected ($P > 0.05$) by monensin supplementation (means at 3 h post-feeding: 53.9 µmol/mL, 57.0 µmol/mL, and 0.95, respectively). Contrary to some in

vitro data, our study suggests that monensin does not increase the risk of S-induced PEM when cattle are fed 60% DDGS diets.

Key words: cattle, dried distillers grains, monensin

M290 Carcass composition of mature cows subjected to a nutritional restriction and two levels of compensatory growth. K. O. Barros[1], H. J. Fernandes*[1], G. L. D. Feijó[2], M. A. Rezende[2,3], H. O. A. Santana[1], E. Rosa[1], L. M. Paiva[1], and J. C. Souza[4], *[1]State University of Mato Grosso do Sul, Aquidauana, MS. Brazil, [2]EMBRAPA Beef Cattle Center, Campo Grande, MS. Brazil, [3]Federal University of Grande Dourados, Dourados, MS. Brazil, [4]Federal University of Mato Grosso do Sul, Aquidauana, MS. Brazil.*

The objective of this study was to evaluate the effect of nutritional restriction followed by 2 ADG rates (0.5 and 1.5 kg/d) during the compensatory growth phase. Fifteen Nellore mature cows were maintained on pasture during May to August in 2010 (dry season). Five cows were kept under maintenance level (i.e., without BW variation) and 10 cows were kept under nutritional restriction by adjusting the stocking rate of the pastures. In August, the animals were moved to a feedlot and had their diet adjusted according to the following 3 treatments: animals in the maintenance group were fed to maintained no BW change (Control) and animals in nutritional restriction group were divided into 2 groups that received diets to allow ADG of 0.5 (T1) or 1.5 (T2) kg/d. Cows were slaughtered after 84 d. The percentage of bone, muscle, and fat tissues were estimated using the composition of the 9–11th rib section (Hankins and Howe procedure). The effects of the nutritional restriction and of the ADG after nutritional restriction were evaluated by orthogonal contrasts. Animals subjected to nutritional restriction (T1 and T2) had more bone tissues (13.4%) than those in the control group (11.5%) ($P = 0.022$). In animals subjected to nutritional restriction, those inT1 had greater (14.5%) content of bone than those in T2 (12.4%) ($P = 0.043$). Animals in T1 and T2 showed a lower content of adipose tissue in the carcass (28.9%) than the control ones (35.5%) ($P = 0.031$). The ADG after nutritional restriction did not affect the fat content in the carcass. The content of muscle in the carcass was not affected by the nutritional restriction or the ADG after this nutritional restriction.

Key words: cattle, nutritional restriction, growth

M291 Combined use of ionophore and virginiamycin on feeding behavior of Nellore steers fed high concentrate diets. A. J. C. Nuñez*[1], V. V. Almeida[2], R. C. Gomes[1], F. T. Mercado[1], I. E. Borges[1], J. Guerra[1], F. Pinese[1], P. R. Leme[1], and J. C. M. Nogueira Filho[1], *[1]USP/FZEA, Pirassununga, SP, Brazil, [2]USP/ESALQ, Piracicaba, SP, Brazil.*

The objective in this research was to evaluate feeding behavior of zebu cattle fed high grain diets and supplemented with salinomycin (SL), virginiamycin (VM) or their combinations. Eight ruminally cannulated Nellore steers, weighing 321 ± 25 kg, were randomly allocated in a 4 × 4 replicated Latin square design (16-d periods), in a 2 × 2 factorial arrangement, with 2 SL levels (0 and 13 ppm) and 2 VM levels (0 and 15 ppm). Animals were housed in individual pens and fed a total mixed ration once daily at 0800 h, with 80% concentrate (60.1% dry ground corn) on DM basis. Feeding behavior was monitored visually over a 24-h period, when eating and ruminating activities were noted every 5 min and assumed to persist for the entire 5-min interval. Total chewing time was calculated as the sum of total time spent eating and ruminating, and total resting time was calculated as the difference between 1440 min and total chewing time. A ruminating bout was defined as at least 5 min of ruminating activity followed by at least 5 min of any other activity. Statistical analyses were conducted using the GLM procedure of SAS. There were no interactions between SL and VM levels for any analyzed variable. Total time spent eating (min/d) and number of ruminating bouts per day were not influenced ($P > 0.05$) by treatments. Steers receiving VM spent 47.8 min/d longer ruminating (376.9 ± 62.9 vs. 424.7 ± 52.9 min/d for 0 and 15 ppm of VM, respectively; $P < 0.01$) and tended to spend 2.5 min more per ruminating bout (27.1 ± 2.5 vs. 29.6 ± 2.0 min/bout for 0 and 15 ppm of VM, respectively; $P = 0.06$) when compared with non-supplemented animals. As a result of longer rumination time, VM treated animals also spent more time chewing (580.3 ± 72.6 vs. 625.9 ± 74.8 min/d for 0 and 15 ppm of VM, respectively; $P = 0.03$) and less time resting (859.7 ± 72.6 vs. 814.1 ± 74.8 min/d for 0 and 15 ppm of VM, respectively; $P = 0.03$) in comparison with non-supplemented steers. These results suggest that Nellore steers receiving 15 ppm of VM may spend more time chewing as a consequence of a healthier ruminal environment.

Key words: antibiotics, beef cattle, salinomycin

M292 Performance and carcass traits of beef bulls fed crude glycerin in the diet. J. P. I. S. Monnerat, P. V. R. Paulino*, S. C. Valadares Filho, I. M. De Oliveira, L. H. P. Da Silva, R. Mezzomo, M. S. Duarte, and S. F. Dos Reis, *Universidade Federal de Viçosa, Viçosa, Minas Gerais, Brazil.*

The purpose of this study was to evaluate the effect of replacing corn grain with crude glycerin (CG) on performance, carcass traits, and yield of commercial carcass cuts of beef bulls finished on feedlot. The CG used was derived from soybean biodiesel production (84.41% glycerol, 6.94% fat, and 8.64% methanol). Thirty-four Nellore × Angus bulls were used in the study, with an average initial body weight of 343.9 ± 16.56 kg. Four animals were randomly chosen and slaughtered at the beginning of the experiment to determine initial dressing percent. The remaining animals (n = 30) were randomly distributed into 5 treatments (6 replicates): 0, 5, 10, 15 and 20% of CG on diet DM, replacing finely ground corn in the concentrate. The animals were fed isoproteic diets (13% CP) containing 50% corn silage and 50% concentrate, DM basis. At the end of the experiment, all animals were slaughtered, and their gastrointestinal tracts were emptied to determine their empty body weight (EBW). Statistical analyses were conducted using PROC GLM of SAS. No significant effects ($P > 0.05$) of increasing CG levels on the diet were observed for most of the variables evaluated: average daily gain (1.98 kg), dry matter intake (9.56 kg/d), feed efficiency (0.207), EBW gain (2.04 kg/d), carcass daily gain (1.45 kg/d), subcutaneous fat thickness (5.28 mm), rib eye area (75.08 cm^2) and dressing (59.72%). On the other hand carcass length increased linearly ($P < 0.05$), chuck yield increased quadratically, while shoulder clod yield decreased in a quadratic manner ($P < 0.05$) as CG inclusion in the diet increased. There was no effect ($P > 0.05$) of CG inclusion on the diet on the yield of other carcass cuts: flank (13.75%), sirloin (17.82%) and round (27.47%). It can be concluded that CG inclusion up to 20% of DM on beef bulls diets (roughage to concentrate ratio of 50:50) of DM does not compromise animal performance and carcass traits.

Key words: biodiesel, by-product, Nellore

M293 Effect of dietary urea-N levels on growth performance and blood biochemical indexes of growth-finishing cattle. L. Jiang*, Y. L. Huo, L. P. Ren, Z. M. Zhou, and Q. X. Meng, *State Key Labora-*

tory of Animal Nutrition, College of Animal Science and Technology, China Agricultural University, Beijing 100193, China.

As an economic non protein nitrogen (NPN) source, urea is widely used as a substitute of intact feed proteins in ruminant animals, especially in beef cattle. A 91-d feeding trial was conducted using 60 growing-finishing Limousin crossbred bulls to determine the effect of dietary urea levels on growth performance and blood biochemical indexes in a randomized complete block design. The treatment diets were 6 supplemental urea levels in the diets (% DM basis): 0, 0.4, 0.8, 1.2, 1.6 and 2.0, respectively. All experimental diets (60: 40 ratio of concentrate to roughage) were iso-nitrogenous (14% CP on DM basis) with urea-N accounting for 0, 8, 16, 24, 32 and 40% of total dietary N on DM basis. The concentrations of dietary metabolic energy (ME) were balanced at similar levels (ranged from 2.70 to 2.74 Mcal/kg) by using different level of corn grains, corn starch and cottonseed meal. The results showed that as dietary urea level increased, daily DM intake and feed conversion efficiency were not affected significantly ($P > 0.10$), but ADG was quadratically decreased (Q; $P < 0.01$) with a breaking point appearing at 24% urea-N level, suggesting urea-N level at less than 24% of total dietary N had no adverse effect on growth performance of growing bulls. Increasing dietary urea-N level from 24% to 40% resulted in remarkable increased concentrations of blood biochemical indexes such as serum urea-N (Q; $P < 0.05$), total proteins (Q; $P < 0.01$), free ammonia (L; $P < 0.01$), alanine aminotransferase (ALT) (L; $P < 0.01$), aspartate aminotransferase (AST) (L; $P < 0.001$) and creatine kinase (L; $P < 0.05$), respectively. These observations indicated that when urea included diets with about 2.7 Mcal ME/kg DM and 14% CP were fed growing-finishing crossbred bulls, the dietary urea-N up to 24% of total dietary N may have somewhat adverse effect on their physiological or metabolic functions. In conclusion, when safe and effective utilization of dietary urea-N was considered for growth-finishing cattle, the urea-N supplementation level at less than 24% of total dietary N should be recommended in practice.

Key words: growing-finishing cattle, growth performance, urea

M294 In situ ruminal protein degradability of distiller's grain varying grain source and milling process in beef cattle. C. Li*[1,2], W. Z. Yang[1], J. Q. Li[2], Y. L. Li[3], and A. Furtado[1], *[1]Agriculture and Agri-Food Canada, Research Centre, Lethbridge, AB, Canada, [2]College of Animal Science, Inner Mongolia Agricultural University, Hohhot, Inner Mongolia, China, [3]Feed Research Institute, Chinese Academy of Agricultural Sciences, Beijing, China.*

An in situ study was conducted to determine ruminal protein degradability of grain and dried distillers grains with solubles (DDGS) varying grain sources (corn vs. wheat) and milling processes (traditional vs. fractional) using fistulated steers. Five different batches of wheat, wheat DDGS (WDDGS), corn, corn DDGS (CDDGS) and fractional DDGS (FDDGS) were collected from 3 different plants located in western Canada or USA. The cattle were fed a diet containing 60% barley silage and 40% barley concentrate. Ruminal microbes were labeled using $^{15}N(NH_4)_2SO_4$ to correct the ruminal bacterial contamination. Five grams of feed were incubated in situ in the rumen of 3 steers for 0, 2, 4, 6, 12, 16, 24 and 48 h. The model $y = a+b(1-e^{-ct})$ was fitted to determine degradation kinetics of CP, where y is CP degraded, a is soluble fraction, b is slowly degradable fraction, c is degradation rate constant, and t is incubation time. Effective degradability (ED) was determined by $ED = a+ [bc/(c+k)]$, where $k = 0.06$/h. Protein contents were 16, 38, 8, 29 and 42% of DM, respectively, for wheat, WDDGS, corn, CDDGS and FDDGS. The fraction a was the highest ($P < 0.05$) for wheat (27%), WDDGS (27%), corn (28%), the medium for CDDGS (24%), and the lowest for FDDGS (7%). In contrast, the fraction b was higher ($P < 0.05$) for FDDGS (60%) than for CDDGS (49%), and was not different for other 3 feeds (66 to 72%). The degradation rate varied ($P < 0.01$) substantially from 3 to 23%/h among 3 feeds. The ED of CP was reduced ($P < 0.01$) by 35%, 28% and 45%, respectively, for WDDGS, CDDGS and FDDGS compared with the parent grains. Correction for bacterial CP contamination on the in situ residues increased ($P < 0.01$) 10% of the ED for corn and FDDGS, but had no change in the ED of other 3 feeds. The results indicate that ruminal CP degradability of DDGS vary considerably with grain source and milling process.

Key words: DDGS, in situ, ruminal protein degradation

M295 Effects of monensin and probiotics on finishing Nellore bulls performance, carcass characteristics, and liver abscesses. C. Sitta[1], A. M. Pedroso[2], G. B. Mourão[1], R. Carareto[1], J. R. R. Dórea[1], T. G. Neri[1], D. A. Rodrigues[1], W. F. Angolini[1], and F. A. P. Santos*[1], *[1]University of São Paulo, Piracicaba, SP, Brazil, [2]Embrapa Catle Southeast, São Carlos, SP, Brazil.*

The objective of the present study was to determine the effect of feeding no feed additives, monensin, yeast culture and a commercially available combination of yeast and probiotic bacteria, on performance and carcass characteristics of cattle fed high starch diets. Ninety-three Nellore bulls with an initial BW of 320 kg were used in a 109-d randomized complete block design feeding trial. Animals were blocked by initial BW and assigned randomly to 16 pens. Animals were raised on pasture and they were adapted to the final diet during the first 21 d of the experimental period. The final diet contained (%DM): 12% tifton grass hay, 78.1% finely ground corn, 6% sugar cane molasses, 1.4% urea, 2.5% mineral and vitamin premix and respective feed additives. Treatments consisted in: 1) Control (no feed additives); 2) Sodium monensin, 30mg/kg DM; 3) Yeast (*Saccharomyces cerevisiae*), 10 g/animal/ day (10^9 cfu/g); 4) Yeast + probiotic bacteria, 3 g/animal/day [*Saccharomyces cerevisiae* (3.33×10^5 cfu/g) + *Bifidobacterium bifidum* (3.33×10^6 cfu/g), *Lactobacillus acidophilus* (3.33×10^6 cfu/g), *Lactobacillus plantarum* (1.66×10^6 cfu/g), *Enterococcus faecium* (1.66×10^6 cfu/g)]. Data were analyzed using the mixed procedure of SAS (1999) with pen as experimental unit. Monensin decreased DMI ($P < 0.1$) compared with the control diet. Average daily gain, feed efficiency and carcass characteristics were not affected by treatments ($P > 0.05$), however, the not significant ($P > 0.05$) 6% better feed conversion for monensin compared with the control diet is in agreement with most of the literature data. The NE values of the diets for BW maintenance and gain (calculated based on DMI, BW and ADG) were not affected by treatments ($P > 0.05$). No liver abscesses were observed.

Table 1. Performance and carcass characteristics of finishing bulls fed differing feed additives for a 109-d period

	Control	Monensin	Yeast	Yeast + bacteria	*P*-value
Initial BW, kg	321.5	321.5	321.4	321.5	0.587
Final BW, kg	485.71	474.98	488.91	481.2	0.743
DMI, kg	9.35	8.25	9.33	9.20	0.094
ADG, kg	1.50	1.41	1.53	1.46	0.758
DMI/ADG	6.27	5.89	6.09	6.28	0.652
Dressing, %	52.06	55.36	53.56	55.9	0.524
Fat thickness, mm	3.43	3.50	3.60	3.59	0.985
LM area, cm^2	70.81	67.51	69.30	69.0	0.368
NEm, (Mcal/kg DM)	1.87	1.98	1.90	1.86	0.34
NEg, (Mcal/kg DM)	1.23	1.33	1.25	1.22	0.31

Key words: additives, feedlot, monensin

M296 Effect of feeding alfalfa hay and starter concentrate containing two different levels of fiber on feed intake, body weight gain and feed efficiency. A. Salary Neya*, M. H. Fathi, H. Naeemipour, and H. Farhangfar, *Birjand University, Birjand, Southern Khorasan, Iran.*

The experiment was conducted to determine the effect of alfalfa hay and starter fiber on feed intake, feed efficiency and daily gain. In this study, 32 male Holstein calves at the age of 3 d were assigned to 4 diets with a 2 × 2 factorial completely randomized design, with 8 replications. The experiment was ended 3 weeks after weaning. Two main factors included adding alfalfa hay to diet and the level of Starter fiber, so the 4 experimental treatments were as follows: T1: starter with low fiber and without hay, T2: starter with low fiber along with hay, T3: starter with high fiber and without hay, and T4: starter with high fiber along with hay. The data were analyzed by a linear model in which the effects of fiber and alfalfa and interaction between them were included. Statistical comparisons among different means were carried out by Tukey-Cramer test. The model was fit by SAS software. Results showed that effect of adding hay to the diet and level of starter fiber had no significant effect on feed intake before weaning, after weaning, and throughout entire trial. The level of fiber on Starter had significant on daily gain of calves in the whole period ($P < 0.05$), so that T2 and T4 had greater weight gain than T1 and T3 as well as feed efficiency after weaning and during the entire period by treatments was affected significantly so that T2 and T4 had a higher efficiency than T1 and T3 ($P < 0.05$). It could be therefore concluded that addition of starter fiber to the diets of young calves appears to favorably alter the rumen environment, resulting in an increased daily gain and feed efficiency.

Key words: male Holstein calves, fiber, starter

M297 Effects of supplementation of organic, inorganic or a 50/50 mix of selenium on gene expression profiles in the longissimus dorsi muscle of maturing Angus beef heifers. K. M. Brennan*[1], J. A. Boling[2], R. Xiao[1], D. Mallonee[1], R. F. Power[1], and J. C. Matthews[2], *[1]Alltech Center for Animal Nutrigenomics and Applied Animal Nutrition, Nicholasville, KY, [2]Department of Animal and Food Sciences, University of Kentucky, Lexington.*

The aim of this study was to investigate gene expression patterns in the longissimus dorsi (LD) muscle of beef heifers in response to different sources of selenium (Se) supplementation. Forty Angus heifers were assigned (n = 10) to 4 Se treatments for 224d. The basal diet contained 0.08 mg Se/d, whereas the mineral supplements provided no additional Se (control, C), or 3 mg Se/d as inorganic (sodium selenite, SS), organic (Sel-Plex, SP), or a 50/50 mix (Mix). On d224, heifers were slaughtered and samples (~1g) were taken from the LD and flash frozen. Se content in the LD was greater in SP and Mix heifers than C or SS ($P \leq 0.01$). Gene expression profiles were evaluated using the Affymetrix bovine genome array. In the LD, 79, 127 and 170 genes were differentially expressed ($P \leq 0.05$, fold-change ≥ 1.2) in SS, SP and Mix heifers, respectively. Of these genes, only 19 were commonly affected by all 3 Se treatments. Ingenuity pathway analysis revealed that heifers supplemented with SS, SP or Mix had both common and differential pathway enrichment. Top biological functions (molecular and cellular function) upregulated with SS supplementation included cell cycle, cell death and amino acid metabolism. Top upregulated biological functions associated with SP included cell morphology, cellular assembly and organization, and cellular development. Top upregulated biological functions associated with Mix supplementation included lipid metabolism, molecular transport and small molecule biochemistry. All 3 Se sources commonly affected the top biological functions: cellular movement, cell cycle and cell to cell signaling and interaction. Taken together these data indicate that gene expression patterns in longissimus dorsi tissue of beef heifers are dependent on both Se supplementation and on Se source.

Key words: selenium, beef heifer, microarray

M298 Effect of zilpaterol hydrochloride supplementation feeding duration on growth performance and carcass characteristics of feedlot heifers. J. C. Robles-Estrada*[1], H. Dávila-Ramos[1], A. Estrada-Angulo[1], A. Plascencia[2], F. G. Ríos[1], and R. A. Zinn[3], *[1]Universidad Autónoma de Sinaloa, Culiacán, Sinaloa, México, [2]Universidad Autónoma de Baja California, Mexicali, B.C., México, [3]University of California-Davis, El Centro.*

Forty-eight crossbred heifers (392.1 ± 24 kg) were used in a 50-d feeding trial (4 pens per treatment in a randomized complete design to performance and hot carcass weight as covariate in carcass traits) to evaluate the effect of feeding duration of zilpaterol hydrochloride (0.15 mg/kg of live weight daily) on growth performance and carcass characteristics. Heifers were fed a diet based on steam flaked corn (2.07 Mcal of NE_m /kg). Cattle fed zilpaterol for the last 0, 20, 25 or 30 d at the end of the finishing period and withdrawn from zilpaterol for the last 3 d on feed. Daily DMI averaged 8.11 ± 0.73 kg and was not affected ($P \geq 0.84$) by treatments. Compared with the controls, zilpaterol increased ($P = 0.01$) carcass adjusted final live weight (3.62%), ADG (27%, $P = 0.03$), gain:feed ratio (28.4%, $P < 0.01$) and apparent dietary NE_m (17.2%, $P < 0.01$). Zilpaterol supplementation did not affect yield grade ($P = 0.09$), USDA quality grade ($P = 0.17$), fat thickness ($P = 0.30$) and KPH fat ($P = 0.73$), but compared with the control group, increased HCW (2.9%, $P = 0.02$), carcass dressing percentage (2.5%, $P = 0.04$) and LM area (8.2%, $P = 0.05$). Reducing zilpaterol feeding duration from 30 to 20 d did not affect ($P > 0.45$) both, growth performance or carcass characteristics. We conclude that zilpaterol administration improved growth performance, HCW, carcass dressing percentage and LM area. Responses to zilpaterol supplementation could be observed since 20 d of zilpaterol supplementation.

Key words: heifers, performance, zilpaterol

M299 Feeding tannins to reduce nitrogen losses from feedlot cattle fed high protein diets containing distillers grains 1. Animal performance and plasma urea nitrogen. K. M. Koenig*, K. A. Beauchemin, and S. M. McGinn, *Agriculture and Agri-Food Canada, Research Centre, Lethbridge, Alberta, Canada.*

Inclusion of distillers grains as an energy source in diets of feedlot cattle increases the protein concentration to levels often exceeding requirements. Excess feed N is largely excreted as urea in urine, a labile form of N with potential for loss to the environment. A completely randomized design with 148 crossbred steers (425 ± 4.3 kg, initial BW) was conducted to determine the effects of feeding condensed tannins (CT), recognized for protein binding effects, with high protein diets on performance and plasma urea N (PUN). Steers were allocated to 16 pens with 4 pens per treatment. The basal diet contained 92% barley grain concentrate and 8% barley silage (DM basis) and was fed as a total mixed ration once per day. The 4 dietary treatments included control (no corn distillers dried grains and solubles, DG0), 20% DG (DG20), 40% DG (DG40) and 40% DG with 2.5% CT (DG40CT) from *Acacia mearnsii* (black wattle tree). Cattle were weighed on 2 d at the start and end of the experiment and on 1 d every 3 wk in between. The DMI was determined from feed offered daily and orts at the end of each 3-wk period. Blood samples were collected from 5 cattle per pen when they were weighed, and PUN was determined as a relative indicator of protein status and urinary excretion of urea N. Data for DMI for each pen, BW, ADG, G:F and PUN for each animal were analyzed as a mixed linear model with diet, time (repeated measure) and diet x time as fixed effects and pen as the experimental unit. The CP content of the diets was 13.2, 15.9, 20.4 and 19.4% for DG0, DG20, DG40 and DG40CT, respectively. There was no effect ($P > 0.05$) of the treatments on DMI (12.0 ± 4.3 kg/d), final BW (621 kg ± 2.5), ADG (1.98 ± 0.07 kg/d), G:F (165 ± 5 g/kg) and carcass traits. The PUN ($P < 0.05$, SEM 6.0 mg N/L) was lowest in cattle fed DG0 (113 mg N/L), highest in cattle fed DG40 (170 mg N/L) and intermediate in cattle fed DG20 (153 mg N/L) and DG40CT (146 mg N/L). Feeding CT to beef cattle fed a high protein diet reduced PUN without altering performance, suggesting lower urinary urea N excretion.

Key words: condensed tannins, distillers grains, finishing cattle

M300 Feeding tannins to reduce nitrogen losses from feedlot cattle fed high protein diets containing distillers grains 2. Nutrient digestibility and route of nitrogen excretion. K. M. Koenig*, K. A. Beauchemin, and S. M. McGinn, *Agriculture and Agri-Food Canada, Research Centre, Lethbridge, Alberta, Canada.*

Eight ruminally cannulated beef heifers (427 ± 41 kg, initial BW) were used in a replicated 4 × 4 Latin square to determine the effects of feeding condensed tannins (CT) with high protein diets containing corn distillers grains on nutrient digestibility and route of N excretion. Periods were 5 wk with 2 wk for transition to the diet, 1 wk for adaptation to CT and 2 wk for measurements. The basal diet contained 92% barley grain concentrate and 8% barley silage (DM basis) and was fed as a total mixed ration once per day. Dietary treatments included control (no corn distillers dried grains and solubles, DG0), 20% DG (DG20), 40% DG (DG40) and 40% DG with 2.5% CT (DG40CT) from *Acacia mearnsii* (black wattle tree). Data were analyzed using a mixed linear model with diet as a fixed effect, and square, period within square and animal within square as random effects. The CP content of the diets was 12.9, 16.8, 20.4 and 20.5% for DG0, DG20, DG40 and DG40CT, respectively. Feed offered and refused were measured daily. Urine and feces were quantitatively collected for 5 d. There was no effect ($P > 0.05$) of CT on DMI, but the inclusion of 40% DG (without and with CT) in the diet decreased ($P < 0.05$) DMI compared with 20% DG. As a result, N intake was similar among heifers fed DG20, DG40 and DG40CT (313 g N/d), and was lower ($P < 0.05$, SEM 18 g N/d) for heifers fed DG0 (220 g N/d). Total tract digestibility of N was similar ($P > 0.05$, SEM 1.1%) among heifers fed DG0, DG20 and DG40 (78.4%), and due to the protein binding effects of CT, was reduced ($P < 0.05$) in heifers fed DG40CT (70.6%). Reduction of N digestibility reflected a shift in N excretion from urine to feces in heifers fed DG40CT compared with DG40 ($P < 0.05$). Feeding CT with 40% DG reduced the amount of N excreted in urine by 17% compared with heifers fed 40% DG and was equivalent to the amount excreted by heifers fed 20% DG. Feeding CT to cattle fed high protein diets shifted the route of N excretion from urine to feces, although there was a 3% decrease ($P < 0.05$) in total tract OM digestibility.

Key words: condensed tannins, distillers grains, nitrogen excretion

M301 Potential modulation of the inflammatory response associated with enteropathogenic *Escherichia coli* infections in young calves using Actigen. A. Aris[1], E. Rodriguez*[1], A. Tort[1], M. Terré[1], F. Fàbregas[1], K. A. Jacques[3], and A. Bach[1,2], *[1]Ruminant Production, Institut de Recerca i Tecnologia Agroalimentàries (IRTA), Caldes de Montbui, Barcelona, Spain, [2]Institució Catalana de Recerca i Estudis Avançats (ICREA), Barcelona, Barcelona, Spain, [3]Center for Animal Nutrigenomics and Applied Animal Nutrition, Alltech, Nicholasville, KY.*

Ten male Holstein calves were distributed in 2 groups to evaluate the potential of Actigen (Alltech) to modulate the inflammatory response elicited by enteropathogenic *Escherichia coli* (EPEC). The control (CTR) calves were fed a basal milk replacer, and Actigen (ACT) calves were fed the same milk replacer plus Actigen at the rate of 1g/head/day. After 42 d, calves were euthanized and segments of mid-jejunum harvested. Explants were retreated again with 0.5 mg Actigen ex vivo or incubated with a control media for 1 h at 37°C. Tissues were then either incubated in a control medium (CTR) or the same medium with $1x10^8$ cfu of EPEC for 7h in a 5% CO_2 at 37°C. Supernatant and tissue samples were taken to analyze cytokines. Data were analyzed using a mixed-effects model accounting for the fixed effects of in vivo, ex vivo, infection, and all their 2-way interactions, and the random effect of animal nested within the interaction between in vivo and ex vivo. The ex vivo infection with EPEC infection triggered an inflammatory response by increasing ($P < 0.05$) the levels of pro-inflammatory cytokines IL–1β (135.64 and 206.44 pg/ml for CTR and EPEC, respectively) and IFN-γ (30.80 and 46.51 pg/ml for CTR and EPEC, respectively) and decreasing ($P < 0.05$) the levels of anti-inflammatory cytokine TGF-γ (107.77 and 68.72 mRNA ratio to β-actin for CTR and EPEC, respectively). Both Actigen supplementation in vivo and in vivo plus ex vivo modulated EPEC inflammatory response through the downregulation of IFN-γ (12.39, 0.07, and 1.18 pg/ml for CTR, ACT in vivo, and ACT in vivo-ex vivo, respectively) and the upregulation of IL-10 (1.16 and 1.46 mRNA ratio to β-actin for CTR and ACT in vivo-ex vivo, respectively). At tissue level the production of IL-1β was lower ($P < 0.05$) in ACT (121.51 pg/ml) than in CTR (230.44 pg/ml). These results indicate that Actigen has a positive effect on intestinal tract, regulating not only the inflammatory response triggered by an infection, but also modulating the basal inflammatory response of the tissue.

Key words: inflammation, EPEC infection, Actigen

M302 Effects of crude protein levels on the concentrate supplement on gas production from carbohydrate in vitro degradation of Elephant grass. M. A. C. Danes*, J. R. R. Dorea, and F. A. P. Santos, *University of Sao Paulo/Esalq, Piracicaba, SP, Brazil.*

The trial was conducted to evaluate the effects of concentrate crude protein (CP) levels on gas production from carbohydrate in vitro degradation of Elephant grass (*Penisetum purpureum*) intensively managed. Hand-plucked samples of intensively managed Elephant grass 'Cameron' (18.5% CP; 58.7% NDF) were dried at 55°C, ground at 1 mm and incubated alone or in a 60:40 forage:concentrate ratio with concentrates based on fine ground corn and soybean meal with 3 levels of CP (8.7 – only corn, 13.4 and 18.1% DM). Ruminal inoculum was collected from a protein supplemented grazing animal. Degradation rates (kd) were estimates by the cumulative gas production semi-automated method (Mauricio et al., 1999). Gas pressure was measured at 1, 2, 3, 4, 6, 8, 10, 12, 14, 17, 20, 24, 28, 36, 48, 72 96 and 120 h after incubation. The final gas volume and kd from fibrous (F) and non-fibrous (NF) carbohydrate and lagtime were calculated according to Pell and Schofield (1993) model. The energy concentrate (8.7% CP) affected fibrous degradation, increasing ($P < 0.05$) its kd, decreasing ($P < 0.05$) lagtime and increasing ($P < 0.05$) gas production per unit of NDF incubated (corrected fibrous carbohydrate volume, cFvol). Those results suggest that the limiting nutrient in diets based on intensively managed tropical grasses is the energy and the supply of that nutrient through an energetic concentrate can improve fiber degradation and might result in better animal performance. The addition of protein through soybean meal did not result in any further improvements and reduced cFvol, most likely due to lack of energy.

Table 1. Volume of gas (vol; mL) and kd (%/h) from non-fibrous (NF) and fibrous (F) carbohydrates, corrected Fvol (mL/g FDN) and lagtime (h) of Elephant grass (P) incubated alone or mixed with concentrates with 8.7, 13.4 or 18.1% CP

	P	P+8.7	P+13.4	P+18.1	SE
NFvol	73.8^{c}	121.9^{b}	157.7^{a}	139.3^{ab}	5.5
NFkd	3.55^{b}	5.20^{a}	4.34^{ab}	4.20^{ab}	0.15
Lagtime	4.97^{a}	3.38^{b}	4.80^{a}	4.53^{ab}	0.26
Fvol	101.7^{a}	81.9^{b}	57.0^{c}	55.5^{c}	1.9
cFvol	577.4^{b}	696.4^{a}	481.9^{c}	444.0^{c}	15.6
Fkd	0.99^{b}	1.72^{a}	1.10^{b}	1.07^{b}	0.09

$^{a\text{-}c}$Means within the row with different letters differ ($P < 0.05$).

Key words: ruminal degradation, supplementation, tropical pasture

M303 Effect of 2,4-thiazolidinedione in finishing beef cattle growth performance and carcass traits. M. Arévalo*, L. González-Dávalos, A. Kunio, J. D. Garza, J. L. Dávalos, O. Mora, and A. Shimada, *Universidad Nacional Autónoma de México, Querétaro, Querétaro, México.*

Thiazolidinediones (TZDs) are insulin sensitizing agents, which are used as adipogenic agents. 2, 4-TZD, is a synthetic ligand of peroxisome proliferator activated receptor- γ (PPARγ the main adipogenic transcription factor). The objective of this study was to evaluate the effect of 2, 4-TZD on bovine carcass characteristics. Seventeen Limousin bulls (18 mo old and 350 kg BW) were assigned into 2 treatments: control and 2, 4-TZD (8mg/70 kg BW). The bulls received daily 2 kg of alfalfa hay and 6 kg of a 15% CP; 2.8 Mcal ED/kg DM supplement based on corn, sorghum, soybean meal; the amount offered was adjusted throughout the feeding trial. Orts were removed, weighed, and recorded daily. Bulls were weighed and blood samples obtained from the coccygeal vein at 28-d intervals to determine glucose, triglycerides, and 2, 4-TZD. Animals were slaughtered when they reached 500 kg BW. DNA, RNA and protein were determined in liver, subcutaneous, kidney and omental adipose tissue and skeletal muscle to determine protein synthesis rate and cellular size. PPAR α, δ and γ mRNA expression was measured by qPCR in liver and skeletal muscle and PPARγ mRNA expression in subcutaneous adipose. All data were statistically analyzed, growth performance and carcass data as a randomized blocks; laboratory measurements were analyzed using a model for a completely randomized design. No significant differences were found ($P > 0.1$) in productive (daily weight gain, days at feedlot) and carcass quality (carcass yield, rib eye area, fat thickness) parameters. Muscle synthesis was greater in control animal ($P < 0.05$), while size was greater in 2, 4-TZD treatment ($P < 0.05$). Respect to PPARs expression in liver PPAR α, δ and γ were lower in 2, 4-TZD treatment vs. control ($P < 0.01$), in muscle; in subcutaneous adipose tissue no differences were found for PPARγ mRNA expression. The results suggest the potential use of 2, 4-TZD in beef cattle diets, because it not only improves adipose tissue differentiation, but also liver and muscle fatty acid oxidation (by an increase in PPARα expression), that therefore could result in improvements in energy efficiency.

Key words: TZD, PPAR, beef cattle

M304 Evaluation of rumen protozoa counting under influence of a polyclonal antibody preparation against lactate-producing and proteolytic bacteria in cows fed different energy sources. C. Marino*[2], W. Otero[1], C. Barreto[3], V. Pellizari[3], F. Ferreira[1], M. Arrigoni[2], and P. Rodrigues[1], *[1]University of Sao Paulo, FMVZ-USP, Pirassununga, Sao Paulo, Brazil, [2]University of Sao Paulo State, FMVZ-UNESP, Botucatu, Sao Paulo, Brazil, [3]University of Sao Paulo, ICB II-USP, Sao Paulo, Sao Paulo, Brazil.*

Nine ruminally cannulated cows fed different energy sources were used to evaluate an avian-derived polyclonal antibody preparation (PAP) against specific ruminal bacteria *Streptococcus bovis*, *Fusobacterium necrophorum*, *Clostridium aminophilum*, *Peptostreptococcus anacrobius* and *Clostridium sticklandii* and monensin (MON) on rumen protozoa counting. The experimental design was 3 Latin squares 3 × 3 distinguished by the main energy source in the diet [dry-ground corn grain (CG), high moisture corn silage (HMCS) or citrus pulp (CiPu)]. Inside each Latin square, animals received one of the feed additives per period (21 d) [none (CON), MON or PAP]. Sample collection for quantitative protozoa analysis were performed at 21 d of each period at 4 h after morning meal collected by manual scanning of rumen floor. Data were analyzed by MIXED 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 PDIFF. Differences were declared at $P < 0.05$. Relative count of *Entodinium* was influenced by the type of energy source ($P = 0.0467$). Animals treated with CG and HMCS showed greater values of these protozoa when compared with animals receiving CiPu but do not differ between them. It was observed feed additive effect for *Isotricha* ($P = 0.0404$). The group treated with PAP showed great values for relative count compared with CON. The MON group did not differ from the others 2. Also, it was observed an energy source effect for *Isotricha* ($P = 0.0008$), where the animals fed CiPu showed greater relative count than animals fed HMCG and CG that did not differ between them. Polyclonal antibodies plus CiPu addition in the diet resulted in

an increase of relative counting of *Isotricha* protozoa that indicates a possible effect on ruminal microbial population.

Key words: feed additive, microorganism, passive immunization

M305 Inclusion of triticale dried distiller grains with or without oilseeds reduces growth performance but increase alpha-linolenic acid and lowers *trans* 10 C18:1 fatty acid of subcutaneous fat in finishing beef cattle. M. L. He*[1,2], T. A. McAllister[1], H. Sultana[1], M. Oba[3], M. E. R. Dugan[4], J. P. Kastelic[1], and J. J. McKinnon[2], *[1]Lethbridge Research Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, Canada, [2]University of Saskatchewan, Saskatoon, SK, Canada, [3]University of Alberta, Edmonton, AB, Canada, [4]Lacombe Research Centre, Agriculture and Agri-Food Canada, Lacombe, AB, Canada.*

Flaxseed (FS) and sunflower seed (SS) have been included in finishing diets of beef cattle to increase beef omega-3 fatty acids. Triticale dried distiller's grain with solubles (TDGGS) is a byproduct of the ethanol industry that has been substituted for barley grain in finishing diets. Steers (n = 90; 455 ± 31 kg) were housed in individual pens (n = 15 per treatment) and given ad libitum access to 1 of 6 diets: 1) control (CON) diet (DM basis) consisted of 90% barley grain - 10% barley silage, with barley concentrate substituted for; 2) 30% TDDGS; 3) 10% FS; 4) 30% TDDGS – 8.5% FS (FS+TDDGS); 5) 10% SS; and 6) 30% TDDGS – 8.5% SS (SS+TDDGS). The diets provided 1.3, 1.4, 1.3, 1.4, 1.4 and 1.5 Mcal NEg per kg, 13, 20, 14, 21, 14 and 21% CP, and 3, 4, 7, 8, 8 and 8% EE (DM basis), respectively. During a 12-wk feeding period SQ fat biopsies were collected once monthly for fatty acid analysis. Inclusion of TDDGS in the diet decreased ($P < 0.01$) ADG and feed conversion (FC), whereas inclusion of oil seeds improved ($P < 0.05$) FC. After 12 wk, the concentration of α-linolenic acid (ALA) increased ($P = 0.02$), whereas C18:1 t10 - a major *trans* fatty acid decreased ($P < 0.01$) in SQ fat in cattle fed TDDGS. Inclusion of oilseeds also increased ($P < 0.01$) ALA in SQ fat. In conclusion, inclusion of 30% TDDG in a barley grain finishing diet with or without FS or SS, lowered growth performance but increased omega-3 fatty acids and lowered *trans* fatty acids.

Key words: beef cattle, triticale dried distiller grains, fatty acid

M306 Substitution of wheat dried distiller grains with solubles for barley silage in a barley based finishing diet increases beef alpha-linolenic acid. M. L. He*[1,3], W. Z. Yang[1], T. A. McAllister[1], M. E. R. Dugan[2], K. A. Beauchemin[1], and J. J. McKinnon[3], *[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, SK, Canada.*

Wheat dried distiller grain with solubles (WDDGS) contains low levels of starch but is high in protein and fiber, and has been used as a substitute for barley grain in beef cattle finishing diets. This study investigated the effects of WDDGS on carcass quality and the meat fatty acid profile when it was substituted for barley silage in a barley based finishing diet. Steers (n = 200; 489 ± 30 kg) were fed one of 4 finishing diets consisting of barley concentrate (barley grain plus additives), barley silage and WDDGS (dry matter basis) in ratios of 85:15:0 (CON), 65:10:25 (DG25), 65:5:30 (DG30), and 65:0:35 (DG35) over a 12 wk period. Carcass quality parameters including weight, dressing percentage, back fat thickness, rib eye area, marbling score, quality grade, and meat yield, did not differ among treatments. Substitution of WDDGS for barley silage improved *pars costalis diaphragmatis* (PCD) muscle fatty acid profiles through increasing ($P < 0.01$) concentrations of total polyunsaturated fatty acids (PUFA) including α-linolenic acid (ALA) without affecting major trans fatty acids. WDDGS replacement of 10 and 15% silage in addition to 20% barley grain in the diets increased ($P < 0.05$) ALA from 0.32 g in CON to 0.40 and 0.41 g per 100 g total fatty acids with 24.4 and 26.6% improvement in DG30 and DG35, respectively. The results indicate that replacement of barley silage with up to 35% WDDG increases total PUFA and omega-3 fatty acids in beef without affecting carcass quality.

Key words: beef cattle, wheat dried distiller grains, carcass quality

M307 Effect of early grain feeding on ADG and signaling proteins for protein synthesis in the muscle tissues of beef animals. W. A. D. Nayananjalie*, M. Bell, J. M. Scheffler, H. Jiang, M. A. McCann, D. E. Gerrard, J. Escobar, and M. D. Hanigan, *Virginia Polytechnic Institute and State University, Blacksburg.*

Early weaning followed by a period of high grain feeding in beef cattle enhances growth rate and reduces lifetime feed intake. High grain feeding leads to absorption of more glucose precursors which can enhance muscle protein synthesis by signaling through mammalian target of rapamycin (mTOR). This response is partially mediated by insulin, but glucose can also improve ATP levels leading to inactivation of AMP-activated protein kinase and induction of mTOR signaling. The objective of this study was to investigate the effects of early weaning followed by a period of high-grain feeding on signaling protein phosphorylation in muscle. Twelve fall-born, Angus × Simmental steers were either weaned at 106 ± 4 d of age in December (EW, n = 6) and fed a high-gain diet as a group for 148 d or remained with their dams (NW, n = 6) on pasture until weaning at 251 ± 5 d of age in May. Both groups were on pasture (predominantly tall fescue) from 253 ± 5 d to 392 ± 5 d of age. Longissimus muscle tissue biopsies were collected at 253 ± 5 and 392 ± 5 d of age. Total and phosphorylated forms of Akt (Ser473), ribosomal protein S6 (rpS6, Ser235/236), eukaryotic initiation factor 4E binding protein 1 (4EBP1, Thr37/46), and eukaryotic elongation factor 2 (eEF2, Thr56) were determined by Western immunoblotting. The experimental unit was steer. Total:phosphorylated forms and ADG were statistically analyzed for effects of treatment using the MIXED procedure of SAS. ADG was regressed on period and total:phosphorylated forms. EW calves had greater ADG (1.4 ± 0.01 kg/d) during the early grain feeding period than NW calves (0.9 ± 0.01 kg/d; $P < 0.01$). However, NW calves had greater ADG during the subsequent grazing period (0.7 ± 0.04 vs. 0.3 ± 0.04 kg/d; $P < 0.01$). There were no treatment differences in signaling protein phosphorylation ratios for either sampling time. Phosphorylation ratios of Akt, 4EBP1, rpS6 and eEF2 were not correlated with ADG. In conclusion, early weaned calves gained more weight during the early grain feeding period than normal weaned calves and grazing ADG was greater for normal weaned calves.

Key words: ADG, signaling proteins, weaning

M308 Slow release urea can replace nitrogen from soybean meal in dry-rolled corn-based finishing diets for yearling steers. B. P. Holland*[1] and J. S. Jennings[2], *[1]Department of Animal and Range Sciences, South Dakota State University, Brookings, [2]Alltech Inc., Brookings, SD.*

One hundred 92 British crossbred steers (initial BW = 410 ± 23.6 kg) were blocked by BW and allotted to 3 pens within block (12 or 13

steers/pen). Pens were allotted to 3 experimental diets (n = 5 pens per treatment). Diets were dry-rolled corn-based with 3 sources of supplemental CP (N basis): 100% soybean meal (SBM); 50:50 blend of soybean meal and Optigen® (SBM/OPT), a slow release urea; or 100% (OPT). All diets contained a supplement that provided 1.25% equivalent CP from non-protein N, and were formulated to target 12% CP. Steers were individually weighed on (d −1 and 0) and implanted with Revalor-S. Steers were fed at 0800 daily and weighed on a pen basis on d 29, 57, 85, and 117 and individually one day before slaughter (d 117 for blocks 3, 4, and 5 and d 145 for blocks 1 and 2). Blood samples were collected 4 h after feeding on d 1, 22, 50, and 78 (6 steers/pen) for plasma urea N (PUN) analysis. Mixed models were used to analyze data and repeated measures were used to analyze PUN data. Slaughter date x N source interactions were not observed for any variables. Final BW, ADG, DMI, and G:F were similar across N sources ($P \geq 0.31$). However, steers fed SBM/OPT tended to gain faster (1.64 vs. 1.41 kg/d; $P = 0.10$) and be more efficient (0.163 vs. 0.146; $P = 0.08$) than OPT steers from d 57 to 85. Standard carcass measurements were similar ($P \geq 0.22$) across treatments. No interaction ($P = 0.11$) between N source and sampling day were observed in PUN, but concentrations were greatest ($P < 0.001$) on d 1 (15.0 mg/100 mL), intermediate on d 50 (13.7 mg/100 mL) and 78 (13.6 mg/100 mL), and least on d 22 (11.0 mg/100 mL). When supplemental N was provided by OPT, PUN concentrations increased ($P < 0.001$). Plasma urea N concentrations were 11.9, 13.4, and 14.6 mg/100 mL when N was supplied by SBM, SBM/OPT, and OPT, respectively. Data suggest SBM nitrogen can be replaced by OPT in dry-rolled corn-based finishing diets, but increased PUN in steers fed OPT may indicate decreased N efficiency.

Key words: beef cattle, nitrogen, plasma urea N

M309 Acetate clearance rates and postabsorptive capacity to utilize acetate by beef steers. W. A. D. Nayananjalie*, T. R. Wiles, S. Arriola, M. Aguliar, J. Escobar, M. A. McCann, D. E. Gerrard, M. L. McGilliard, and M. D. Hanigan, *Virginia Polytechnic Institute and State University, Blacksburg.*

Weaning beef calves at 200 d of age may not be economically advantageous in all management systems. Early weaning followed by high-grain feeding can improve performance and increase marbling deposition. Because fat synthesis utilizes acetate as a substrate, we hypothesized that early grain feeding may enhance acetate conversion to fat. The objective of this study was to determine the effects of early grain feeding on acetate utilization in growing steers. Eight Angus x Simmental steers were weaned at 105 ± 4 d of age and fed a high-grain diet for 148 d (EW, n = 4) or remained with their dams on pasture until 249 ± 5 d of age (NW, n = 4). Both groups were on grass from 251 ± 5 to 393 ± 5 d of age. Acetate clearance was assessed at 114 ± 5 d (129 ± 12 kg, P1), 141 ± 5 d (160 ± 14 kg, P2), 227 ± 5 d (276 ± 18 kg, P3) and 348 ± 5 d (330 ± 17 kg, P4) of age. A bolus of acetate (4 mmol/kg of BW) was infused into the jugular vein. Jugular blood was collected at −15 min, at 5-min intervals over the first 30 min and 15-min intervals over the next 60 min. Plasma acetate levels were determined by isotope dilution using a GC-MS and plasma glucose levels were determined using a YSI glucose analyzer. Acetate clearance and appearance rate constants were determined by steer by fitting a one-pool model to the data using the Nelder Mead algorithm in acslX. Resulting rate constants were statistically analyzed for fixed effects of period, treatment and period by treatment and blood glucose concentrations were analyzed for fixed effects of treatment, period, time and the covariate effect of acetate concentration using the GLIMMIX procedure of SAS. Acetate clearance rate constants were less ($P = 0.06$) and appearance rate greater ($P < 0.05$) in EW steers during grain feeding. Acetate appearance rate constants were greater ($P < 0.05$) in NW steers in P4. Blood glucose concentrations were greater in NW steers ($P < 0.05$) only in P1. Infusion of acetate did not significantly affect glucose concentrations. Grain feeding increases rates of acetate appearance, yet reduces acetate clearance and suggests feeding high concentrate diets alters acetate metabolism in growing steers.

Key words: acetate, glucose, weaning

M310 Blood profile of bulls fed different levels of crude glycerin. J. R. R. Carvalho, M. M. Ladeira*, M. L. Chizzotti, T. M. Gonçalves, D. M. Oliveira, P. D. Teixeira, A. Nogueira Neto, and P. T. Silva, *Federal University of Lavras, Lavras, MG, Brazil.*

This study was carried out to analyze the effect of crude glycerin on blood concentrations of the enzymes aspartate aminotransferase (AST), alanine aminotransferase (ALT), gamma-glutamyl aminotransferase (GGT), creatine kinase (CK) and glucose and creatinine metabolites, after 84 d on feedlot. Forty-four Red Norte bulls received the following levels of crude glycerin (83% glycerol): 0, 6, 12 and 18% of DM. The basal diet consisted of 30% of corn silage, 12% of soybean meal, 56% of ground corn grain and 2% of mineral mixture. Glycerin was added to partially replace corn and corn gluten meal (21% of CP) was added to maintain diets isonitrogenous. Blood samples were collected on d 84 of the experimental period, after 16 h of overnight fasting. The experiment was conducted in a completely randomized design and data were analyzed using PROC GLM of SAS 9.1. The levels of glycerol did not affect the blood concentration of enzymes and metabolites (Table 1). Increased levels of blood glucose could be expected due to gluconeogenic pathway. However, the absence of this effect indicates that glycerol could be used by the liver and enteric tissues. The AST enzyme showed high concentration, which could indicate liver injury, which can be attributed to the low forage:concentrate ratio and absence of ionophores or buffers in the diet. The GGT enzyme appeared in normal concentrations There was not effect for ALT, which is normally present in low concentrations in large animals.. Creatinine remained low and within normal limits, which may indicate absence of toxic effect of methanol (0.02% in glycerin). The level of 18% of crude glycerin in diet DM did not result in health impairment and could be used in feedlot diets. Funded by Fapemig, CNPq, CAPES, and INCT-CA

Table 1. Biochemistry of the blood of bulls fed different levels of crude glycerin

	Crude glycerin level, DM basis					
Item	0%	6%	12%	18%	SEM	*P*-value
Glucose, mg/dL	83.2	73.1	85.1	71.9	5.40	0.21
Creatinine, mg/dL	1.53	1.41	1.47	1.48	0.09	0.83
AST, U/L	93.0	95.4	85.8	84.9	6.80	0.62
ALT, U/L	28.7	28.5	28.9	29.4	1.48	0.98
GGT, U/L	12.5	12.2	15.7	17.5	2.36	0.32
CK,U/L	284.1	461.0	274.0	244.9	73.0	0.16

Key words: enzymes, glucose, glycerol

M311 Effect of specific polyclonal antibody preparation doses on ruminal variables in cattle fed high concentrate diets. J. Bastos*[2], C. Marino[1], D. Millen[2], R. Pacheco[2], J. Magalhaes[1], J. Carvalho[3], M. Arrigoni[2], and P. Rodrigues[1], [1]*University of Sao Paulo,*

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The objective of the present study was to evaluate the effects of different doses of polyclonal antibody preparation (PAP) against specific ruminal bacteria *Streptococcus bovis*, *Fusobacterium necrophorum*, *Clostridium aminophilum*, *Peptostreptococcus anacrobius* and *Clostridium sticklandii* on rumen fermentation parameters (pH, total concentration of volatile fatty acids (tVFA) which included acetate, propionate and butyrate, ammonia nitrogen (NH3-N) and lactate) in cattle fed high concentrate diets. Eight rumen cannulated cows were used in a latin square 4x4, twice replicated. The treatments were T1: 0.0 g/anim/d, (control); T2: 1.5 g/anim/d; T3: 3.0 g/anim/d; T4: 4.5 g/d with 4 experimental periods with 21 d each. Sample collection was carried out at the last day of each period with 2 h of interval between each collection. Data were analyzed by MIXED procedure, which separated the effects of treatments, period, animal nested in square and square. The effect of treatments was evaluated by polynomial regression. Differences were declared at $P < 0.05$. There was no interaction between time and treatment ($P > 0.05$) for any of the rumen variables studied. Independently from time of sampling, there was no linear or quadratic effect on rumen pH, tVFA, molar proportion of acetate, propionate and butyrate and NH3-N. Thus, it can be concluded that different levels of PAP were not sufficient to alter rumen environment with the necessity of more studies to validate or not this observation.

Key words: feed additive, passive immunization, ruminal fermentation

M312 Corn grain processing methods and forage levels in finishing diets for Nellore bulls. R. Carareto[1], F. A. P. Santos*[1], G. Mourão[1], A. M. Pedroso[2], C. Sitta[1], M. P. Soares[1], M. R. Paula[1], R. S. Marques[1], and M. C. Soares[1], *[1]University of Sao Paulo, Piracicaba, São Paulo, Brazil, [2]Embrapa Cattle Southeast, Sao Carlos, São Paulo, Brazil.*

The trial was conducted at the Animal Sciences Department of the University of São Paulo in Piracicaba, SP. One hundred and 90 2 (192) finishing Nellore bulls (403 kg) BW in 32 pens were fed for 99 d to compare diets containing fine ground (FG), dry rolled (DR), high moisture (HM) or steam flaked flint corn (SF) and 2 levels (12 or 20% on DM) of sugar cane bagasse. Data were analyzed as a randomized complete block using the Mixed procedure of SAS, with pens serving as the experimental units. There was no interaction between corn processing methods and diet forage levels ($P > 0.05$). DMI was greater ($P < 0.05$) for dry rolled corn compared with the other 3 processing methods (Table 1). ADG was greater ($P < 0.05$) for steam flaked and high moisture corn than for ground or rolled corn (Table 1). Feed efficiency (ADG/DMI) was greater ($P < 0.05$) for steam flaked corn than for fine ground or dry rolled corn, and greater ($P < 0.05$) for high moisture and ground corn than for dry rolled corn. The greatest ($P < 0.05$) diet net energy values were observed for steam flaked and high moisture corn. DMI was less and ADG, feed efficiency, dressing and diet energy values were greater for cattle fed 12% than 20% forage diets ($P < 0.05$). Forage level had no effect on diet starch digestibility ($P > 0.05$). In conclusion, steam flaked corn and high moisture corn are the greatest, ground corn is intermediate and dry rolled corn is the least in net energy for finishing Nellore bulls. Performance of finishing Nellore bulls is improved with 12% sugar cane bagasse forage diets compared with 20% forage diets.

Table 1. Influence of corn processing on growth performance of feedlot Nellore bulls and dietary net energy values

Variable	FG	DR	HMC	SF	SE	Pr>F
ADG, kg/d	1.12^{b}	1.09^{b}	1.21^{a}	1.25^{a}	0.031	0.0057
DMI, kg	9.37^{b}	10.18^{a}	9.41^{b}	9.26^{b}	0.168	0.0034
ADG/DMI	0.121^{b}	0.108^{c}	0.129^{ab}	0.136^{a}	0.004	<0.001
NEm (mcal/kg/DM)	1.73^{b}	1.58^{c}	1.821^{ab}	1.93^{a}	0.0386	<0.001
NEg (mcal/kg/DM)	1.11^{b}	0.97^{c}	1.18^{ab}	1.28^{a}	0.0339	<0.001

Key words: corn grain processing, fiber lever, Nellore

M313 Effect of sugar and sodium propionate for barley grain in dairy calves starter on weaning and performance. H. Beiranvand, M. Khorvash, G. R. Ghorbani*, A. Homayouni, M. Mirzaei, and S. Kargar, *Isfahan University of Technology, Isfahan, Iran.*

Replacing dietary starch with sugar and sodium-propionate has been reported to improve performance in ruminant animals. This experiment was conducted to determine the effects of replacing different sources of energy with barley grain in dairy calves′ starter on weaning, dry matter intake, average daily gain (ADG), feed efficiency, skeletal growth, and fecal score. A total of 21 male calves (42 ± 4 kg; mean ± SD) were assigned randomly to one of 3 following treatments: 1) no replacing (Control); 2) replacing sugar at 5% of dietary DM with barley (Sugar); and 3) replacing sodium-propionate at 5% of dietary DM with barley (Propionate). These parameters were measured and reported during 3 time periods (d 1 to 42, 43 to 70 and 1 to 70). All data were analyzed as completely randomized design using the MIXED procedure of SAS (SAS, 2003). Each calf was housed in an individual box with unlimited access to water. All dietary treatments were provided ad-libitum in addition to milk (4 kg/head/day). The base of weaning was consumption of 1 kg solid feed during 3 consecutive days. Feeding Sugar significantly decreased age of weaning compared with Propionate (50 vs. 60 d), however, Propionate negatively affected this variable compared with Control ($P < 0.02$). Dry matter intake, ADG, feed efficiency, skeletal growth indices and fecal score were not affected by treatments. Results of current experiment showed that using sugar but not sodium-propionate as an alternative for barley grain in dairy calves starter can be an option based on its cost and availability.

Key words: dairy calves, propionate, sugar

M314 Evaluation of content and epithelial attached bacterial community in the rumen of steers differing in susceptibility to rumen acidosis. Y. Chen*, M. Oba, and L. L. Guan, *Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Alberta, Canada.*

Rumen acidosis is a common digestive disorder problem in ruminant livestock industry. The objective of this study was to determine if ruminal bacteria diversity and density are different between acidosis-susceptible (AS) and acidosis-resistant (AR) beef cattle. Six steers were selected from a pool of 17 steers fed a feedlot diet containing grain at 85% of dietary DM. Based on continuous rumen pH measurements for a 3-d period, steers that were highest (n = 3) and lowest (n = 3) in severity of rumen acidosis, indicated by the area under pH 5.8 (pH units × min/d), were classified as AS and AR animals, respectively. Rumen papillae and digesta were collected at 0, 2, 4 and 6h after feeding and bacterial diversity was characterized using PCR-denaturing gradient gel electrophoresis (PCR-DGGE) and quantitative real time PCR (qRT-PCR) analysis. Bacterial profiles of rumen digesta samples from AR group was 69.7% similar to those from AS group while the epimural bacterial (bacteria attached to the ruminal papillae) profiles from AR group was 73.5% similar to those from AS group. The copy number of total 16S rRNA genes in the rumen digesta of AS steers was 10-fold higher than that of AR steers, while it was not different between AR and AS epimural communities. However, the copy number of 16S rRNA gene of *Selenomonas ruminantium* was higher for AS compared with AR steers ($P = 0.05$) for both digesta and epimural samples. In addition, the copy number of total 16S rRNA genes of epimural bacteria was positively correlated with ruminal pH (r = 0.59, $P = 0.04$) and negatively correlated with total VFA concentration (r = −0.59, $P = 0.05$) for AR steers, but no such relationship was found for AS animals. Furthermore, the copy number of total 16S rRNA genes of content bacteria was positively correlated with molar proportion of butyrate (r = 0.74, $P = 0.006$) for AR animals, while it was negatively correlated with molar proportion of butyrate (r = −0.73, $P = 0.007$) for AS animals. These results suggest that the diversity and population of some bacterial species can be different between AS and AR animals.

M315 Supplementing rumen-protected Met and Lys in alfalfa and red clover silage diets fed to lactating dairy cows. G. A. Broderick*[1], R. P. Walgenbach[1], M. J. de Veth[2], and N. D. Luchini[3], *[1]U.S. Dairy Forage Research Center, Madison, WI, [2]Balchem Corporation, New Hampton, NY, [3]Adisseo, Alpharetta, GA.*

Action of polyphenol oxidase reduces NPN formation in red clover silage (RCS). In 7 previous trials, RCS averaged (% of total N) 36% NPN vs. 54% NPN in alfalfa silage (AS). Feeding RCS increased intestinal protein absorption but with no improvement in N utilization, suggesting depressed utilization of one or more essential AA. This trial tested effects of adding rumen-protected Met (RPM) and Lys (RPL) to AS and RCS diets. Forty-eight lactating Holstein cows were blocked by DIM and parity into 6 squares in an incomplete 8x8 Latin square with a 2x2x2 arrangement of diets: AS or RCS, with or without RPM (15 g/d of Smartamine-Mproviding 10.5 g/d of total Met), with or without RPL (69 g/d of AminoShure-L providing 26 g/d of total Lys). Diets were formulated to contain (DM basis): 50% AS and 20% corn silage or 63% RCS and 7% corn silage; plus 24% corn, 3% solvent soybean meal; and 16% CP and 31% NDF. Periods were 4-wk (total 16 wk); data from the last 2 wk were analyzed using Proc Mixed in SAS. LS-means are reported in the table. Feeding AS increased DMI, yield of ECM, milk fat content and yield, and protein content. However, RCS improved ECM/DMI and MUN. RPM increased DMI and milk fat and protein content. No responses to RPL were detected but RPM × RPL interactions suggested differential responses to RPL versus RPL plus RPM. Lack of silage × RPAA interactions suggested there was no specific impairment of Met or Lys utilization on RCS.

Table 1.

	Forage			RPM, g/d			RPL, g/d		
Variable	AS	RCS	P > F	0	15	P > F	0	69	P > F
DM intake, kg/d	23.9	22.7	<0.01	23.1	23.6	0.01	23.3	23.3	0.98
Milk, kg/d	35.0	34.8	0.47	34.9	34.9	0.92	35.1	34.7	0.23
ECM, kg/d	34.0	33.2	0.03	33.5	33.7	0.47	33.7	33.5	0.64
ECM/DMI	1.43	1.47	0.02	1.46	1.43	0.07	1.45	1.44	0.65
Fat, %	4.06	3.93	<0.01	3.95	4.04	0.05	3.98	4.01	0.43
Fat, kg/d	1.40	1.34	<0.01	1.37	1.38	0.46	1.38	1.38	0.81
Protein, %	3.04	3.01	0.03	2.99	3.06	<0.01	3.01	3.04	0.12
Protein, kg/d	1.04	1.03	0.09	1.03	1.04	0.11	1.04	1.03	0.66
MUN, mg/dl	15.1	12.9	<0.01	14.0	14.0	0.63	13.9	14.1	0.12

Key words: alfalfa silage, red clover silage, rumen-protected AA

M316 Steam-flaked soybeans in lactating dairy cow diets. H. R. Bruns*[1], K. F. Kalscheur[1], D. J. Schingoethe[1], R. Rosenboom[2],

G. Doppenberg[2], and A. R. Hippen[1], *[1]South Dakota State University, Brookings, [2]Deluxe Feeds, Sheldon, IA.*

While most soybean feedstuffs have been extensively investigated for use in ruminant diets, there is a lack of information regarding steam-flaked soybeans (Deluxe Feeds – EnRG Flakes; Sheldon, IA). This research evaluated various inclusion rates of steam-flaked soybeans (SFSB) in lactating dairy cattle diets. Twelve multiparous Holstein cows (103 ± 39 DIM) were used in a 4 × 4 Latin-square experiment with 28-d periods, 14-d for diet transitioning followed by a 14-d sampling period. Treatments were inclusion of SFSB at 0, 5, 10 and 15% of dietary DM, replacing a mixture of soybean meal, soyhulls, calcium salts of fatty acids, and choice white grease. Animals were fed typical lactating dairy cow diets formulated to be isonitrogenous and isoenergetic containing 60% of DM as forage and 40% of DM as concentrate. Dry matter intake (30 kg/d) was similar for all treatments and milk production was also not different with 42.1, 43.1, 41.9, and 41.9 kg/d for 0, 5, 10, and 15% SFSB, respectively. Milk fat percentage (3.6%) and yield (1.5 kg/d) was similar across treatments. Milk protein percentages (3.6%) and yields (1.15 kg/d) and lactose concentrations (4.9%) were also unaffected by the amount of SFSB in the diet. Feed efficiency (1.4 kg milk / kg DMI) was consistent throughout all dietary treatments. Milk urea nitrogen concentration and yield decreased linearly (14.6, 14.2, 13.9 and 13.3 mg/dL and 6.2, 6.2, 5.8 and 5.6 g/d; $P < 0.01$) as the amount of SFSB in the diet increased. Body weight changes (−3.69, 3.43, 7.97 and 14.8 kg; $P < 0.10$) tended to increase linearly, and body condition score changes (0.07, 0.06, 0.03 and −0.03; $P < 0.05$) decreased linearly as the amount of SFSB in the diet increased. This research demonstrates that steam-flaked soybeans can be substituted for soybean meal and commercial fat sources while maintaining milk and milk fat production and significantly decreasing milk urea nitrogen production.

Key words: steam-flaked soybeans, full-fat soybeans, lactating cows

M317 Effects of different amounts of dietary protected and unprotected niacin on intake and milk production. F. C. Cardoso*[1], J. Garrett[2], and J. K. Drackley[1], *[1]University of Illinois, Urbana, [2]QualiTech, Chaska, MN.*

Oral supplementation of niacin has been reported to increase milk yield in dairy cows. However, its effects on milk yield and components have been variable among studies. Protection of niacin against degradation by rumen microbiota might help achieve consistent response to niacin. Our objective was to determine the effects of 3 levels of protected niacin (PN) in comparison with unprotected niacin (UN) either in the diet or infused into the abomasum. Six multiparous rumen–cannulated Holstein cows (BW = 656 kg) after peak lactation (128 ± 23 d in milk) were assigned to 1 of 6 treatments in a completely randomized 6 × 6 Latin Square with an extra period to measure carryover effects. Periods consisted of a 7-d adaptation period followed by a 7-d measurement period. Cows were fed according to NRC (2001) recommendations. Treatments were: CON, no niacin; INF, abomasal infusion of 12 g unprotected niacin (UN); N12, 12 g UN; BN3, 3 g PN; BN6, 6 g PN; and BN12, 12 g PN. Treatments N12, BN3, BN6, and BN12 were top-dressed on the TMR twice daily. The daily dose of treatment INF was divided in 5 equal portions and infused during the day every 4 h. Cows receiving treatments other than INF were infused with the same volume of water at the same time. Statistical analysis was performed using the MIXED procedure of SAS. Least squares means were separated using the Tukey adjustment. Milk yield tended ($P = 0.06$) to be greater for N12 (37.1 ± 2.3 kg) than for BN12 (33.4 ± 2.3 kg). The DMI was lower ($P = 0.02$) for BN12 (21.5 ± 1 kg) than for N12 (24.3 ± 1 kg). The linear effect among BN3, BN6, and BN12 was significant ($P = 0.04$) for DMI. Feed efficiency (FE = energy-corrected milk/DMI) was greater ($P = 0.04$) for BN12 (1.7 ± 0.1) than for N12 (1.5 ± 0.1).Furthermore, the positive linear effect among BN3, BN6, and BN12 was significant ($P = 0.03$) for FE. The milk fat/protein ratio (F/P) was higher ($P = 0.03$) for BN12 (1.28 ± 0.09) than for N12 (1.15 ± 0.09). The positive linear effect among BN3, BN6, and BN12 was significant ($P < 0.01$) for F/P. In conclusion, cows receiving BN12 had higher F/P and FE but lower milk yield than cows receiving the same amount of UN.

Key words: niacin, milk yield, feed efficiency

M318 Effect of malate supplementation to dairy cows on milk production: A meta-analysis. J. Alcañiz*[1], J. J. Mallo[1], M. Puyalto[1], M. I. Gracia[2], and J. Sánchez[2], *[1]Norel, S.A., Madrid, Spain, [2]Imasde Agroalimentaria, S.L., Madrid, Spain.*

We evaluated the effect of malate supplementation on milk production in lactating dairy cows. Four trials involving 516 dairy cows assessed the efficacy of malate. A blocked design was applied in each study with 2 treatments: 1) Control, and 2) Malate (48–84 g/cow/day). The studies were similar in basic design and each treatment group (T1 Control and T2 Malate) equivalence in terms of parity, pretrial milk yield and days in milk. Three trials supplemented the additive at 48 g/cow/day in the TMR and one study at 84 g/cow/day in the concentrate. Milk production was recorded daily during 71–90 d of lactation and averages calculated in a weekly basis. Data were tested for homogeneity, pooled and combined in a meta-analysis. Data were analyzed using mixed models ANOVA with terms included for the fixed effect of treatment and the random effect of study. Animal (cow) within treatment and study were considered as a random effects. Pretrial milk yield and DIM were included as a covariate. A repeated measures ANOVA was conducted with time. Malate supplementation significantly increased milk production by 2.3% across the lactation weeks studied (41.81 vs. 42.85 kg/d; $P = 0.0107$, SE = 0.33). An interaction between lactation week and treatment was detected ($P = 0.0015$). Malate supplementation increased milk production from the beginning of the trial until the fourth week of trial (41.8 vs. 41.1 kg/d, SE = 0.46; 42.2 vs. 42.3 kg/d, SE = 0.45; 41.6 vs. 42.1 kg/d, SE = 0.44; 41.5 vs. 42.7 kg/d, SE = 0.42; for wk 1 to wk 4, respectively), maintaining the improvement afterward. It can be concluded that the supplementation of dairy cow rations with malate increases milk production under farm conditions.

Key words: dairy cows, malate, milk yield

M319 Independent effects of diet chemical fiber and physical measurements on dairy cows. D. Sauvant*[1], W. Z. Yang[2], D. R. Mertens[3], and K. A. Beauchemin[2], *[1]AgroParisTech-INRA, Paris, France, [2]Agriculture and Agri-Food Canada, Lethbridge, AB, Canada, [3]Innovation & Research, Belleville, WI.*

Fiber effectiveness has been defined by peNDF, which is the product of NDF and the fraction retained on a 1.18-mm sieve. To evaluate the concept of using an index (product of fiber and particle size) for predicting cow responses, a meta-analysis was performed to assess the independent and interaction effects of chemical fiber (NDF) and alternative physical measurements (PM). A database was compiled from 24 published experiments using lactating dairy cows and 104 (n) treatments where dietary NDF and PM were reported. Forages were long, chopped or grounded. Dietary NDF averaged 35.3 ± 7.1% of DM.

Three PM were considered: mean particle size (MPS; 3.72 ± 2.02 mm, n = 44), particles retained on a 2-mm sieve (P2; 42.4 ± 15.5% DM, n = 40) or on 19-mm and 8-mm sieves of the Penn State Particle Separator (P8; 49.5 ± 12.7% DM, n = 36). As the PM was not measured with the same criteria across the experiments, a dummy variable (0 or 1) was created to systematically code the short or long PM, respectively. The effects of NDF and PM were tested on chewing index (CI; 37.5 ± 11.9 min/kg DMI, n = 78), rumen pH (6.08 ± 0.26, n = 60), acetate to propionate ratio (A:P; 2.70 ± 0.73, n = 52), milk yield (MY; 29.0 ± 10.6 kg/d, n = 96) and milk fat percentage (MF; 3.75 ± 0.62%, n = 82). Meta analyses were carried out using GLM procedure including the effects of experiment, NDF, PM and the interaction. NDF was a continuous covariable. The mean differences between treatments were: NDF = 4.3%DM; MPS = 1.31mm; P2 = 7.5%DM; and P8 = 8.6%DM. Experiment was systematically significant ($P < 0.01$). For CI, pH and A:P, influences of NDF and PM were significant ($P < 0.01$), but there was no interaction between them. For MY and MF, only the effect of NDF was significant ($P < 0.01$). As expected, MF was negatively affected ($P < 0.01$) by pH (MF = −1.05 + 0.76 pH, n = 48, RMSE = 0.05%). In conclusion, the effects of NDF and PM appeared to be additive in published trials, which questions the principle and the validity of their product (peNDF) for predicting lactating cow responses.

Key words: effective fiber, meta-analysis, dairy cattle

M320 Effect of feeding *Camelina sativa* seeds or meal on lactation performance and milk fatty acid composition in lactating dairy cows. J. P. Sarramone*[1,2], C. Benchaar[3], Y. Lebeuf[1,2], R. Gervais[1], and P. Y. Chouinard[1,2], *[1]Département des sciences animales, Université Laval, Québec, QC, Canada, [2]Institute of Nutraceuticals and Functional Foods (INAF), Québec, QC, Canada, [3]Agriculture and Agri-Food Canada, Dairy and Swine R&D Centre, Sherbrooke, QC, Canada.*

Camelina sativa and flaxseed are both sources of *c*9,*c*12,*c*15–18:3. The objective of the current study was to evaluate the effects of feeding camelina seeds, camelina meal, flaxseed, or dried distillers grains with solubles (source of *c*9,*c*12–18:2) on milk yield and composition in lactating dairy cows. Four Holstein cows were used in a 4 × 4 Latin square design with 21-d periods, including 14 d of adaptation followed by 7 d of sampling. Four isolipidic dietary treatments (4.5% fat) were formulated: DDGS) 18% corn dried distillers grains with solubles; CM) 9.5% camelina meal; CS) 4.2% camelina seeds; FS) 4.7% flaxseed (DM basis). Differences between treatments were declared significant at $P \leq 0.05$ using the Tukey correction for multiple comparisons. Body weight, DM intake, milk protein content and yield, milk lactose content, MUN, and SCC were similar among treatments. Milk yield was higher for DDGS (37.4 kg/d;*b*), intermediate for CM (37.0 kg/d;*ab*), and CS (36.5 kg/d;*ab*), and lower for FS (35.6 kg/d;*a*). Milk fat content and yield were lower for CM (2.71%, 1000 g/d;*a*) compared with DDGS (3.63%, 1355 g/d;*b*), FS (3.73%, 1328 g/d;*b*), and CS (3.48%, 1258 g/d;*b*). Concentrations (mg/g FA) of *c*11–20:1 and *c*13–22:1 were lower for DDGS (0.9*c* and 0.2*c*), and FS (0.5*c* and 0.1*c*), intermediate for CS (3.4*b* and 1.0*b*), and higher for CM (8.1*a* and 1.8*a*). Cows fed FS had a higher content of *c*9,*c*12,*c*15–18:3 (6.4*a*) in milk fat compared with DDGS (3.5*c*), CM (4.5*bc*), and CS (5.0*b*). Feeding CM and FS increased milk fat content of *c*9,*t*11,*c*15–18:3 compared with DDGS and CS (0.4*a*, 0.4*a*, 0.2*b*, and 0.3*b*, respectively). Milk fat contents of *t*11,*c*15–18:2, *c*9,*t*13–18:2, and *t*13/*t*14–18:1 were higher for CM (7.2*a*, 2.9*a*, and 17.6*a*) intermediate for CS (2.3*b*, 1.9*ab*, 13.4*b*) and lower for FS (1.2*bc*, 1.5*b*, and 8.0*c*) and DDGS (0.8*c*, 1.6*b*, and 8.2*c*). Milk fat contents of *t*10–18:1 and *t*11–18:1 were higher for CM (22.0*a* and 29.2*a*) compared with DDGS (5.4*b* and 17.9*b*), CS (6.4*b* and 17.2*bc*), and FS (3.2*b* and 8.6*c*). In conclusion, FS was more efficient to increase *c*9,*c*12,*c*15–18:3 in milk fat compared with camelina fed as meal or seeds.

Key words: *Camelina sativa*, linseed, milk fatty acids

M321 Milk fatty acid profile of dairy goats fed increasing levels of an unprotected conjugated linoleic acid (UCLA) supplement. D. Fernandes[1], J. Souza[2], M. M. Almeida[3], M. Baldin[1], R. Dresch[1], F. Batistel[2], E. Ticiani[2], M. A. S. Gama[4], and D. E. Oliveira*[2,1], *[1]Centro de Ciências Agroveterinárias, UDESC, Lages, SC, Brasil, [2]Centro de Educação Superior do Oeste, UDESC, Chapecó, SC, Brasil, [3]Universidade Federal de Juiz de Fora, Juiz de Fora, MG, Brasil, [4]Embrapa, CNPGL, Juiz de Fora, MG, Brasil.*

The aim of this study was to evaluate the dose-response changes in milk fatty acid profile associated with the reduction observed in milk fat content and yield of dairy goats fed increasing levels of UCLA (Fernandes et al., 2010, JDS, 93:456). Eight Toggenburg goats (4 primiparous and 4 multiparous; 120–150 DIM) received 4 levels of UCLA 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 UCLA; 3) CLA30: 15 g/d of CSSO plus 30 g/d of UCLA and 4) CLA45: 45 g/d of UCLA. Each experimental period lasted 12 d, with 6 d of washout intervals. The UCLA contained 29% of t-10, c-12 CLA and 29% of c-9, t-11 CLA. Lipid supplements were mixed into the concentrate (1.0 kg/d) fed twice a day. Milk samples were collected on the last day of each experimental period for fatty acid analysis. Data were analyzed using GLM procedures, including animal, period, LS, and treatment as sources of variation. The UCLA reduced linearly the desaturase indexes (Table 1). Concentration of fatty acids < 16C in milk fat was linearly reduced as the CLA dose increased, suggesting that inhibition of de novo synthesis was more pronounced with the highest CLA dose. The secretion of t-10, c-12 CLA in milk increased with the CLA dose (Control = 0.02g/d; CLA15 = 0.08g/d; CLA30 = 0.13g/d; CLA45 = 0.17g/d; $r^2 = 0.77$; $P < 0.001$). The transfer efficiency of t-10, c-12 CLA into milk fat decreased with the CLA dose (CLA15 = 1.82%; CLA30 = 1.48%; CLA45 = 1.33%; $r^2 = 0.71$; $P < 0.001$). The milk fatty acid profile was changed in a dose-response way.

Table 1. Fatty acid profile of dairy goats fed increasing levels of UCLA

	Control	CLA15	CLA30	CLA45	SEM	*P*-value
g/100g of total FA						
CLA isomers						
cis-9,trans-11	0.5	0.6	0.7	0.8	0.03	0.001
trans-10,cis-12	0.03	0.1	0.3	0.5	0.02	0.001
Desaturase indexes						
14:1/14:0+14:1	0.01	0.008	0.006	0.005	0.0005	0.001
16:1/16:0+16:1	0.02	0.018	0.017	0.01	0.001	0.003
18:1/18:0+18:1	0.59	0.53	0.49	0.46	0.01	0.001
CLA/18:1t11+CLA	0.30	0.27	0.26	0.27	0.01	0.05
Ratios						
<C16	28.7	26.7	24.3	23.3	0.7	0.004
C16+C16:1	25.1	24.7	23.6	21.9	0.3	0.001
>C16	42.2	44.8	47.5	49.4	0.8	0.001

Key words: dairy products, fatty acid profile, desaturase index

M322 Performance and milk fatty acid profile of dairy goats fed a total mixed ration (TMR) containing an unprotected conjugated linoleic acid (UCLA) supplement. M. Baldin[1], J. Souza[2], M. M. Almeida[3], R. Dresch[1], D. Fernandes[1], F. Batistel[2], E. Ticiani[2], F. C. F. Lopes[4], M. A. S. Gama[4], and D. E. Oliveira*[2,1], *[1]Centro de Ciências Agroveterinárias, UDESC, Lages, SC, Brasil, [2]Centro de Educação Superior do Oeste, UDESC, Chapecó, SC, Brasil, [3]Universidade Federal de Juiz de Fora, Juiz de Fora, MG, Brasil, [4]Embrapa, CNPGL, Juiz de Fora, MG, Brasil.*

Lactating goats have been shown to be less prone to trans-10 cis-12 CLA-induced milk fat depression (MFD) than cows and ewes on a metabolic live-weight basis. This study aimed to evaluate the effects of UCLA, fed as a TMR ingredient, on performance and milk fatty acid (FA) profile of dairy goats. Eighteen Toggenburg goats (83 ± 17 DIM) were used in a crossover design with 14 d experimental periods and 6 d washout interval. The treatments were: 1) Control (C): 30 g/d of calcium salts of soybean oil or 2) CLA: 30 g/d of UCLA (29% of trans-10 cis-12 CLA). Lipid supplements were mixed into 1.0 kg of concentrate and then with corn silage (50:50, DM basis) and fed 3 times a day. After complete consumption, corn silage was fed ad libitum and orts recorded. Milk samples were taken every 2 d to determine its solid contents and on the last day of each experimental period for milk FA analysis. Data were analyzed as a repeated measurement design using PROC MIXED of SAS, assuming period and treatment sequence as random effects. Milk yield (1.91 vs. 1.90 kg/d, SEM = 0.28), body weight (45.6 vs. 45.2 kg, SEM = 10.5), dry matter intake per metabolic weight (7.66 vs. 7.53%, SEM = 0.87), milk protein content (2.80 vs. 2.81%, SEM = 0.18) and milk protein yield (51.3 vs. 51.4 g/d, SEM = 7.06) were unchanged ($P > 0.05$) by CLA. CLA reduced ($P < 0.001$) milk fat content (4.10 vs. 3.29%, SEM = 0.39) and yield (75.0 vs. 61.1 g/d, SEM = 9.5). CLA reduced the concentrations of C4:0 to C14:0 chain FA (24.8 vs. 29.0%, SEM = 1.58) and C16:0 (22.9 vs. 26.6, SEM = 1.27), but increased long chain FA in milk fat (45.9 vs. 38.7%, SEM = 2.41, $P < 0.001$). Milk fat trans-10 cis-12 CLA was strongly increased by CLA (0.42 vs. 0.02%, SEM = 0.03, $P < 0.001$), whereas all desaturase indexes were reduced ($P < 0.05$). Results showed that milk fat synthesis was partially reduced despite the large increase in milk fat trans-10 cis-12 CLA content, corroborating previous data indicating that goats are less responsive to CLA-induced MFD than cows and ewes (Acknowledgment: FAPEMIG).

Key words: milk fatty acids, milk fat depression, goats

M323 Effects of feeding levels of a milk replacer on growth performance, digestion and metabolism of nutrients, and serum biochemical markers in calves. X. Xu, J. Wang, Y. Tu*, N. Zhang, C.-G. Jiang, and Q. Diao, *Key Laboratory of Feed Biotechnology of Ministry of Agriculture/Feed Research Institute, Chinese Academy of Agricultural Sciences, Beijing, P. R. China.*

This study investigated the effect of feeding levels of a milk replacer on growth, digestion and absorption of nutrients and serum biochemical markers in calves. Twenty-four newborn Holstein calves were allotted to 3 groups with 8 calves each and each group was fed a milk replacer at 9.5%(group L), 11.0% (group M) or 12.5% (group H) of body weight (BW), respectively, for 8 weeks. Feed intake(FI), BW and body measurement of the calves were measured and blood samples were collected at 0, 2, 4, 6 and 8 weeks of age. A digestion trial was conducted by total collection of feces and urine during 3–4 and 5–6 weeks of age, respectively. Data were analyzed by GLM progress of SAS software. FI differed among 3 groups (519.8, 625.5 and 711.1 g/d, $P < 0.05$). The average daily gain of calves from group M or H was greater than that from group L (357.6 or 349.3 vs. 250.0 g/d, $P < 0.05$) during 3–4 weeks of age. Body length, wither height and heart girth did not differ among 3 groups. During 3 to 4 weeks of age, the apparent digestibility of dry matter (DMD) or organic matter (DOM) were greater in group L than in group H (84.16% vs. 80.69% or 86.55% vs. 82.02%, $P < 0.05$), and the apparent digestibility of crude protein was greater in group M than in group H (68.65% vs. 61.51%, $P < 0.05$). During 5 to 6 weeks of age, DMD, DOM and the apparent digestibility of calcium were greater in group M than in group H (87.11% vs. 85.40%, 88.07% vs. 86.70%, and 67.75 vs. 58.04%, $P < 0.05$). At 2 weeks of age, the serum albumin concentration was greater in group L or M than that in group H (31.49 or 31.38 vs. 29.40 g/L, $P < 0.05$), the serum triglyceride concentration was greater in group H than in group L ($P < 0.05$), and serum urea nitrogen was greater in group M than in group L (3.43 vs. 2.59 mmol/L, $P < 0.05$). At the other ages, serum biochemical markers were not influenced by the treatments. The milk replacer fed at 11.0%BW was better than those fed at 9.5 or 12.5%BW in growth of the calves, especially at 2–4 weeks of age. But the digestion and absorption of nutrients decreased as feeding level increased.

Key words: calves milk replacer, feeding level, growth and digestion

M324 Effect of dietary starch content on response to an intravenous glucose tolerance test in early lactation dairy cows. B. H. Nelson*, K. W. Cotanch, R. J. Grant, and H. M. Dann, *William H. Miner Agricultural Research Institute, Chazy, NY.*

Multiparous Holstein cows (n = 24) were used to evaluate the effect of dietary starch content in corn silage-based diets fed from 1 to 21 d in milk (DIM) on blood metabolites following an intravenous glucose tolerance test (GTT). Cows were fed either 1) a low-starch diet (L; 21.0% starch; 76.5% in vitro 7-h starch digestibility (IVSD); 1.65 Mcal NE_L/kg), 2) a medium-starch diet (M; 23.2%; 76.7% IVSD; 1.67 Mcal NE_L/kg), or 3) a high-starch diet (H; 25.5%; 74.5% IVSD; 1.68 Mcal NE_L/kg). Corn meal was replaced partially with soyhulls and wheat middlings in the L and M diets. The GTT was done on d 15 ± 2. Cows were fasted 1 h before and during the GTT. Glucose (dextrose 50% w/v) was infused via a jugular catheter at 0.25g/kg of body weight. Blood samples were collected at −15, −10, 0, 10, 15, 20, 25, 30, 45, 60, 90, 120, 150, and 180 min relative to glucose administration and analyzed for plasma glucose, serum insulin, and serum nonesterified fatty acids (NEFA). The NLIN procedure of SAS was used to fit exponential curves for [glucose] during the first 60 min of the GTT to calculate clearance rate (CR), time to reach half maximal concentration ($T_{1/2}$), and time to reach basal level (T_{basal}). Area under the curve (AUC) was calculated using the trapezoidal method and actual concentration values discounted for the mean basal concentration (mean of −15, −10, and 0 min). Data were analyzed as a completely randomized design by ANOVA with the MIXED procedure of SAS using treatment as a fixed factor and cow within treatment as a random factor. Treatment did not affect ($P > 0.10$) peak [glucose] (218 ± 13 mg/dL), nadir [glucose] (46 ± 3 mg/dL), CR_{60} (3.46 ± 0.38%/min), $T_{1/2}$ (21.4 ± 2.0 min), Tbasal (42.1 ± 1.7 min), AUC_{60} (3018 ± 203 mg/dL × min) or AUC_{180} (2782 ± 366 mg/dL × min). The insulin response (peak: 119 ± 21 μIU/mL; AUC_{60}: 2905 ± 534 μIU/mL × min; AUC_{180}: 2657 ± 518 μIU/mL × min) was unaffected ($P > 0.10$) by treatment. The peak (1151 ± 211 μEq/L) and nadir (212 ± 1 μEq/L) [NEFA] were not different ($P > 0.10$) among treatments. Dietary starch content did not affect glucose metabolism in early lactation cows.

Key words: starch, transition cow, glucose tolerance test

M325 Effect of milk feeding level on pre- and post-weaning performance of dairy calves. E. K. Miller-Cushon[1], R. Bergeron[2], K. E. Leslie[3], and T. J. DeVries*[1], *[1]Dept. Animal and Poultry Science, University of Guelph, Kemptville Campus, Kemptville, ON, Canada, [2]Dept. Animal and Poultry Science, University of Guelph, Campus d'Alfred, Alfred, ON, Canada, [3]Dept. Population Medicine, Ontario Veterinary College, University of Guelph, Guelph, ON, Canada.*

There is evidence that milk feeding level influences growth and solid feed intake of calves early in life. The objective of this study was to determine the effects of milk feeding level on intake and growth of calves, particularly once transitioned to a novel diet post milk-weaning. Twenty individually housed Holstein bull calves were randomly assigned at birth to a daily milk allotment, fed via a teat for 6 wk: 1) ad libitum (ADL), or 2) a rate of 5 L/d, in 2 feedings (LIM). Concentrate was provided ad libitum during the milk-feeding stage. Calves were weaned during wk 7 by reducing milk allotment by 15%/d. After milk weaning, all calves were fed a complete pelleted diet ad libitum for 7 wks. Intake was recorded daily and calves were weighed 2x/wk. Data was analyzed using a repeated measures mixed model. During milk-feeding, ADL calves consumed more milk (12.2 L/d vs. 4.9 L/d, SE = 0.8, $P < 0.001$), but LIM calves had greater DMI (0.48 vs. 0.09 kg/d, SE = 0.08, $P < 0.001$). ADL calves had greater ADG than LIM during milk-feeding (1.2 vs. 0.6 kg/d, SE = 0.07, $P < 0.001$); before weaning, ADL calves had greater weights (94.2 vs. 68.2 kg, SE = 4.8, $P < 0.001$). During the 7 d of weaning, LIM calves experienced no growth check, while ADL calves plateaued in weight gain (0.7 vs. −0.03 kg/d, SE = 0.15, $P < 0.001$). Upon transition to solid feed, DMI was similar between all calves (in wk 8, 1.9 kg/d, $P = 0.2$), indicating that differences in early feed intake did not influence later willingness to consume a novel ration. Calves had similar ADG immediately after weaning (in wk 8, 0.7 kg/d, $P = 0.9$) and there was no long-term treatment effect on ADG (post-weaning mean of 1.2 kg/d, $P = 0.9$). Thus, greater body weights for calves previously fed ADL were maintained in the post-weaning period (in wk 14, 143.5 vs. 123.5 kg, SE = 5.5, $P = 0.002$); daily DMI as a % of body weight was less for ADL calves (2.7 vs. 3.3%, SE = 0.2, $P = 0.01$), indicating greater efficiency of growth during that time period. The results indicate that calves fed different milk levels had similar long-term intakes and ADG; however, ADL calves maintained their advantage in body weight during the post-weaning period.

Key words: dairy calf, milk feeding level, growth

M326 Effects of methionine hydroxy copper supplementation on lactation performance, fertility, nutrients digestibility and some metabolic indices in dairy cows. F. Wang[1], S. L. Li*[1], Y. J. Wang[1], X. Jin[1], H. Cao[2], F. C. Guo[2], and Y. M. Wan[2], *[1]State Key Laboratory of Animal Nutrition, College of Animal Science and Technology, China Agricultural University, Beijing, China, [2]Novus International Research Center, Beijing, China.*

The objective of the study was to investigate the effects of chelated copper ((HMTBA)2-Cu; MINTREX Cu Novus International Inc., St. Charles, MO) on lactation and reproductive performance of dairy cow. Thirty lactating Holstein cows were assigned into 3 groups using randomized block design: 1) S: 12 ppm Cu in concentrate provided by CuSO4; 2) SM: 6 ppm Cu provided by CuSO4 plus 6 ppm by (HMTBA)2 Cu; 3) M: 12 ppm Cu provided by (HMTBA)2 Cu, and the level of diet Cu was determined according to NRC (2001) requirement. The trial was completed in 120 d, including 20 d for adaptation. The results showed that the average milk yield and 4% FCM yield of cows in SM were increased significantly compared with those in the S and M($P = 0.08$; $P = 0.06$). Cows fed SM had lower milk lactose compared with S or M fed cows. Reproductive performance showed that the number of follicles and ovarian score of SM and M increased numerically ($P > 0.05$) . ADF apparent digestibility of SM increased compared with S ($P < 0.1$), while the digestibility of NDF increased compared with M ($P < 0.1$). According to the comprehensive analysis of serum at fasting and hours 1, 2, and 4 after first feeding, Significantly decrease was observed for serum Cu concentration of SM ($P < 0.01$) while significantly increase was observed for serum K concentration in SM and M compared with S ($P < 0.05$). It is concluded that feeding 6 ppm chelated Cu plus 6 ppm CuSO4 optimized performance of dairy cows.

Key words: fertility, methionine hydroxy copper, nutrient digestibility

M327 Effects of methionine hydroxy zinc supplementation on lactation performance, fertility, nutrients digestibility and some metabolic indices in dairy cows. F. Wang[1], S. L. Li*[1], H. Cao[2], F. C. Cao[2], and Y. M. Wang[2], *[1]State Key Laboratory of Animal Nutrition, College of Animal Science and Technology, China Agricultural University, Beijing, China, [2]Novus International Research Center, Beijing, China.*

The objective of the study was to investigate the effects of chelated zinc ((HMTBA)2-Zn; MINTREX Zn Novus International, Inc., St. Charles, MO) on lactation and reproductive performance of dairy cow. Thirty lactating Holstein cows were assigned into 3 groups using randomized block design: 1) S: 42 ppm Zn in concentrate provided by ZnSO4; 2) SM: 21 ppm Zn provided by ZnSO4 plus 21 ppm by HMTBA)2 Zn; 3) M: 42 ppm Zn provided by HMTBA)2 Zn, and the level of diet Zn was determined according to NRC (2001) requirement. The trial was completed in 120 d, including 20 d for adaptation. The results showed that milk yields of the 3 groups showed slight downward trends overall and the average milk yield of all cows during the trail was 29.89kg/d. The average milk yield and 4%FCM of S (28.79kg; 29.28kg) were lower than the SM (30.40kg; 32.49kg) and the M (30.49kg; 31.04kg), but no significant difference were found between groups ($P = 0.42$; $P = 0.53$). Cows fed SM had lower milk lactose compared with S or M fed cows ($P = 0.08$). Numerically, the apparent digestibility of organic matter, crude protein, crude fat and acid detergent fiber of S were the lowest The serum alkaline phosphatase and Lactate dehydrogenase contents in M cows were significantly higher than the S and the SM ($P < 0.05$). According to the comprehensive analysis of serum at fasting and hours1, 2, and 4 after first feeding, the serum zinc concentration of S was significantly lower than SM and M group ($P = 0.01$), while K ion content was significantly higher than the SM and M ($P = 0.04$). It is concluded that feeding 42 ppm of chelated zinc optimized the performance and Zn status of dairy cows.

Key words: fertility, methionine hydroxy zinc, nutrient digestibility

M328 Effect of metabolizable protein level on milk production and composition of early lactating Holstein cows. A. Laki, K. Rezayazdi, and M. Dehghan-Banadaky*, *Animal Science Department, Campus of Agricultural and Natural Resources, University of Tehran, Karaj, Tehran, Iran.*

The objective of present study was to investigate the effects of metabolizable protein (MP) levels on milk production and milk composition in early lactating cows. Twenty 4 Holstein cows in early lactation (days

in milk = 30.67) were assigned to 4 diets with different MP levels included: 1) 10.60%, 2) 11.07%, 3) 11.54%, and 4) 12.00% basis of dry matter (DM). MP values for diets were determined by CNCPS software (V 5.2). Experiment lasted in 8 weeks. Cows were milked 3 times a day and milk yield was recorded at each milking times. Milk samples were taken every week. Milk compositions were analyzed by infrared test method. The results of this study showed that fat corrected milk (FCM) yield and protein yield increased as MP level increased until 11.54% (DM) and then decreased ($P < 0.05$). Milk fat percentage and yield not affected by MP level ($P > 0.05$). Milk lactose, solids not fat, total solids percentage and yield were the highest at 11.54% (DM) level (diet 3). Increasing MP level more than 11.54% (DM) did not improve milk composition. Milk urea nitrogen increased linearly as MP level increased. We conclude that nitrogen efficiency decrease linearly as MP level increased and relationship between FCM yield and milk protein yield with MP level is nonlinear.

Table 1. Effects of MP offered to dairy cows in early lactation on milk yield and milk composition

Item	1	2	3	4	SEM
Milk yield (kg/d)	34.78^{b}	35.0^{b}	36.01^{a}	36.44^{a}	0.60
FCM 4% (kg/d)	29.81^{b}	30.28^{ab}	32.2^{a}	31.68^{ab}	0.64
fat%	3.06	3.0	3.29	3.13	0.11
protein%	2.56^{b}	2.79^{a}	2.77^{ab}	2.6^{ab}	0.07
lactose%	4.72^{b}	4.74^{ab}	4.94^{a}	4.71^{b}	0.04
MUN (mg/dl)	15.0^{c}	16.89^{b}	18.54^{a}	19.16^{a}	0.90
fat (kg/d)	1.06	1.08	1.18	1.14	0.04
protein (kg/d)	0.89^{c}	0.97^{ab}	1.0^{a}	0.95^{b}	0.02
lactose (kg/d)	1.64^{c}	1.66^{bc}	1.78^{a}	1.72^{b}	0.02

$^{a–c}$Means within same row with different superscripts differ ($P < 0.05$).

Key words: Holstein cows, metabolizable protein, milk composition

M329 The effect of reducing dietary phosphorus on bone metabolism in lactating dairy cows. L. Puggaard[1], A. Liesegang[2], J. Sehested*[1], and P. Lund[1], *[1]Department of Animal Health and Bioscience, Aarhus University, Tjele, Denmark, [2]Vetsuisse Faculty, University of Zurich, Zurich, Switzerland.*

The effect of dietary phosphorus (P) on P balance and concentration of bone resorption marker carboxyterminal cross-linking telopeptide of Type 1 bone collagen (CTX) and bone formation marker osteocalcin (OC) were investigated in 18 Danish Holstein cows (676 ± 73 kg BW) in the period −6 to 36 weeks relative to calving. However, only data from wk 2, 6 and 12 will be presented here. Cows were blocked by calving date and randomly assigned to one of 3 dietary treatments: Low P (LP), Medium P (MP) or High P (HP) providing 2.2, 2.8 and 3.5 g P/kg DM. A pre-mix LP concentrate was composed of sugar beet pulp, soybean meal, molasses, rapeseed oil, feed salt and urea. The LP ration was composed of (g/kg DM): 461 (premix), 287 (corn silage), 163 (grass silage) and 88 (molasses). MP and HP diets were obtained by adding NaH2PO4 to the LP pre-mix. All diets were fed ad libitum. Individual P balances (difference between P intake and P in milk, feces and urine) were recorded at wk 2, 6 and 12 relative to calving. Milk yield and DMI were recorded over 2 d and corresponding fecal outputs were estimated by grab sampling and feed INDF as marker. Urinary output was estimated from 6 h quantitatively sampling. Blood samples were collected from the tail vein. Concentrations of CTX and OC were determined in serum using commercial available immunoassays. Intake of DM (kg/d) was significantly ($P = 0.0003$; SEM = 1.2) lower in LP (15.4) compared with HP (21.4) and MP (20.3). Milk production was similar among treatments (33.8 kg/d, $P = 0.51$; SEM = 3.0). Concentration of CTX (ng/mL) was significantly ($P = 0.005$; SEM = 1.3) higher in LP (5.4) compared with HP (2.7) and MP (2.9), whereas OC was similar among treatments (58.6 ng/mL, $P = 0.41$; SEM = 12.1). Balance of P (g/d) was significantly ($P = 0.01$; SEM = 5.8) lower in LP (−24.4) compared with HP (−10.2) and tended ($P = 0.06$) to be lower in MP (−19.5) compared with HP. The results suggest that cows were not able to maintain DMI at LP. The results also indicate that plasma CTX reflects P balance, which is influenced by dietary P level in early lactation.

Key words: bone markers, CTX and OC, phosphorus balance

M330 Evaluation of rumen microbial diversity population under influence of a polyclonal antibody preparation against lactate-producing and proteolytic bacteria in cows fed different energy sources. C. Marino*[2], W. Otero[1], C. Barreto[3], V. Pellizari[3], F. Ferreira[1], M. Arrigoni[2], and P. Rodrigues[1], *[1]University of Sao Paulo, FMVZ-USP, Pirassununga, Sao Paulo, Brazil, [2]University of Sao Paulo State, FMVZ-UNESP, Botucatu, Sao Paulo, Brazil, [3]University of Sao Paulo, ICB II-USP, Sao Paulo, Sao Paulo, Brazil.*

Nine ruminally cannulated cows fed different energy sources were used to evaluate an avian-derived polyclonal antibody preparation (PAP) against specific ruminal bacteria *Streptococcus bovis*, *Fusobacterium necrophorum*, *Clostridium aminophilum*, *Peptostreptococcus anaerobius* and *Clostridium sticklandii* and monensin (MON) on rumen protozoa counting. The experimental design was 3 Latin squares 3 × 3 distinguished by the main energy source in the diet [dry-ground corn grain (CG), high moisture corn silage (HMCS) or citrus pulp (CiPu)]. Inside each Latin square, animals received one of the feed additives per period (21 d) [none (CON), MON or PAP]. 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 (DGGE). Data were analyzed by MIXED 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 PDIFF. Differences were declared at $P < 0.05$. An interaction between feed additive and energy source ($P = 0.0423$) was observed for the count of bands that were amplified in DGGE for *Archaea* community. In animals fed HMCS, the number of bands amplified in DGGE for *Archaea* community was greater in CON group (5.67) compared with MON (2.33) and PAP (2.67). 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.

Key words: denaturing gradient gel by electrophoresis, ionophore, microorganism

M331 Effect of poly-unsaturated fatty acid on plasma and milk fatty acid composition in early lactating dairy cows. B. Vlaeminck*[1], M. Hostens[2], E. Colman[1], S. De Campeneere[3], G. Opsomer[2], and V. Fievez[1], *[1]Laboratory for Animal Nutrition and Animal Product Quality, Ghent University, Melle, Belgium, [2]Department of Reproduction, Obstetrics and Herd Health, Ghent University, Merelbeke, Bel-*

gium, [3]Department of Animal Sciences, Institute for Agricultural and Fisheries Research, Melle, Belgium.

Twenty 4 Holstein cows were randomly assigned to 3 groups to evaluate the effect of feeding n-6 (18:2n-6 or 20:4n-6, from 2 weeks before expected calving date to 2 weeks after parturition, period 1 (P1)) followed by n-3 poly-unsaturated fatty acids (FA) (18:3n-3 or 22:6n-3, P2) on plasma and milk FA. FA (140 g/d 18:2n-6 or 18:3n-3 and 22 g/d 20:4n-6 or 22:6n-3) were supplied as plant (soybean oil and extruded linseed; treatment 1) or as marine oils (Vevodar and DHA-gold, treatment 2). In the control treatment, palm prills were used to obtain iso-energetic, isoproteinic and isolipidic diets. Milk parameters were monitored weekly during the first 7 weeks of lactation in milk samples obtained during 4 consecutive milkings per week. Plasma was sampled on day −14, −7, 0, 8, 14, 20, 26, 33, 40 and 46 relative to parturition. Supplementation with 18:2n-6 (P1) did not increase plasma FA proportions (g/100g FA) of 18:2n-6 whereas trans-10–18:1 (0.07 vs. 0.12, $P < 0.01$) and trans-11–18:1 (0.44 vs. 0.73, $P < 0.05$) increased compared with the control. Supplementation with 20:4n-6 (P1) increased its proportion in plasma (3.13 vs. 3.78, $P < 0.05$). In P2, 18:3n-3 supplementation increased 18:3n-3 (5.4 vs. 8.6, $P < 0.001$). Feeding 22:6n-3 increased trans-10–18:1 (0.07 vs. 0.63, $P < 0.001$), trans-11–18:1 (0.40 vs. 1.55, $P < 0.001$) and 22:6n-3 (0.16 vs. 0.87, $P < 0.001$), whereas 18:0 decreased (12.4 vs. 10.1, $P < 0.001$). Changes in plasma FA were largely reflected in milk with an increase in 18:3n-3 (0.36 vs. 0.68, $P < 0.001$) when 18:3n-3 was supplemented. Feeding 22:6n-3 increased trans-10–18:1 (0.57 vs. 2.03, $P < 0.001$), trans-11–18:1 (1.18 vs. 3.24, $P < 0.001$) and 22:6n-3 (0.02 vs. 0.05, $P < 0.001$), whereas 18:0 decreased (12.0 vs. 8.5, $P < 0.001$). The increase in plasma 20:4n-6 in P1 was not reflected in milk whereas 18:2n-6 in milk fat increased (1.52 vs. 1.74, $P < 0.05$) through 18:2n-6 supplementation despite similar proportions in plasma FA. In the current experiment, supplementation of n-3 FA from 2 to 7 weeks in lactation increased their plasma concentration in a form which allows extraction by other tissue as shown by changes in milk FA.

Key words: dairy, fatty acids

M332 Effect of extruded flaxseed or alfalfa protein concentrate in interaction with two levels of concentrate on milk protein and Ca synthesis. C. Hurtaud*[1], G. Chesneau[2], D. Coumier[3], and J. L. Peyraud[1], *[1]INRA-Agrocampus Ouest UMR1080 Production du Lait, Saint-Gilles, France, [2]Valorex, Combourtillé, France, [3]Desialis, Paris, France.*

Feeding extruded flaxseed (FLAX) and alfalfa protein concentrate (APC) to dairy cows increased milk omega-3 content but their effect on other milk components is not known yet. The objective of this study was to compare the effect of FLAX and APC in interaction with the level of concentrate on milk protein composition and Ca content. The corn silage based diets were composed with 30% (C0) or 65% concentrate (C+) and supplemented with FLAX (1 kg.d^{-1}) or APC (2 kg.d^{-1}). The diets supplied the same level of energy, protein and Ca. The trial was carried out according a nested reversed design using 24 dairy cows averaging 117 ± 14 DIM with 2 periods of 14 d. Data were analyzed according a split plot design using proc mixed procedure. The significance threshold was set at $P \leq 0.05$. There was no significant interaction between the sources of omega 3 and the level of concentrate. C+ significantly increased milk yield (+ 3.7 kg), milk protein content (0.16%) and yield (141 g.d^{-1}). C+ largely decreased casein/protein ratio (−2.6% units) and increased total and colloidal Ca (respectively +172 and +148 mg.kg^{-1}). Increase in milk soluble protein might reflect a loss of integrity of mammary epithelium and/or a production of inflammatory proteins (such as haptoglobulin) associated with subacute ruminal acidosis. High level of concentrate could have induced bone mobilization to produce bicarbonate thus making more available Ca for mammary gland. Compared with FLAX, APC tended to decrease milk yield (0.9 kg.d^{-1}, $P = 0.061$), despite no effect on DMI. APC increased both total protein and casein contents without impact on casein/protein ratio and protein yield. It decreased milk urea content. These results suggest that APC might have not changed the total supply of metabolic protein while reducing the supply of ruminal soluble nitrogen. APC decreased soluble Ca content. This result suggests that biodisponibility of Ca is lower for APC than for CaCO3 and minerals. This experiment shows that the source of omega-3 affects milk casein content whereas large increase of concentrate level does not increase milk casein content even though protein content increased.

Key words: concentrate, lipids, milk Ca

M333 Effect of cow variation on the efficiency of nitrogen recycling to the rumen in dairy cattle. M. Aguilar*[1], M. E. Van Amburgh[2], W. A. D. Nayananjalie[1], and M. D. Hanigan[1], *[1]Virginia Polytechnic Institute and State University, Blacksburg, [2]Cornell University, Ithaca, NY.*

Milk urea nitrogen (MUN) and blood urea nitrogen (BUN) are correlated with nitrogen balance and nitrogen excretion. Wood et al. (2003) found that cows in lactations 1, 2, and 3 had a heritability for MUN of 0.44, 0.59, and 0.48, respectively. The genetic components of MUN concentrations may be associated with differences among urea transporters in the kidney and the rumen wall. We hypothesized that on a common diet, MUN concentrations would be inversely correlated with gastrointestinal entry rates (GER) of urea. Eight lactating cows with similar milk production but varying MUN levels were selected for the study. Cows remained on a common diet, and nitrogen balance and urea kinetics (using [^{15}N^{15}N] urea) were assessed during a 4 d period. Urea synthesis (UER), GER, and urinary urea excretion (UUE) were calculated from ^{15}N enrichments (Lobley, 2000). MUN levels ranged from 10.3 – 16.7 mg/dl and averaged 14.91 ± 2.06 mg/dl. Milk yield and body weight averaged 26.34 ± 4.39 and 505.64 ± 61.87 kg, respectively. N intake and fecal N output averaged 0.51 ± 0.06 and 0.49 ± 0.09 kg of DM, respectively. Despite the common diet and similar milk production, UER was variable averaging 21.26 ± 2.61g/h. GER, UUE, and UUE/UER were also variable averaging 13.57 ± 1.98 g/h, 7.69 ± 2.01 g/h, and 0.36 ± 0.08, respectively. UER was positively correlated with GER, but not with N intake due to minimal dietary N variation, indicating GER is a significant determinant of UER. Further, UER was also positively correlated with MUN ($P = 0.03$) indicating MUN variation is driven by UER. MUN was also positively correlated with UUE ($P = 0.1$), but contrary to our hypothesis, MUN was not correlated with GER ($P = 0.42$). GER variation may be driven more by fermentable carbohydrate supply, than by urea concentrations in blood. Thus MUN was driven by UER, and UUE was driven by blood urea concentrations as reflected by MUN. MUN was not an indicator of GER.

Key words: gut entry rate, recycling, urea

M334 Effect of enhanced feeding rates of conventional milk replacer 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], N. Litherland[3], D. Ziegler[4], and H. Chester-Jones[4], *[1]Milk Products, Chilton, WI, [2]Hubbard Feeds Inc.,*

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Holstein heifer calves [n = 100, 2–4 d old, average bodyweight (BW) = 39.9 kg] were used in an experiment to evaluate the effects of enhanced (ENH) feeding rates of conventional milk replacer (MR) on calf growth, starter intake, and health during pre- (d 1–42) and post-weaning (d 43–56) periods. Calves were housed in individual calf pens within a naturally ventilated barn with curtain sidewalls. All calves were fed a 20% CP, 20% fat all-milk MR reconstituted to 15% solids, an 18% CP (as-fed basis) texturized calf starter and free-choice water. Calves were assigned randomly to 1 of 4 treatments: 1) 0.57 kg/d (as-fed MR powder weight) d 1–35 and 0.28 kg/d d 36–42 (CON), 2) 0.68 kg/d d 1–21, 0.45 kg/d d 21–35 and 0.23 kg/d d 36–42 (ENH21), 3) 0.68 kg/d d 1–28, 0.45 kg/d d 28–35 and 0.23 kg/d d 36–42 (ENH28), and 4) 0.68 kg/d d 1–35 and 0.34 kg/d d 36–42 (ENH35). Calf BW on d 56 was greater ($P < 0.05$) for ENH35 (79.2 kg) and ENH28 (78.5 kg) calves compared with CON (75.1 kg), whereas BW of ENH21 (76.6 kg) calves did not differ from CON. Average daily gain from d 1–56 tended to be greater ($P = 0.10$) for ENH35 (0.70 kg/d) than for CON (0.63 kg/d) calves, with ENH21 (0.65 kg/d) and ENH28 (0.69 kg/d) calves having intermediate growth rates. Frame growth from d 1–56 also differed due to treatment; ENH35 (10.5 cm) and ENH28 (9.91 cm) calves had greater ($P < 0.05$) hip height gain than CON (8.81 cm), while ENH21 (9.47 cm) calves had similar changes in frame growth compared with CON. Coinciding with decreased MR intake, calves on the ENH21 treatment had greater ($P < 0.05$) starter intake from d 22–35 compared with ENH35, whereas ENH28 calves consumed more ($P < 0.05$) starter than ENH35 calves from d 29–35. Overall, starter intake from d 1–42 and 1–56 did not differ ($P > 0.10$) among treatment. Total MR intake (as-fed) was 22.6, 22.9, 24.5, and 26.6 kg/calf for CON, ENH21, ENH28, and ENH35, respectively. Health parameters did not differ among treatments. Compared with CON, feeding ENH rates of a conventional MR (0.68 kg/d) for at least 28 d increased d 56 BW and d 1–56 hip height gain without affecting starter intake.

Key words: calves, milk replacer, feeding rate

M335 Form of trace mineral supplementation on complete lactation performance, reproduction, and locomotion in Holstein cows. G. I. Zanton*[1], D. E. Diaz[1], M. Vazquez-Anon[1], and J. E. Nocek[2], *[1]Novus International Inc., St. Charles, MO, [2]Spruce Haven Farm and Research Center, Auburn, NY.*

When formulating to meet the absorbable trace mineral requirements of the cow, the level of trace mineral required in the diet can vary depending on source and form due to differences in bioavailability. The objective of this experiment was to evaluate the effects of feeding the chelated trace mineral, Mintrex (Zn, Cu, and Mn) at a reduced level compared with inorganic trace minerals (ITM) supplied as sulfates on a commercial level, on complete lactation (305 d) performance, reproductive performance, and locomotion in Holstein cows. To accomplish this objective, 216 Holstein cows were housed in 4 pens (2/treatment) for a complete lactation and fed diets containing ITM formulated to supplement Zn, Cu, and Mn at commercial levels or all ITM replaced by Mintrex and formulated to supplement at approximately half commercial levels. Group DMI and individual milk production was monitored daily, milk composition was evaluated monthly, locomotion scores were evaluated at 150 and 300 DIM, and reproduction performance was monitored. Data were analyzed with pen as the experimental unit and treatment differences are considered significant when $P < 0.05$ and trending toward significance when $P < 0.15$. Twenty-six percent of cows were removed from the trial for various reasons, but the number removed ($P > 0.67$), time of removal ($P > 0.95$) and reason for removal ($P > 0.35$) did not differ between treatments. Complete lactation performance did not differ between treatments ($P > 0.60$) with milk yield, fat, and protein percent averaging 36.75 kg, 3.53%, and 3.04%, respectively. Somatic cell count linear score tended to be reduced in cows fed Mintrex (ITM: 3.11, Mintrex: 2.70; $P < 0.11$). Conception at each individual service did not differ between treatment ($P > 0.16$) and days open also did not differ ($P > 0.25$), however ordinal logistic analysis indicated the cows fed Mintrex tended to have greater odds to conceive at earlier services ($P < 0.08$). Locomotion scores did not differ between treatment ($P > 0.24$). In conclusion, cows fed Mintrex at reduced levels with no dietary ITM had similar performance as cows fed higher levels of ITM.

Key words: trace minerals, lactation performance, reproduction

M336 Effect of replacing corn grain and soybean meal with a treated wheat grain on the performance of dairy cows. J. Benninghoff*[1], G. Hamann[2], H. Steingaß[3], F.-J. Romberg[2], K. Landfried[2], and K.-H. Südekum[1], *[1]University of Bonn, Bonn, Germany, [2]DLR Westpfalz, Münchweiler/Alsenz, Germany, [3]University of Hohenheim, Stuttgart, Germany.*

This study evaluated a wheat grain which was treated to reduce ruminal degradation of starch and crude protein. The wheat grain (WeiPass) was treated with xylose in aqueous Ca-Mg lignosulphonate solution at elevated temperatures. Two isocaloric and isonitrogenous diets were formulated with, on dry matter (DM) basis, either 16% corn grain and 6.4% soybean meal (control group, CON) or 17.8% WeiPass and 4.6% soybean meal (wheat group, WHEAT). The DM of both diets contained 30.6% grass silage, 16.4% corn silage, 6.8% grass hay, 16% barley-wheat grain mixture, 6.4% rapeseed meal, and 1.4% mineral and vitamin mixture. Diets were offered as total mixed rations. Thirty-six German Holstein dairy cows were assigned to one of the 2 groups according to parity, body weight after calving, and milk yield during the previous lactation. The DMI and milk production were recorded from 20 d in milk (DIM) to 120 DIM. Blood samples were obtained from each cow 21 d before the expected calving date to 14 DIM at weekly intervals and then every second week until 120 DIM. Response variables were DM intake (DMI), milk production and composition, and blood metabolites. All data were analyzed using a mixed model procedure with treatment, lactation number, calving month, and week of lactation as fixed factors, and cow as random factor. The average of DMI, energy-corrected milk (ECM) yield, and milk fat and protein yields (all given as kg/day) were 18.9, 28.7, 1.25, and 1.02 for CON cows and 19.3, 32.5, 1.36, and 1.11 for WHEAT cows, respectively. Only ECM and milk protein yields were greater ($P < 0.05$) for WHEAT cows, all other variables were similar ($P > 0.10$) for both groups. Blood metabolites indicated that cows in both groups were healthy throughout the trial and no differences were observed between groups. In conclusion, a treated wheat grain could replace corn grain and part of the soybean meal in a diet for lactating dairy cows and overall performance might be slightly improved. Thus, treated wheat grain may be an alternative to corn grain in diets of lactating dairy cows depending on availability and costs of grain sources.

Key words: dairy cow, grain, starch

M337 Comparison of models to predict ruminal methane from milk fatty acids. J. M. Castro-Montoya, V. Fievez, and B. Vlae-

minck*, *Laboratory of Animal Nutrition and Animal Product Quality, Gent University, Gent, Belgium.*

Increased awareness of livestock's contribution to the greenhouse effect enhanced interest in monitoring methane emissions from dairy cattle through models based on milk fatty acids (FA). A first aim of this study was to assess the correlation between these models using a data set from 12 experiments (n = 180), covering a wide range of diets. These FA data allowed to compare 3 models described by Castro-Montoya et al. (2011) with CH_4 proportions (mmol/mol total VFA) predicted from the odd- and branched-chain FA (OBCFA) *iso* C14:0, *iso* C15:0, C15:0, *iso* C16:0 and the sum of C17:0 and *cis*–9 C17:1; Weill et al. (2009) with CH_4 (g/L milk) = Sum FA ≤ C16 × 11.37 × (milk production (kg/year) $^{-0.427}$) (model 1); and Dijkstra et al. (2011) with CH_4 (g/kg DMI) = 25.5 + (0.302 × C18:0) – (10.2 × *cis*–11 C18:1) – (2.5 × *trans*–10+11 C18:1) (model 2). Pearson correlations between CH_4 output from the OBCFA–model and model 1 (r = 0.2) and 2 (r = 0.54) were poor to modest which could be related to differences in units to express methane, inclusion of additional variables (e.g., milk production) and dietary conditions from which models were developed. To overcome the differences in units, multiple linear regression with forward variable selection and 7–fold cross validation was performed to predict CH_4 (mmol/mol total VFA) based on the milk fatty acids retained in each of the models. A random experiment effect was included. The models developed from Dijkstra et al. [CH_4 = 323.3 – (18.8 × *cis*-11 C18:1) – (72.2 × *trans*-10+11 C18:1)] and from OBCFA [CH_4 = 329.9 + (221 × *iso* C14:0) + (116.5 × *iso* C15:0) – (38.9 × C15:0) – (61.9 × *iso* C16:0) – (33 × C17:0 + *cis*-9 C17:1)] performed similarly (Adj R^2 = 0.67; RMSPE = 4%). A third model from regression of the sum of FA ≤ C16 correlated modestly with CH_4 proportions (Adj R^2 = 0.52; RMSPE = 5.0%). Finally, by individually introducing 17 FA ≤ C16, the model CH_4 = 283 + (12.6 × C8:0) + (147.7 × *iso* C14:0) + (104.6 × *iso* C15:0) – (7.6 × C14:1) – (49.9 × C15:0) – (20 × *iso* C16:0) + (0.9 × C16:0) performed similarly to the former two models (Adj R^2 = 0.73; RMSPE = 3.7%). In this last model the predominance of OBCFA worth notice.

Key words: methane, milk fatty acids

M338 Effects of methionine analog supplementation on milk yield and composition of primiparous dairy cows in a Brazilian dairy herd. L. Alegransi[1], V. L. Souza[1], M. C. Doska[1], G. F. Zanetti[1], E. M. Ribas[2], A. Ostrensky[3], and R. Almeida*[1], *[1]Universidade Federal do Paraná, Curitiba, PR, Brazil, [2]Nutron Alimentos, Brazil, [3]Pontifícia Universidade Católica do Paraná, Curitiba, PR, Brazil.*

The objective of this trial was to evaluate the effects of methionine analog supplementation on milk yield and composition in a commercial dairy herd at Paraná State, south of Brazil. Eighty-eight Holsteins and 12 Brown Swiss primiparous cows were paired blocked based on breed, milk yield, and days in milk. The treatment consisted on the daily supplementation of 25 g of methionine hydroxyl analog (MFP, Novus International, Inc., USA). Both groups, with 50 first-lactation cows each, were fed simultaneously twice daily the same basal diet in a TMR, had received bST injections every 10 d and were milked thrice daily. Each group of cows was housed in a side of a free stall and no cow entrance was allowed during the trial. Cows (220 DIM and 31.5 mo) were allocated to a sequence of 2 treatments in a crossover design with 42-d periods, and the response variables were measured on d 40 to 42 of treatment allocation. Twenty-six cows were lost due to dry off, death, and mastitis treatment. Data was analyzed with the GLM of SAS with a model containing the effects of block, cow within block, period, and treatment. The DM, CP and NDF contents of the offered diets were similar between treatments, as well as cow′s body condition score. The estimated nutritional levels of this diet using CPM-Dairy were 45.2%DM, 1.73 Mcal/kg NE_{lac}, 17.6% CP, 34.9% NDF, 19.7% ADF, 21.7% $_{pe}$NDF, 37.8% NFC, 5.2% EE, 0.80% Ca, and 0.43% P. With the MFP® supplementation, the estimated lysine:methionine relationship was 3,10:1 (6,40% Lys and 2,07% Met). Milk yield was 33.3 kg for Control and 34.2 kg for methionine-treated cows (P = 0.19). MFP treated cows produced 53 g more fat yield per day (P = 0.03) than non-treated cows. It was observed a tendency (P < 0.10) of methionine-treated cows produced more 3.5%fat-corrected milk, more energy-corrected yield, 30 g more protein yield, and a higher total solids content. Supplementation with methionine analog did not increase milk yield, but it was shown a tendency of higher milk components on methionine-treated cows.

Key words: amino acids, metabolizable protein, nitrogen balance

M339 Dry matter digestibility of dairy goats diets during pregnancy. A. R. Rivera*, I. A. M. A. Teixeira, C. J. Härter, L. D. Lima, D. S. Castagnino, T. R. Delphino, H. G. O. Silva, T. T. Berchielli, and K. T. Resende, *Universidade Estadual Paulista, Jaboticabal, SP, Brasil.*

Physiological stage influences feed intake and digestibility of nutrients and has been observed that during pregnancy females change their feeding pattern and intake. Many studies have focused on late pregnancy and/or early lactation of cows and ewes, with scarce results evaluating the diet digestibility during the entire pregnancy. Thus the objective of this study was to evaluate the effect of number of fetuses on the diet digestibility of 2 dairy goat breeds during the pregnancy. A total of 12 multiparous goats with average body weight of 52.3 ± 9.56kg were used. At the beginning of pregnancy (d 35 post mating) the goats were distributed into 4 groups, as such: 1-fetus-Saanen (n = 3), 2-fetuses-Saanen (n = 3), 1-fetus-Oberhasli (n = 3) and 2-fetuses-Oberhasli. Four digestibility assays were performed (initiating at 45, 75, 105 and 135 d of pregnancy) with the goats allocated into digestibility cages that allowed total feces collection in a 5-d period. Statistical analyses were performed considering a repeated measure design. A significant interaction between breed and fetuses number (P < 0.05) was observed for apparent dry matter (DM) digestibility. In Saanen goats, DM digestibility with 2-fetuses was significantly lower (70.9 ± 3.21%). than 1-fetus (77.2 ± 1.88%). The significant interaction between days of pregnancy and fetus number (P < 0.05) indicated that the number of fetuses influenced DM digestibility with a linear increase as pregnancy advanced in single pregnant goats. On the other hand, in twin pregnancies the DM digestibility showed a quadratic pattern as pregnancy progressed. These previous results indicates that stage and type of pregnancy have major effects on digestibility which probably is modified to allow better nutrient absorption to meet the extra nutrient demand due to pregnancy. This research is in progress (Fapesp project number 2008/57302–0).

Key words: days of pregnancy, goats, nutrient absorption

M340 Effect of different levels of a mycotoxin deactivating feed additive on Holstein crossbred dairy cows in Southeast Asia fed rations naturally contaminated with mycotoxins. U. Hofstetter*[1], I. Rodrigues[1], and K. Kiyothong[2], *[1]Biomin Holding GmbH, Herzogenburg, Austria, [2]School of Agriculture, Food and Rural Development, University of Newcastle, Newcastle, UK.*

The objectives of this study, carried out in Thailand, were to determine the impact of mycotoxins on lactating dairy cows and to evaluate the effects of different levels of a mycotoxin deactivating product. Twenty-four early lactating multiparous Holstein-Friesian x local dairy cows with an average body weight of 420kg and an average daily milk yield of 13.7kg were allocated according a randomized complete block design (RCBD) with 4 dietary treatments and 6 animals per treatment. The trial consisted of a 2-week adaptation period followed by a 10-week experimental period. Diets were fed as a total mixed ration (TMR). Mycotoxin analyses showed a contamination of 38µg/kg aflatoxin B1, 541µg/kg zearalenone, 720µg/kg deoxynivalenol, 701µg/kg fumonisin B1, 270µg/kg T-2 toxin and 74µg/kg ochratoxin A. The trial groups consisted of the contaminated TMR and contained different levels of the feed additive (groups 1–4 with 0, 15, 30 or 45g/cow/day). Data were subjected to ANOVA procedure for a randomized complete block design experiment using the general linear model (GLM) of the SAS System. Treatment means were compared using Duncan's New Multiple Range test. Total milk yield and milk protein yield were significantly higher ($P < 0.05$) in cows fed rations containing the mycotoxin deactivator. Cows in treatments 2, 3 and 4 produced approximately 2kg more milk than cows fed the unsupplemented ration (see table). Milk from cows in treatment 1, the negative control, contained 0.7µg/kg of AFM1. Milk from cows fed any of the 3 rations containing the feed additive had non-detectable levels of AFM1 . Additionally somatic cell count was significantly lower ($P < 0.05$) in these groups, which is a strong indicator that the immune system of the cows was improved by eliminating the immune suppressing effects of mycotoxins. The results confirm that mycotoxin contaminated rations impair health and performance of lactating dairy cows by affecting somatic cell count and milk production. The trial results also demonstrate that a feed additive can ameliorate these detrimental effects.

Table 1. Milk production and quality

Parameter	Treatment 1 (neg. control)	Treatment 2	Treatment 3	Treatment 4
Milk yield [kg/cow/day]	12.6[a]	14.7[b]	14.7[b]	14.9[b]
Protein [g/kg]	31.0[a]	34.2[b]	34.3[b]	36.1[b]
AFM1 [µg/kg] (detection limit = 0.06 µg/kg)	0.7	nd	nd	nd
Somatic cell count [x 10^3 cell/ml]	547[a]	385[b]	346[c]	346[c]

[a-c]Values within a row with different superscripts differ significantly ($P < 0.05$).

Key words: aflatoxin M1, mycotoxins

M341 Voluntary selection of starter ingredients offered separately to nursing calves. C. Montoro*[1] and A. Bach[1,2], *[1]Ruminant Production, IRTA, Caldes de Montbui, Barcelona, Spain, [2]ICREA, Barcelona, Spain.*

An experiment was conducted to determine whether calves exposed to different ingredients would consume the similar amounts of nutrients to calves offered all ingredients in a single starter. Forty Holstein male calves (initial BW = 41.5 ± 0.9 kg, age = 7 ± 0.5 d) individually housed on wood shavings were randomly assigned to either Control (CTR): a common starter ad libitum composed of ground corn (47.2%), soybean meal (20%), oats (11%), barley (10.1%), soybean hulls (8%) and soybean full fat (1.2%), or Choice (CH): the same 6 ingredients offered in separate buckets to each animal ad libitum. All calves were offered 2 L of milk replacer (MR) at 12.5% DM twice daily in a bucket during the 5 wk of study. Differences between treatments in total daily feed consumption, nutrient consumption (CP, EE, NFC, and NDF), and individual consumption of each ingredient were analyzed using a mixed-effects model with repeated measures that included initial BW as a covariate, dietary treatment, time (day or week of study) and their 2-way interaction as fixed effects, and animal as a random effect. Time entered the model as a repeated measure. No differences were observed between treatments on total DM, NDF, and NFC consumption (Table 1). Contrary, consumptions of CP and EE were greater ($P < 0.01$) in CH animals than in CTR calves. These differences in nutrient intakes were a consequence of a greater ($P < 0.01$) consumption of soybean full fat by CH calves (159 g/wk) and a lesser ($P < 0.01$) consumption of corn (194 g/wk) and oats (12 g/wk) compared with CTR calves (15, 573, and 133 g/wk, respectively). It is concluded that calves showed a marked preference for soybean full fat and rejected carbohydrate-rich ingredients such corn and oats. Further research is needed to determine whether this preference was due to hedonic or metabolic control.

Table 1. Nutrient composition of total solid DM consumed (g/d) as affected by treatment

	DM	CP	EE	FND	NFC
Control	247	44[a]	10[a]	50	159
Choice	261	77[b]	16[b]	61	137

[ab]Values with different superscripts within column differ at $P < 0.05$.

Key words: regulation, nutrient, intake

M342 Duodenal flows and milk yields of odd- and branched-chain fatty acids in response to N underfeeding and energy source in dairy cows. R. Gervais*[1], B. Vlaeminck[2], A. Fanchone[3], P. Nozière[4], M. Doreau[4], and V. Fievez[2], *[1]Département des sciences animales, Université Laval, Québec, Québec, Canada, [2]Lanupro, Ghent University, Melle, Belgium, [3]Unité de Recherches Zootechniques, INRA, Petit Bourg, Guadeloupe, France, [4]Unité de Recherche sur les Herbivores, INRA, Theix, St-Genès-Champanelle, France.*

To assess the effects of a decrease in dietary N supply in dairy cows and its interaction with the nature of energy (E) on the duodenal flows of odd- and branched-chain fatty acids (OBCFA), and secretions in milk, 4 Holstein cows, fitted with rumen, duodenum, and ileal cannulas, were used in a 4 × 4 Latin square design (28-d periods). Treatments were 2 N levels (low and high) combined with 2 E sources rich in starch (S) or fiber (F). The high level of N met 110% of N requirements, with an adequate supply in rumen degradable N, whereas the low level covered 80% of N requirements with a shortage in rumen degradable N. The 4 isoenergetic diets had a forage:concentrate ratio of 60:40. No interaction between level of N and E source was observed for OBCFA duodenal flows, and milk yields. Compared with high N, low N diets reduced the duodenal flows of iso (7.2 vs. 9.4 g/d; $P < 0.01$), and linear odd-chain fatty acids (FA; 7.6 vs. 9.6; $P < 0.01$) and tended to reduce the flow of anteiso FA (8.0 vs. 10.0; $P = 0.06$). Low N diets decreased milk yield of iso FA (7.5 vs. 9.1 g/d; $P < 0.05$) and tended to reduce milk anteiso (7.4 vs. 8.8; $P = 0.09$) and linear odd-chain FA (12.7 vs. 14.5; $P = 0.08$). Compared with S, F diets increased duodenal flow of iso FA (8.9 vs. 7.7 g/d; $P < 0.05$), and tended to increase the flow of linear-odd chain FA (9.3 vs. 7.9; $P = 0.06$). Feeding F diets increased milk iso (9.6 vs. 6.9 g/d; $P < 0.01$) and linear odd-

chain FA (15.2 vs. 12.1; $P < 0.05$), and tended to increase milk anteiso FA (9.0 vs. 7.3 g/d; $P = 0.08$). N supply had no effect on the apparent transfer of duodenal iso, anteiso, and linear odd-chain FA to milk, and no interaction with E source was observed. Compared with F, S diets decreased the apparent transfer of anteiso FA by 25% ($P < 0.05$), and tended to reduce transfer of iso FA (−17%; $P = 0.07$). In conclusion, because the apparent transfer of some OBCFA from the duodenum to milk was affected by treatments, further research is needed to establish which milk OBCFA can be used as robust markers to estimate OBCFA and microbial protein flow at the duodenum and/or which corrections should be applied.

Key words: duodenal flow, milk fatty acids, OBCFA

M343 Effects of a direct-fed microbial and fibrolytic enzyme product on somatic cell counts in milk produced by crossbred dairy cows in the Brazilian Cerrado. R. D. Sainz*[1,2], C. U. Magnabosco[3,4], E. A. Filgueiras[5], R. Guimarães[3], F. M. C. Freitas[4,6], and L. R. Mattos[4,6], *[1]University of California, Davis, [2]Embrapa, Brasilia, DF, Brazil, [3]Embrapa Cerrados, Planaltina, DF. Brazil, [4]Embrapa Arroz e Feijão, Santo Antonio de Goiá, GO, Brazil, [5]Biofórmula, Goiânia, GO, Brazil, [6]Embrapa Gado de Leite, Juiz de Fora, MG, Brazil.*

Two experiments were conducted on commercial dairy farms to test the effect of a product (Bioformula, Goiania, Brazil) containing direct-fed microbial (DFM) and fibrolytic enzymes on milk quality. In Exp. 1, 38 Holstein cows were fed corn silage on an *ad libitum* basis, and received up to 6 kg/d concentrate according to production level. In Exp. 2, 22 Girolando (crossbred Holstein x Gir) cows grazed *Panicum maximum* cv. Mombaça pastures plus corn silage and received up to 5 kg/d concentrate according to production level. In both experiments, cows were blocked by age, parity, stage of lactation and current production level into control and treated groups. Treated group cows received 2 g/d of a product containing live yeast (1 × 109 cfu/g), mannan oligosaccharide (10%), and *Lactobacillus acidophilus*, *Bacillus subtilis*, and *Enterococcus faecium* (2 × 107 total cfu/g), plus cellulose (6 U/g), hemicellulase (10 U/g), and xylanase (3U/g) while controls received 2 g/d of the vehicle alone. Milk composition was monitored weekly for 16 wk. Data were analyzed by ANOVA, with treatment as main effect and initial composition as the covariate. Somatic cell counts were log-transformed to overcome non-normality, but back-transformed data are presented here. There were no differences in milk production, or in the percentages of fat, protein, lactose, and non-fat solids, nor in total bacterial count, throughout both experiments ($P > 0.10$). In Exp 1 SCC in milk increased ($P < 0.05$) over time in both experiments, from 247,172 to 606,736 (controls) or 260,016 (treated). In Exp. 2 it increased ($P < 0.05$) from 117,490 to 584,490 (controls) or 270,396 (treated). In both experiments, SCC were similar ($P > 0.10$) for the first 8 weeks, then diverged. These results suggest that DFM may enhance immune function and improve milk quality in crossbred dairy cows under tropical conditions.

Key words: direct-fed microbials, somatic cell counts, tropics

M344 Effects of abomasal dosing of ferrous lactate in lactating dairy cows. O. N. Genther*, J. A. Zyskowski, T. H. Herdt, and D. K. Beede, *Michigan State University, East Lansing.*

We hypothesize that the majority of Fe naturally occurring in drinking water is in the ferrous (Fe^{2+}) state, and if present in great enough concentrations, could negatively affect Fe status and potentially cause toxicity. Our objective was to evaluate the short-term effects of abomasally infused ferrous lactate on Fe status of mid-lactation dairy cows given amounts to simulate total daily Fe intake from high-Fe drinking water. Six mid-lactation Holstein cows were assigned in a replicated 3 × 3 Latin Square balanced for treatment sequences. There were 7 d between experimental periods. Treatments were: 1) 0 mg Fe; 2) 0.75 mg of Fe from ferrous lactate per kg BW; and, 3) 1.5 mg of Fe from ferrous lactate per kg BW. Treatments were calculated to approximate 0, 4.5 and 9 ppm Fe concentrations in drinking water, respectively. All treatments were iso-lactate. Treatments were dosed in ~1 min directly into the abomasum via the ruminal fistula in 1 L of deionized water to avoid any potential ruminal impacts on Fe valence. Blood samples were taken hourly before dosing via jugular catheter for 6 h, and post-dosing hourly for 12 h. Liver biopsies were taken at 0 (before dosing), 18 and 36 h of each period. Mean of the pre-dosing blood samples was used as a covariate for each dependent variable in statistical analysis. There were no treatment by time interactions ($P > 0.10$) for serum Fe, unsaturated iron-binding capacity (UIBC), total iron-binding capacity (TIBC), percent Fe saturation, α-tocopherol, and Cu concentrations, as well as for liver Fe, Cu and Zn. There was no main effect of treatment on any response variables. There was an effect of hour pooled across treatments on serum Fe ($P = 0.022$), UIBC ($P = 0.012$), percent Fe saturation ($P < 0.0001$); and, for liver Cu ($P = 0.023$) and Zn concentrations ($P = 0.022$). There was a treatment by time interaction for serum Zn concentration ($P = 0.055$) and a tendency for liver Cu concentration ($P = 0.155$). Results indicate that infusion of ferrous Fe at rates used in this study do not have major impacts on short-term Fe status of lactating dairy cows.

Key words: iron, lactating dairy cows, iron status

M345 Glycerin as a replacement for corn in dairy Holstein cows diets. J. B. D. Sancanari*[1,2], J. M. B. Ezequiel[1], E. H. C. B. van Cleef[1,2], V. R. Fávaro[1], A. P. D'Áurea[1,2], A. C. Homem[1], Z. F. Silva[1], D. A. V. Silva[1,2], and J. W. Cattelan[1], *[1]São Paulo State University, Jaboticabal, São Paulo, Brazil, [2]FAPESP, São Paulo, São Paulo, Brazil.*

Six multiparous dairy Holstein cows cannulated in the rumen, after the peak of lactation, were used to evaluate the effect of inclusion of glycerin, originated from the biodiesel production, replacing the dietary corn on milk production (MP), milk composition and DMI. Cows were housed at individual tie-stall barn and fed with 3 isoenergetic and isonitrogenous diets containing 0 (G0), 15 (G15) and 30% (G30) of crude glycerin in diets dry matter. The experiment was a double 3 × 3 Latin Square, where each period lasted 23 d. Milk samples were obtained from 2 milking on the 18th and 19th d of each period. The MP obtained were 17.1, 16.4, and 18.9 kg/d ($P > 0.05$) for G0, G15, and G30, respectively. DMI was depressed ($P < 0.05$) in the G30 without affecting the MP, resulting in increased feed efficiency ($P < 0.05$). Cows fed with G0 and G15, respectively, the DMI showed 17.1 and 13.8% higher than G30. This effect could be attributed to the high salt content (6%, which 99% were NaCl) present in glycerin. Furthermore, it was observed that the milk urea nitrogen (MUN) was influenced ($P < 0.05$) by treatments, being 31% higher in G15 compared with G30, indicating greater efficiency of utilization of dietary protein on the G30. The concentrations of milk fat were 3.2, 3.3, and 3.2%, respectively, for G0, G15, and G30 ($P > 0.05$). Lactose obtained in G15 (4.7%) were 4% higher ($P < 0.05$) than the other treatments (4.5%). The crude protein of milk was 15.6 and 12.9% higher ($P < 0.05$) in G0 (3.2%) and G15 (3.1%), respectively, than in G30 (2.7%). This reduction can be caused by NFC deficiency in the diets and decrease in digestibility due to the high ratio NDF/NFC caused by replacement

of corn (main source of NFC in the diet) by glycerin. Possible deficiencies of essential amino acids, particularly methionine and lysine in duodenal digesta, must also be taken into account. It was concluded that the inclusion of 30% of glycerin in the diet improves feed efficiency, but may alter some components of milk. Further studies are needed to elucidate this mechanism.

Key words: biodiesel, co-products, milk composition

M346 Rolled barley grain treated with lactic acid and heat altered postprandial rumen mineral availability in lactating dairy cows. U. Farooq*, A. Mazzolari, S. M. Dunn, and B. N. Ametaj, *University of Alberta, Edmonton, Alberta, Canada.*

Presence of phytic acid (PA) in the grain kernels is associated with decreased bioavailability of phosphorus (P), calcium (Ca), and magnesium (Mg) as well as increased P loss in feces of dairy cow. Treating grain with lactic acid and heat might increase bioavailability of those minerals. Therefore, the objective of this investigation was to evaluate rumen mineral bioavailability in cows fed rolled barley grain steeped in lactic acid (LA) and treated with heat. Eight clinically healthy, rumen-fistulated primiparous Holstein cows (153 - 179 DIM) were assigned to a paired 2 × 2 crossover design. Each period consisted of 11 d of adaptation and 10 d of measurements. All cows were fed once daily a TMR containing rolled barley grain (31.5% in DM) steeped for 48 h in equal quantity of tap water (CTR) or in 1.0% LA and heat at 55°C (LAH). Rumen fluid samples were taken on the last day of the experimental period (d 21) at 0, 2, 4, 6, 8, 10, and 12 h after the morning feeding. Samples were analyzed by atomic absorption spectrometry for Ca, Mg, sodium (Na), and potassium (K) and a modified colorimetric method for inorganic P (P*i*). Statistical analyses were performed by JMP using the GLM procedure. Because there was a carryover effect only results from the 1st period were considered. Overall data showed that concentrations of P*i* ($P < 0.05$; CTR, 278.5; LAH, 231.1 mg/L), Ca ($P < 0.01$; CTR, 87.35; LAH, 64.55 mg/L), and Mg ($P < 0.01$; CTR, 98.13; LAH, 75.52 mg/L) in the ruminal fluid were lower in LAH cows versus CTR group. Furthermore, concentration of Na in the ruminal fluid was greater ($P < 0.01$; CTR, 80.15; LAH, 90.09 Meq/L) in LAH cows, whereas no changes in the concentration of K were observed among the 2 groups. Postprandial time influenced ($P < 0.01$) concentrations of all ruminal minerals, except for P*i*. In conclusion, results of this study indicated that treating rolled barley grain with LA and heat increased the bioavailability of P*i*, Ca, and Mg and has the potential to be used by dairy industry to lower mineral supplementation and environmental pollution.

Key words: barley grain, lactic acid and heat, rumen minerals

M347 Phosphorus feeding for second lactation dairy 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 - Health Sciences Center, New Orleans.*

The objective of this experiment was to evaluate the effect of dietary P on production performance of 28 s lactation cows. Cows were fed either 0.38% or 0.42% ± 0.01% P (DM basis; averages ± standard deviation) from 3 to 45 DIM (treatment period). Both groups of cows were fed 0.42% ± 0.01% P thereafter until the end of the experiment at 110 DIM (carry-over period). Both treatment diets contained 16.5% ± 0.52% CP, and 0.80% ± 0.12% Ca. Pregnant cows were brought to the barn at least 21 d before expected calving. Cows were housed in a free-stall barn fit with electronic gates. Close-up TMR containing 0.28% ± 0.05% Ca and 0.34% ± 0.03% P (DM basis) was fed until 2 d after calving date. Treatments were randomly assigned to cows before their first lactation, when these cows were subjected to similar treatments. Intake and milk yield were recorded daily. Weekly averages during treatment period (wk 3 to 6) and carry-over period (wk 7 to 15) were analyzed as repeated measurements using the Mixed procedure (SAS, version 9.2). Cows fed diet containing 0.42% P tended ($P = 0.09$) to eat more than those fed 0.38% diet during the treatment period but intake was similar ($P = 0.86$) during carry-over period. Milk yield was not significantly ($P = 0.12$) different throughout the experiment, although cows fed 0.42% P produced 3.5 kg more than those in the treatment containing 0.38% P. Following a similar pattern from their first lactation, the 2 groups of cows peaked in milk production 2 weeks apart, on wk 4 and 6, respectively for treatments 0.42% P and 0.38% P. Percentages of milk components were similar ($P \geq 0.16$) between the 2 treatments. Milk fat and protein percentages averaged 3.42% and 2.83%, respectively. Performance of second lactation cows was not significantly different between the 2 levels of P fed during this trial.

Key words: phosphorus, dairy cow, second lactation

M348 Biochemical blood parameters of dairy cows fed with increasing concentration of glycerin. J. B. D. Sancanari*[1,2], J. M. B. Ezequiel[1], E. H. C. B. van Cleef[1,2], V. R. Fávaro[1], A. P. D'Áurea[1,2], A. C. Homem[1], Z. F. Silva[1], D. A. V. Silva[1,2], and J. W. Cattelan[1], *[1]São Paulo State University, Jaboticabal, São Paulo, Brazil, [2]FAPESP, São Paulo, São Paulo, Brazil.*

Blood parameters have been used to assess the health status of animals. The blood biochemical composition reflects the balance between the inflow, the discharge and the metabolism of nutrients in animal tissue. Six multiparous Holstein cows cannulated in the rumen, after the peak of lactation were used in this trial. The animals were distributed in a double 3 × 3 Latin Square to evaluate the effect of inclusion of 0 (G0), 15 (G15), and 30% (G30) of crude glycerin in the diet dry matter (replacing corn) on the blood biochemical parameters. The cows were fed 3 isoenergetic and isonitrogenous diets twice daily. Blood samples were taken on 23 d of each period, by puncturing the coccygeal vein 3 h after the morning milking. There was no effect ($P > 0.05$) on the liver enzymes alanine aminotransferase (ALT), aspartate aminotransferase (AST) and alkaline phosphatase (ALP), with average values of 34.6, 65.6 and 142.7 U/mL, respectively, however, the enzyme gamma-glutamyltransferase (GGT) was changed ($P < 0.05$). GGT concentrations obtained for G0, G15 and G30 were 40.7, 34.4 and 46.8 U/mL, with a superiority of 14.7 and 35.5% in G30 ($P < 0.05$) compared with G0 and G15, respectively. Thus, this can indicate that possible liver changes may have occurred, however, the animals did not showed clinical symptoms of intoxication, probably due to short supplementation period. There were no differences ($P > 0.05$) on plasma concentrations of total protein (TP), albumin (ALB), urea (U), creatinine (CREA), glucose (GLUC), triglycerides (TG) and cholesterol (COL) suggesting no effects on protein and energy metabolism. The average values were 8.4 and 2.1 g/dL, 24.5, 1.2, 70.4, 13.1 and 71.1 mg/dL, respectively, for TP, ALB, U, CREA, GLUC, TG and COL. Further studies are needed to evaluate the effect of inclusion of glycerin in the diet on the metabolism of dairy cows, with particular attention to the supplement for longer periods.

Key words: biodiesel, blood, ruminants

M349 Treating barely grain with lactic acid and heat modulated pre-prandial rumen calcium and magnesium availability in lactating dairy cows. U. Farooq*, A. Mazzolari, S. M. Dunn, and B. N. Ametaj, *University of Alberta, Edmonton, AB, Canada.*

Phytic acid (PA), present in grain kernels, is able to bind minerals and lower their availability to the host, especially those of calcium (Ca) and magnesium (Mg). Treating barley grains with lactic acid and heat might increase rumen degradation of PA, consequently increase availability of Ca and Mg in the rumen fluid. Therefore, this study sought to evaluate rumen availability of selected minerals in lactating dairy cows fed rolled barley grain steeped in lactic acid (LA) and treated with heat. Eight, rumen-fistulated primiparous Holstein cows (153 - 179 DIM) were assigned to a paired 2 × 2 crossover design. Each period consisted of 11 d of adaptation and 10 d of measurements. All cows were fed once daily a TMR containing barley silage (40% DM basis) and rolled barley grain (31.5% DM basis) steeped for 48 h in equal quantity of tap water (CTR) or in 1.0% LA and heat at 55°C (LAH). Rumen fluid samples were taken on d 1, 3, 5, and 7 before morning feeding. Samples were analyzed by atomic absorption spectrometry for Ca, Mg, sodium (Na), and potassium (K) and a modified colorimetric method for inorganic phosphorous (P*i*). Statistical analyses were performed by JMP using the GLM procedure. Results of this study demonstrated that concentrations of Ca ($P < 0.01$; CTR, 39.21; LAH, 24.91 mg/L), and Mg ($P < 0.05$; CTR, 15.21; LAH, 8.02 mg/L) in the ruminal fluid were lower in LAH cows versus the CTR group. Moreover, there was an interaction between treatment and day of sampling for Ca ($P < 0.05$), Mg ($P < 0.01$), and Na ($P < 0.01$). Furthermore, day of sampling effected ($P < 0.01$) concentrations of all minerals, whereas no changes in the concentrations of P*i*, Na, and K were observed among the 2 groups. Overall, treating rolled barley grain with LA and heat improved the bioavailability of Ca and Mg and has the potential to be used by dairy industry to lower mineral supplementation and pollution of the environment.

Key words: barley grain, lactic acid and heat, rumen minerals

M350 Performance variables of dairy cattle fed a commercial micronutrient supplement during the peripartum period. N. Barkley*, A. Kenny, E. Adkins, X. Revelo, and M. Waldron, *University of Missouri, Columbia.*

A time course study was completed to determine the effects of feeding the nutritional supplement OmniGen AF on dry matter intake (DMI), body condition score (BCS), body weight, milk yield, feed to milk conversion efficiency, milk composition [fat, protein, solids–not–fat (SNF), milk urea nitrogen (MUN), 4.0% fat-corrected milk (FCM), somatic cell score (SCS)], plasma concentrations of the metabolites glucose, nonesterified fatty acids (NEFA) and β–hydroxybutyrate (BHBA) in peripartum dairy cattle. Twenty multiparous Holstein cows were fed diets formulated to meet or exceed NRC recommendations for the appropriate physiologic state. Cows were randomly assigned to one of 2 treatment groups (control 56g/cow/day soybean hulls; n = 12 or supplemented 56g/cow/day OmniGen AF; n = 8) balanced for mature equivalent 305-d milk production. Treatment was issued with 225g of sweet feed as a top dressing from d –46 ± 1 through d +31 relative to calving. Feed issue and refusal weights were collected daily to determine DMI. Average BCS (assessed by 2 independent evaluators) and body weights were collected weekly. Blood was sampled on d –47 ± 1, –30 ± 1, –20 ± 1, –11 ± 1, 1, 7, 14 and 30 relative to parturition for plasma glucose, NEFA, and BHBA analysis. Milk yield was recorded daily and milk composition samples were collected during 2 consecutive milkings weekly. All performance variables were analyzed in SAS using mixed model ANOVA procedures with repeated measures. Pretreatment covariates were utilized for BCS, body weight, and all plasma metabolites. No treatment differences or treatment by time interactions were observed for DMI, BCS, body weight, milk yield, feed to milk conversion efficiency, milk composition and plasma metabolites glucose, NEFA and BHBA ($P > 0.10$). Feeding OmniGen AF as a micronutrient supplement during the peripartum period had no statistical effect on the performance variables examined within this study.

Key words: OmniGen AF, micronutrient, dairy

M351 Effect of whole versus chopped sugar cane on dry matter intake in dry dairy cows. J. E. Pérez-De La Ossa[1] and R. P. Lana*[1,2], *[1]Univesidade Federal de Viçosa, MG, Brazil, [2]CNPq and INCT-CA, Brasília, DF, Brazil and Viçosa, MG, Brazil.*

The objective was to evaluate the possibility of use non processed sugarcane in the diet of dry dairy cows. Four crossbred Holstein-Gyr cows with 450 ± 10 kg body weight were used to evaluate the effect of whole vs. chopped sugar cane on intake in dry dairy cows. The animals were housed in individual stalls (24 m^2) with free access to water. Diets consisted in either chopped or whole ad libitum sugarcane plus low intake supplement (400 g/cow/day) containing 25% urea, 25% mineral salt and 50% of a mix of corn meal and soybean meal as nitrogen source. Cows were randomly allocated to a crossover design with 2 animals per treatment in 2 periods of 20 d. In the second period, the treatments changed between the animals, totalizing 4 replicates per treatment or 8 experimental units. Each period consisted of 10 d for adaptation and 10 d for data collection. The experiment was analyzed as a complete randomized design. There was no effect ($P > 0.10$) of sugar cane processing on intake, with values of 22.8 versus 25.5 kg as fed/cow/day for whole and chopped sugarcane, respectively, or 5.24 versus 5.86 kg dry matter/cow/day. Therefore, sugarcane can be fed in a whole form to dry dairy cattle. Feeding whole sugarcane may help to reduce feed costs by reducing machinery use and labor. Also, without processing, the sugarcane decreases losses by fermentation and increases life time of conservation in the feedbunk.

Key words: dry cows, feed, sugarcane

M352 On-farm dry matter testing to improve feed delivery precision on dairy farms. K. R. French* and R. A. Kohn, *University of Maryland, College Park.*

Silage comprises a major portion of total mixed rations (TMR) in most dairy operations. The content of the TMR that is offered to the animals differs from the intended ration. The uncertainty of rations may affect feed efficiency, and consequently milk production, feed expenses, and environmental losses. When silage is measured by weight, unaccounted for changes in silage dry matter (DM) content may substantially change a fed ration. The objective of this study was to measure variation in silage DM on selected dairy farms and determine the potential usefulness of an electronic method of on-farm DM analysis. A field survey of 31 Maryland dairy producers obtained data about on-farm DM analysis frequency, DM analysis methods, ration analysis frequency, feeding regimen, milk production, and number of cows. Of those surveyed, 83% reported testing forage DM more than once per year by any method, and 63% reported testing DM by an on-farm method; mean number of cows was 103, and mean reported RHA was 22,100 lbs. Eight surveyed producers volunteered to collect

on-farm DM data for 21 d. Producers performed daily DM analysis using a Farmex 1210 electronic silage tester, recorded observations on rain events, and recorded ration changes related to the daily DM analysis. Silage samples corresponding to the on-farm DM analyses were retained, and were analyzed for DM after drying at 55°C followed by 100°C (as standard method) and electronic tester (in-lab). There were large differences among farms in how well different methods of DM analysis compared. The difference between on-farm DM (electronic) and standard DM had a mean of 1.82% and SD of 4.99%. Ninety-five percent of observations fell within the limits of agreement (1.96 x SD ± mean) of −7.97 and 11.60%. The electronic method did not compare well to laboratory DM analysis for most farms.

Key words: dry matter, silage, total mixed ration

M353 Effects of the source and amount of sulfur in prepartum diets on plasma metabolites of periparturient Holstein cows. E. Manidari, H. Amanlou, M. Frozanmehr, H. Mirzaei Alamouti*, and M. Shahir, *Department of Animal Science, University of Zanjan, Iran.*

The objective of this study was to determine the effects of concentration and source of sulfur in close-up diets on plasma metabolites in periparturient period. 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. Blood metabolites were measured at −21, 1 and 21 d relative to calving. 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. 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). The Diet 2 significantly decreased plasma concentration of calcium, cupper, albumin, glucose; although increased urea, bilirubin, β-hydroxybutyrate, aspartate aminotransferase, creatin phosphokinase in periparturient period. The Diet 2 also significantly increased phosphorus, total protein and nonesterified fatty acids concentration of plasma in prepartum period. In summary, increasing sulfur concentration (0.41% of DM) using magnesium sulfate in close-up diets compared with other diets used in this study compromised metabolism of periparturient cows.

Key words: Holstein cows, prepartum diet, sulfur

M354 Intake, digestibility and metabolism of nitrogen compounds of dairy cows fed with different urea levels in diets based on sugar cane. A. M. F. Santiago*[1], J. M. de S. Campos[2], A. S. Oliveira[3], S. A. Santos[4], and S. M. Souza[4], *[1]Instituto Federal de Tecnologia, Rio Pomba, MG, Brazil, [2]Universidade Federal de Pernambuco, Guaranhus, PE, Brazil, [3]Universidade Federal de Mato Grosso, Sinop, MT, Brazil, [4]Universidade Federal de Viçosa, Viçosa, MG, Brazil.*

Twelve multiparous Holstein cows (12.6 ± 0.5 kg/d of yield milk, 225 ± 90 DIM and 589 ± 53 kg BW) were distributed in 3 4x4 Latin squares by DIM, with 4 periods of 18 d to evaluate the effect of 4 levels of the mixture urea:ammonium sulfate (9:1) (urea) in diet (0, 1, 2 and 3% of DM) on intake, digestibility and metabolism of N. Diets TMR were isonitrogen (11.8% of CP), containing 74.7% of DM sugar cane (*Saccharum officinarum*, L., RB 73–9735, 21.9o Brix, 28.3% of DM, 2.6% of CP, 42.2% of aNDFom and 50.5% of NFC.). Fecal samples were collected once daily at 1000, 1200, 1400, 1600 e 1800 h, of 12 to 16 d of each period. Indigestible NDF (after 264 h of ruminal incubation) was used to estimate fecal. Milk samples were collected on 14 and 15 d of each period at am and pm milking. Spot urine samples were obtained approximately 4 h postfeeding on 13 d of each period. Urine volume was estimated using creatinine concentration as marker. Data were analyzed using model mixed (PROC MIXED, SAS Inst. Inc., Cary, NC). The urea inclusion increased NNP diet (10.8, 31.6, 51.7 and 69.4% of N). DM (14.1 kg/d), CP (1.6 kg/d), aNDFom (4.8 kg/d) and NFC (7.8 kg/d) intakes were not affected by urea ($P > 0.05$). DM (72.1%), OM (73.3%), CP (80.0%), NDF (44.1%) and NFC (92.2%) digestibility of diets were not affected by urea ($P > 0.05$). The urea used (0% vs. 1 + 2 + 3% of DM) increased ($P < 0.05$) blood urea-N (7.76 vs. 13.15 mg/dL), urinary N-urea (46.7 vs. 98.8 g/d), urinary N (37.8 vs. 53.0% of N intake) and urinary N/yield milk (7.7 vs. 11.2 g of N/kg of milk). However, the urea level (1 at 3% of DM) did not affect ($P > 0.05$) N excretion and efficiency of N utilization for milk production. Although of linear increase ($P < 0.05$) of blood urea-N with urea level from 1 to 3% of DM, the maximum observed (14.31 mg/dL) was below the recommended borderline maximum by NRC (2001) of 20 mg/dL. In diets based on sugar cane with higher NFC, the increased of urea level of 1 to 3% of DM can be used in dairy cows with production below 15 kg/day, without affecting intake, digestibility and efficiency of N diet.

Key words: nitrogen non-protein

M355 Effects of barley grain processing on milk yield and composition of early lactating Holstein cows. H. Amanlou, H. Mirzaei Alamouti*, and A. Aslani, *Department of Animal Science, University of Zanjan, Iran.*

To determine the effects of barley grain processing on milk yield and composition, 12 multiparous Holstein dairy cow; body weight, 560 ± 48.5 kg and days in milk, 31 ± 11.9, were used in an incomplete block design with 4 diets, 3 periods, 4 blocks and 3 cows per block. The diets were different in size of ground barley grain. 1) coarse size with 92.2% processing index (PI), volume weight of barley after processing as a percentage of whole barley, 2) medium size with 76% PI, floury size with 73% PI, and floury and extruded with 54% PI. Cows were individually fed diets containing 70% concentrate and 30% alfalfa hay during 63 d (21 d in each period). Daily milk yield and composition and periodically blood metabolites were determined. Apparent nutrients digestibility of the diets were determined. Data were analyzed using the MIXED procedure of SAS. Dry matter intake, milk yield and composition, and blood metabolites were not different between diets. Extruded barley grain increased ($P < 0.05$) the apparent dry matter digestibility, neutral detergent fiber and non-fiber carbohydrates. Cows fed the extruded barley grain had higher ($P < 0.05$) feed efficiency. Effective rumen degradability of organic matter and protein were increased ($P < 0.05$) by extruding of barley grain. In general, this study showed that although different size of grounded barley grain did not influence milk production and composition, extruding of barley grain can increase the total digestible nutrients.

Key words: barley grain, cows, feed processing

M356 Fate of phosphorus in large intestine of dairy heifers. P. P. Ray*, M. D. Hanigan, and K. F. Knowlton, *Virginia Polytechnic Institute and State University, Blacksburg.*

The objective was to investigate the disappearance of phosphorus (P) from the large intestine of dairy heifers. Uncertainty about the availability of P in different feeds may limit implementation of dietary strategies to reduce fecal P excretion by dairy cows. Derivation of intestinal P digestion and total tract P absorption data are limited by our lack of knowledge of the dynamics of P digestion and absorption in the large intestine. Data on the fate of organic P flowing to the large intestine are especially scarce. Eight ruminally and ileally cannulated Holstein heifers were used in two 4 × 4 Latin squares with 9 d periods including 3 d of washout. All heifers were fed a high forage diet containing 0.14% total P. Ytterbium-labeled corn silage and Co–EDTA were dosed daily as particulate and liquid phase markers, respectively, to measure ileal digesta flow. Markers were mixed with rumen digesta 4 times daily throughout the study. On d 1 to 4 of each period heifers were infused ileally with 0, 5, 15, and 25 g/d of phytate-P solution (0, 1.41, 4.22, and 7.04 g/d P, respectively). Total fecal collection was conducted during the 4 d infusion. When infusion ceased (d 5 and 6) ileal digesta was sampled to measure P flow to the ileum from the basal diet. Feces and digesta samples were dried and ground, digested (nitric-perchloric), and analyzed for total P with the molybdovanadate yellow method. The effect of phytate infusion on fecal P excretion was evaluated using solution statements in Proc Mixed, with basal ileal P flow as a covariate. Fecal excretion of total P increased with increasing phytate P infused ($P \leq 0.0001$). The slope coefficient for infused phytate P to feces was 1.09 ± 0.21 indicating complete P transfer to feces. In contrast, the slope coefficient for the flow of ileal P (from the basal diet) to feces was 0.22 ± 0.24 indicating net absorption from the large intestine. Thus the form of P (e.g., phytate, inorganic, microbial) entering the large intestine may affect absorption from that segment. These data will support mechanistic modeling efforts to improve prediction of P digestion allowing more accurate estimation of P bioavailability in feeds.

Key words: heifer, large intestine, phosphorus

M357 Peripheral blood leukocyte population dynamics during the peripartum period in dairy cattle fed a commercial micronutrient supplement. A. Kenny*, N. Barkley, X. Revelo, and M. Waldron, *University of Missouri, Columbia.*

A time course study was conducted to determine the effects of a dietary micronutrient supplement on blood leukocyte populations in peripartum dairy cows. Twenty Holstein cows were offered diets formulated to meet or exceed NRC recommendations and randomly assigned to one of 2 treatment groups from d –46 ± 1 through d 31 relative to calving: Control (56g/cow/day soybean hulls; n = 12) or Supplemented (56 g/cow/day OmniGen-AF; n = 8). Blood was sampled on d –47 ± 1, –30 ± 1, –20 ± 1, –11 ± 1, 1, 7, 14 and 30 relative to parturition. Leukocytes were isolated and incubated with monoclonal antibodies that identified cells positive for CD4, CD8α, CD14, CD21 or TcR1-N12 markers which represented helper T cells, cytotoxic T cells, monocytes, B cells and γδ T cells, respectively. The percentage of leukocytes positive for these markers was determined by flow cytometry and analyzed using SAS by mixed model ANOVA with repeated measures. A treatment by time interaction was detected with lower percentages of γδ T cells observed in supplemented cows on d –47 and 1 ($P < 0.05$). The proportion of γδ T cells on d –47 was greater ($P < 0.05$) and on d 1 was less ($P < 0.05$) than most time points. A decrease ($P < 0.05$) in the percentage of lymphocytes and an increase ($P < 0.05$) in the percentage of neutrophils was also observed on d 1 compared with most time points. The percentage of cytotoxic T cells on d 1 and 7 decreased ($P < 0.05$) compared with d –30, –11 and 30. The proportion of B cells was greater ($P < 0.05$) during all prepartum samples than all postpartum samples, and was greater ($P < 0.05$) in supplemented cows on d 30. The percentage of helper T cells was greater ($P < 0.05$) on d –47, –20 and 30 than on d –1 and 14. However, the percentage of monocytes on d –47 and –30 was less ($P < 0.05$) than all other time points. The percentage of monocytes was decreased ($P < 0.05$) in supplemented cows on d –30. OmniGen-AF had minimal effects on the blood leukocyte populations of peripartum dairy cattle. However, changes in the proportion of each cell type over time were observed, especially on the day after parturition.

Key words: OmniGen-AF, leukocyte, dairy

M358 Peripheral blood leukocyte population dynamics in peripartum dairy cattle managed under different dry period nutritional strategies. A. Kenny*, N. Barkley, X. Revelo, and M. Waldron, *University of Missouri, Columbia.*

A time course study was conducted to determine changes in blood leukocyte populations in peripartum dairy cows managed under a one– or 2–group dry period nutritional strategy. Twenty-three Holstein cows were randomly assigned to receive a single diet from d –51 ± 2 to parturition (OG; n = 12) or a far–off diet from d –51 ± 2 to d –28 ± 2 and a close–up diet from d –28 ± 2 to parturition (TG; n = 11). The NE_L of the OG diet was 1.43 Mcal/kg and the NE_L for the far–off and close–up diets of TG was 1.21 and 1.32 Mcal/kg, respectively. Blood was sampled on Days –51 ± 2, –29 ± 1, –18 ± 1, –8 ± 1, 1 and 7 relative to parturition. Leukocytes were isolated and incubated with monoclonal antibodies that identified cells positive for CD4, CD8α, CD14, CD21 or TcR1-N12 markers which represented helper T cells, cytotoxic T cells, monocytes, B cells and γδ T cells, respectively. The percentage of leukocytes positive for these markers was determined by flow cytometry and analyzed using SAS by mixed model ANOVA with repeated measures. A treatment by time interaction ($P < 0.05$) was observed in B cells and cytotoxic T cells. The proportion of B cells on d –18 and –8 was greater ($P < 0.05$) in the TG treatment group, and on d 7 the proportion of cytotoxic T cells increased in the TG group and decreased in the OG group ($P = 0.03$). The B cell percentage on d 7 of both treatment groups was less ($P < 0.05$) than on d –51, –29 and –8. On d 1 the proportion of lymphocytes was lower ($P < 0.05$) and the proportion of neutrophils was greater ($P < 0.05$) than all other sample days. The percentage of monocytes was less on d –51 and –29 than all other sample days ($P < 0.05$) and was also less on d –18 and –8 than on d 1 ($P < 0.05$). The proportion of helper T cells was greater on d –51 and –29 than on d 1 and 7. No differences were detected in γδ T cells. The dynamics of most peripheral blood leukocyte populations was similar between dairy cattle managed under a one– or 2–group dry period nutritional strategy. Variations in B cell dynamics were detected during the dry period and also in cytotoxic T cells after parturition.

Key words: far-off, close-up, leukocyte

M359 Digestion and rumen fermentation in precision-fed dairy heifers on low or high forage rations at four levels of dry distillers grain. F. X. Suarez-Mena*, G. J. Lascano, and A. J. Heinrichs, *The Pennsylvania State University, University Park.*

The objective of this study was to determine the effects of forage to concentrate ratio (F:C) and corn dry distillers grain with solubles (DDGS) at various inclusion levels in precision-fed dairy heifer diets on digestion and rumen fermentation. A split plot design with F:C as whole plot and DDGS inclusion level as sub–plot was administered in a 4-period (19 d) 4 × 4 Latin square. Eight ruminally cannulated Holstein heifers (344 ± 15 kg BW) housed in individual stalls were allocated to 2 F:C (50:50 LF or 75:25 HF; DM basis) and to a sequence of DDGS inclusion (0, 7, 14 and 21%; DM basis). Diets were fed to provide equal amounts of nutrients allowing 800 g/d BW gain and fed 1X/d. Ruminal contents were sampled at –2, 0, 2, 4, 6, 8, 10, 12, and 20 h after feeding. Statistical analysis was conducted using the MIXED procedure of SAS. LF rations had greater apparent digestibility (AD) of DM (66.7 vs. 63.2 ± 0.8%; $P = 0.02$) and OM (69.0 vs. 65.2 ± 0.6%; $P < 0.01$). AD responded quadratically for DM, OM, ADF and NDF with 14% DDGS inclusion level having the highest values. Rumen concentration of ammonia tended to be higher for HF (7.68 vs. 6.48 ± 0.44 mg/dL; $P = 0.07$) and tended to increase as DDGS increased (6.46 to 8.14 ± 0.62 mg/dL; $P = 0.08$). Molar proportions (% of total VFA) of acetate tended to be greater for HF (65.8 vs. 64.0 ± 0.6%; $P = 0.07$) and decreased as DDGS increased (65.4 to 63.9 ± 0.5%; $P < 0.01$); propionate increased as DDGS increased (18.8 to 20.6 ± 0.3%; $P < 0.01$). Acetate to propionate ratio decreased as DDGS increased (3.49 to 3.11 ± 0.06; $P < 0.01$). Rumen protozoa count decreased as DDGS increased (24.42 to 11.94 ± 3.15 × 10^4/mL; $P < 0.01$). We conclude that nutrient AD had a greater response when included at 14% DDGS. Ammonia concentration and molar proportion of propionate increased; while molar concentration of acetate, acetate to propionate ratio, and rumen protozoa number decreased with increasing levels of DDGS. LF rations had greater DM and OM AD.

Key words: digestion, dry distillers grain with solubles, fermentation

M360 Effect of live-cell yeast at two dosages on lactation performance by dairy cows. L. F. Ferraretto*, R. D. Shaver, and S. J. Bertics, *Department of Dairy Science, University of Wisconsin-Madison, Madison.*

The objective of this trial was to evaluate the effect of live-cell yeast (LCY; Procreatin-7; Lesaffre Feed Additives) at 2 dosages in high starch (HS) diets (30% starch DM basis) on lactation performance by dairy cows versus HS and low starch (LS; 20% starch DM basis) control diets. Sixty-four multiparous Holstein cows, 114 ± 37 DIM and 726 ± 74 kg BW at trial initiation, were randomly assigned to 32 electronic gate feeders, which were randomly assigned to 1 of 4 treatments in a completely randomized design; a 2-wk covariate adjustment period with cows fed a 50:50 mixture of the HS and LS diets followed by a 12-wk treatment period with cows fed their assigned treatment diets. The HS diets were fed without (HS0) and with 2 (HS2) or 4 (HS4) g/cow/d of LCY. The LS diet did not contain LCY (LS0) and was formulated by partially replacing dry ground shelled corn with soy hulls. Data were analyzed using Proc Mixed in SAS with covariate, treatment, wk and treatment x wk interaction as fixed effects and gate (treatment) as a random effect. Cows fed LS0 consumed ($P < 0.01$) 2.5 kg/d more DM than HS2, and tended ($P < 0.07$) to consume 1.7 kg/d more than HS4. Milk yield averaged 44.3 kg/d and was unaffected ($P > 0.10$) by treatment. Solids- and energy- corrected milk yields tended ($P < 0.09$) to be 2.2 kg/d greater for HS4 than HS2. Milk fat content was greater ($P < 0.03$) for LS0 than HS0, and tended ($P < 0.09$) to be greater for HS2 and HS4 than HS0. Milk fat yield for cows fed LS0 was greater ($P < 0.05$) than HS0 and HS2, but not different than HS4 ($P > 0.10$). Milk protein content tended ($P < 0.08$) to be greater for HS4 than LS0. The MUN contents were greater ($P < 0.02$) for cows fed LS0 than the HS diets. Feed conversion (kg Milk / kg DMI) was 9% greater for HS2 than LS0 ($P < 0.05$), and tended ($P < 0.08$) to be 8% greater for HS0 than LS0. The BW, BW change, and BCS measurements were unaffected by treatment ($P > 0.10$). The LS0 diet increased DMI and milk fat content and yield, but reduced feed conversions. The addition of LCY to HS diets tended to increase milk fat content in dairy cows.

Key words: yeast, lactating cow, starch

M361 Differences in nutrients formulated and nutrients supplied on three California dairies. H. A. Rossow[1], R. J. van Hoeij[2], and G. Acetoze*[1], *[1]University of California, Davis, [2]Utrecht University, Utrecht, the Netherlands.*

Computer models used in ration formulation assume that nutrients supplied by a ration formulation are the same as the nutrients presented in front of the cow in the final ration. Deviations in nutrients due to feed management effects such as dry matter changes (i.e., rain), loading, mixing and delivery errors are assumed to not impact delivery of nutrients to the cow and her resulting milk production. To estimate how feed management impacts nutrients supplied to the cow, weekly total mixed ration (TMR) samples were collected and analyzed (Analab, Fulton, IL) for 4 pens (close up cows, fresh cows and 2 high milk producing cows pens) for 7 weeks on 3 California dairies. Differences among nutrient analyses from these samples and nutrients from the formulated rations were analyzed by GLM procedure of SAS (SAS Institute, 2007). Deviations in nutrients formulated and supplied were significantly different ($P > 0.05$) among dairies except for fat % (mean 0.25, 0.047, 0.074, SE 0.13, 0.12, 0.11), ash % (mean 0.048, 0.39, 1.2, SE 0.28, 0.26, 0.24), magnesium % (mean 0.036, 0.020, 0.015, SE 0.015, 0.014, 0.013) and chloride % (mean 0.071, 0.00097, 0.14, SE 0.026, 0.025, 0.023). Therefore feed management practices on all 3 dairies impacted nutrients supplied to the cow. Differences among all formulated and supplied nutrients were also significantly different among pens and were 6.14 for DM %, 1.39 for crude protein %, 0.55 for ADF %, 2.2 for NDF %, 3.1 for starch %, 0.088 for fat %, 0.67 for lignin % and 0.60 for ash %. However, differences among nutrients supplied due to diet changes for a pen were not significant. Therefore feed management impacts nutrient delivery to the cow but most diet adjustments are small relative to differences among pen rations.

Key words: feed management, nutrient supply, ration formulation

M362 Effect of dietary protein level and rumen-protected amino acids supplementation on ruminal fermentation and nitrogen utilization in lactating dairy cows. C. Lee*[1], A. N. Hristov[1], K. Heyler[1], T. Cassidy[1], H. Lapierre[2], G. A. Varga[1], and C. Parys[3], *[1]Pennsylvania State University, University Park, [2]Agriculture and Agri–Food Canada, Sherbrooke, QC, Canada, [3]Evonik Degussa GmbH, Hanau, Germany.*

The objective of this experiment was to investigate the effect of dietary protein level and rumen–protected amino acid supplementation on ruminal fermentation and N utilization in lactating dairy cows. The experiment utilized 8 ruminally cannulated Holstein cows (102 ± 28 DIM) in a replicated 4 × 4 Latin square design trial with 21-d periods. Treatments were: 15.6% CP diet [HighCP; metabolizable protein (MP) balance: –24 g/d], 14.0% CP diet (LowCP; MP balance: –283 g/d), 14.0% CP diet supplemented with 100 g/cow/d rumen-protected Lys (AminoShure-L, 24 g/d estimated digestible Lys supply; LowCPLys),

and 14.0% CP diet supplemented with 100 g/cow/d rumen-protected Lys plus 24 g/cow/d rumen-protected Met (Mepron, 15 g/d estimated digestible Met supply; LowCPLysMet). Dry matter intake (26.0 ± 0.79 kg/d), milk yield (40.9 ± 1.46 kg/d), milk composition, and rumen fermentation (pH, VFA and ammonia concentrations) were not affected by diet. Blood and milk urea-N concentrations were lower ($P = 0.03$) for the LowCP diets compared with HighCP. Cows on the LowCP diets had lower N intake (585 vs. 641 g/d, $P < 0.001$) than on HighCP. Apparent total tract N digestibility tended to be decreased ($P = 0.07$) with the LowCP diets compared with HighCP. Milk N secretion and fecal N excretion were not affected by diet. Compared with HighCP, the LowCP diets decreased urinary N excretion (by 29%; $P = 0.01$) and as proportion of N intake (by 22%, $P = 0.04$). Supplementation with rumen–protected amino acids did not further decrease N losses. Whole animal N retention did not differ among diets. Ammonia emission from manure was decreased (by 35%; $P = 0.001$) by the LowCP diets compared with HighCP. In this short-term experiment, dietary CP level or rumen-protected Lys and Met supplementation had no effect on ruminal fermentation, nutrient digestibility (except N), and cow productivity. However, urinary N losses as well as ammonia emission from manure were significantly reduced with the LowCP diets.

Key words: dairy cow, dietary protein, rumen-protected amino acid

M363 Effects of additive treatment and glycerol supplementation on in vitro digestibility and fermentation of a total mixed ration. J. H. Han*[1,2], S. C. Kim[2], D. H. Kim[1,2], J. J. Romero[1], H. J. Lee[1,2], J. H. Shin[1], O. C. M. Queiroz[1], K. G. Arriola[1], C. R. Staples[1], and A. T. Adesogan[1], *[1]Department of Animal Sciences, Institute of Food and Agricultural Sciences, University of Florida, Gainesville, [2]Department of Animal Sciences, Institute of Agricultre and Life Sciences, Gyeongsang National University, Gyeongnam, Jinju South Korea.*

Little is known about effects of glycerol supplementation on ruminal fermentation and whether additives can mitigate potential negative impacts. The objective was to estimate effects of additive treatment and glycerol addition on the in vitro DM and NDF digestibilities and fermentation of a TMR for lactating dairy cows. Two isonitrogenous corn silage (34.5%) and alfalfa hay (10.8%)-based TMR containing 0 or 10% glycerol (DM basis) were treated without (Control, CON) or with 4 additives (0.35 g/L of Procreatin 7 yeast, Prince Agri, YE; 500 mg/L of Dry Apex essential oil, EO, BFI Liquid Feeds; 5 mg/kg of monensin, MO, Sigma; or 3.75 mg/L of sodium bicarbonate, SB, Sigma) and incubated for 48 h in buffered-rumen fluid in triplicate. The experimental design was completely randomized. Treatments had a 2 (glycerol) × 5 (additives) factorial structure and both terms and the interactions were included in the statistical model. No glycerol x additive interaction was detected. Adding glycerol tended to increase molar proportion of propionate ($P = 0.07$, 20.7 vs. 19.5), tended to decrease pH ($P = 0.06$, 6.57 vs. 6.75), and decreased molar proportions of acetate ($P = 0.04$, 46.5 vs. 49.4), and iso-butyrate ($P = 0.05$, 5.46 vs. 5.79). In vitro DMD (67.2 vs. 60.1%) and NDFD (63.5 vs. 26.9%) were greatest ($P < 0.05$) for SB and least for MO-treated fermentation. Compared with other treatments, EO and MO produced greater pH ($P < 0.05$, 6.83 vs. 6.62), lower total VFA concentrations ($P < 0.001$, 92.2 vs. 104.0 mM), and less methane ($P < 0.001$; 22.3 vs. 27.7 mol/100 mol of VFA) whereas MO resulted in lower NH3-N ($P < 0.05$; 13.8 vs. 16.3 mg/dl). Butyrate and valerate molar proportions were lowest for MO-treated fermentations ($P < 0.05$; 9.35 vs. 10.2 and 4.07 vs. 4.85). *Streptococcus bovis* counts on de Man, Rogosa, Sharpe broth were greater for EO than for other treatments ($P < 0.05$; 1.7 vs. 1.43 log cfu/ml). Glycerol addition improved the energetic efficiency of ruminal fermentation. SB produced the greatest DMD and NDFD values but MO and EO decreased the extent of fermentation and YE had minimal effects on the fermentation.

Key words: glycerol, essential oil, monensin

M364 Use of an anti-inflammatory additive in preweaning Holstein calves. L. A. Borunda*[1], D. Domínguez[1], G. Villalobos[1], I. Arteaga[1], E. Santellano[1], M. Cook[2], and M. Yang[2], *[1]Universidad Autónoma de Chihuahua, Chihuahua, Chihuahua, México, [2]Aova Technologies Inc., Madison, WI.*

The use of anti-inflammatory additives to regulate the excess of gut inflamation in Holstein calves is a modern approach to maximize nutrient utilization on growth and production. The objective was to determine the impact on animal performance when BIG CALF (Aova Technologies) was fed at 0% (T0), 1% (T1; 5.54 g/a/d) or 2% (T2; 9.08 g/a/d) to Holstein calves during the preweaning period. Forty-four Holstein female calves averaging 35.2 kg (±6.04) were randomly assigned to treatments after colostrum feeding. Calves were housed in individual hutches and fed daily 3 L of raw milk during the first 15 d of trial and then 4 L until weaning. Half daily doses of BIG CALF were mixed with both of the 2 raw milk meals. Calves received ad libitum a commercial starter concentrate (18% CP) after 5 d of age. The length of experimental period was 56 d. Starter concentrate and water intake were recorded daily and individually, as well as disease incidence, body weight, average daily gain, and feed conversion every 14 d. Statistical analysis of animal performance data was done by repeated measures, and disease incidence by chi-squared analysis. Starter concentrate intake (kg) tended ($P \leq 0.10$) to increase by 30.3% in calves of T1 (0.524 ± 0.052) vs. T0 (0.402 ± 0.050). Average daily gain (kg) was not affected by treatments, means for T0, T1 and T2 were 0.417 ± 0.049, 0.529 ± 0.052, and 0.402 ± 0.049, respectively. However, average daily gain during the last period of trial (42 to 56 d) was 46.8% higher ($P \leq 0.01$) for T1 (0.963 ± 0.090) vs. T0 (0.656 ± 0.087). Final body weight (kg) was superior by 14.3% ($P \leq 0.0003$) for calves of T1 (64.4 ± 1.51) vs. T0 (56.3 ± 1.46), and 12.9% ($P \leq 0.0008$) for calves of T1 vs. T2 (57.04 ± 1.46), respectively. Feed conversion tended ($P \leq 0.10$) to improve by 16.3% in animals of T1 vs. T0 (1.751 ± 0.150 vs. 2.094 ± 0.145). Feeding BIG CALF did not affect daily water intake (L), means were 2.785 ± 0.236, 2.386 ± 0.248, and 2.808 ± 0.237 for T0, T1 and T2, respectively. Diarrhea incidence was 28.9% lower ($P \leq 0.046$) in calves of T1 (23.9%) vs. T0 (33.6%). Feeding BIG CALF at 1% increased animal performance compared with control treatment, but did not at 2%.

Key words: animal performance, anti-inflammatory, Holstein calves

M365 Effect of dietary *trans* fatty acids on milk yield and milk composition of early lactating dairy cows. J. S. Watts*, D. L. Sevier, S. M. Clark, M. A. McGuire, and P. Rezamand, *Department of Animal and Veterinary Science, University of Idaho, Moscow.*

Trans fatty acids (tFA) result from either industrial hydrogenation of oils or from biohydrogenation of unsaturated fat in the rumen. The objective was to determine the effect of supplemental dietary tFA on milk yield and composition compared with saturated fat (sFA). Holstein dairy cows 7 d in milk (n = 12) were randomly assigned to a sequence of treatments in a 3x3 Latin square design. Three treatments containing 0, 1.5, and 3% tFA (Virtus Nutrition; Corcoran, Ca), and 3, 1.5, and 0% sFA (Virtus Nutrition; Corcoran, Ca) respectively were

included in a lactation ration. Animals were fed individually and feed intake and milk yield were recorded daily. Each period lasted 14 d. Milk samples were collected on d 10 and 14 of each period with a baseline sample taken on d 0 (pretreatment). Milk composition was determined by near-infrared analysis (Washington DHIA; Burlington, WA) and milk fatty acid (FA) composition was determined by gas chromatography (GC). Data were analyzed with the MIXED procedure of SAS with significance at $P < 0.05$. Addition of tFA had no detectable effect on milk yield or dry matter intake. Additionally, supplementation of tFA did not significantly affect percentages of milk fat, protein, lactose, SNF, or somatic cell count. Dietary tFA linearly increased the total percentage of unsaturated FA in milk ($P = 0.001$) but had no effect on total percentage of saturated FA. Within the saturated FA, C15:0 and C20:0 increased with increasing tFA ($P < 0.02$), whereas C16:0 decreased. Within the unsaturated FA, tFA increased monounsaturated FA ($P = 0.002$), but not polyunsaturated FA. Importantly, total concentrations of 18:1 trans isomers increased in milk with increasing tFA ($P < 0.0001$) with 18:1 t6-t12 all increasing linearly. Overall, inclusion of tFA up to 3% of DM had a significant effect on the FA composition of milk, increasing the percentage of unsaturated FA including 18:1 *trans* isomers. These changes in the FA composition of milk could have negative implications for human health, as consumption of *trans* fat from industrial hydrogenation is associated with increased risk of several chronic diseases.

Key words: *trans* fatty acid, milk composition, transition cow

M366 Effect of nicotinamide on milk yield and retention of cows on commercial California dairies. P. D. French*[1], M. A. DeGroot[2], and J. C. Woodworth[3], *[1]French Consulting, Bon Air, VA, [2]DeGroot Dairy Consulting, Visalia, CA, [3]Lonza Inc., Enterprise, KS.*

A field study was carried out on 8 commercial dairy farms located around Hanford, CA from July 2008 to January 2009. Average herd size was 2,000 milking cows and ranged from 1000 to 5000 milking cows. Farm was the experimental unit and 2 treatments were equally randomized across farm with a 6-wk period sequence of on-off-on-off and off-on-off-on in a double reversal design; where on is close-up dry cow rations with 4 g of added nicotinamide (NM) per kg DM and off is rations without supplemental NM. Supplementation was targeted to deliver 48 g NM/cow/day during the last week of gestation. Data were edited to include only those cows that received the prepartum ration for a minimum of 17 d. Individual cow data were collected using DairyComp 305. All data, except for culling and pregnancy, were analyzed using the MIXED procedure of SAS. Culling and reproductive data were analyzed using the GLIMMIX procedure of SAS. One farm was excluded from the analysis because of failure to follow the daily feeding protocol. Although the culling percentage from calving through 30 DIM did not differ, cull rate from calving through 60 DIM was lower for NM (6.21 vs. 8.81%; $P < 0.05$). Cows that received NM during the prefresh period were 0.68 times as likely to be culled during the first 60 DIM ($P < 0.05$) compared with the controls. Milk fat percentage at 30 DIM was greater ($P < 0.01$) for cows the received NM prefresh and tended ($P < 0.10$) to be greater at 60 DIM. The difference in milk fat percentage along with a numerical difference in milk yield at 30 DIM lead to a very significant increase of 3.4 kg of 3.5% FCM for NM ($P < 0.01$). Nicotinamide did not affect mortality, DIM at culling, or pregnancy rate. Results of this study indicate that feeding nicotinamide during the close-up period reduces early lactation culling and increases FCM yield.

Key words: niacin, prefresh, culling

M367 Periparturient supplementation of saturated and unsaturated fat sources differentially alters the fatty acid profile of colostrum and milk fat of Holstein cows. M. Garcia*[1], L. F. Greco[1], A. Lock[1,2], J. E. P. Santos[1], and C. R. Staples[1], *[1]University of Florida, Gainesville, [2]Michigan State University, East Lansing.*

Information is limited on the effect of supplemental fat on the fatty acid (FA) profile of colostrum. Fat supplements were saturated free FA (SAT; 38% C16:0, 41% C18:0, 7% C18:1cis-9, and 0.7% C18:2n-6 of total FA) or Ca salts of primarily unsaturated FA (USFA) of palm and soybean oil (32% C16:0, 5% C18:0, 23% C18:1cis-9, 27% C18:2n-6, and 3.5% C18:3n-3 of total FA). Prepartum cows (n = 27 fed no supplemental FA; n = 26 fed SAT at 1.7% of dietary DM; n = 24 fed USFA at 2% of dietary DM) were allocated randomly to diets (1.7% FA for base diet, DM basis) starting at 60 d before calculated calving date through 90 DIM. Within 2 h of calving, cows were milked and colostrum was sampled and stored at −20C for later analysis of FA using gas-liquid chromatography. Concentration of total FA (7.4, 6.0, and 7.2% of DM for control, SAT, and USFA, respectively) and proportion of individual shorter chain (C4:0 to C14:0) saturated FA (19.9, 18.9, and 18.1% of FA) were not affected by supplement. Feeding fat decreased ($P < 0.05$) proportion of C14:1 (1.89, 1.70, and 1.57% of FA) and C16:1 (0.54, 0.43, and 0.40% of FA), increased proportion of C18:0 (8.4, 9.6, and 9.6% of FA), but had no effect on proportions of C16:0 (38.1, 37.4, and 37.1% of FA) and C18:1 cis-9 (22.2, 22.6, and 22.1% of FA). Colostrum from cows fed USFA had greater proportions of C18:2n-6 (2.25, 2.31, and 3.35% of FA), total C18:1 trans (1.60, 1.58, and 2.06% of FA), and CLA cis-9, trans-11 (0.20, 0.17, and 0.27%) but not of C18:3n-3 (0.38, 0.39, and 0.41%). The effect of dietary fat source on the FA profile of milk collected wk 5 to 7 postpartum from cows fed the same 3 dietary supplements was different compared with their effects on colostrum. Proportion of each medium chain FA (C10:0, C12:0, and C14:0) was lower and that of C18:0 was elevated by fat supplementation to lactating cows. As with colostrum, feeding USFA increased proportions of total C18:1 trans, C18:2n-6, and CLA cis-9, trans-11 in milk fat. In conclusion, fat supplementation influenced the FA profile of colostrum fat and milk fat differently.

Key words: colostrum, milk, fatty acids

M368 Effects of reduced dietary protein and supplementing rumen protected amino acids on the nitrogen efficiency of dairy cows. A. L. Bell*[1], M. J. de Veth[2], T. R. Wiles[1], O. Becvar[3], and M. D. Hanigan[1], *[1]Virginia Polytechnic Institute and State University, Blacksburg, [2]Balchem Corporation, New Hampton, NY, [3]Virginia-Maryland Regional College of Veterinary Medicine, Blacksburg, VA.*

When fed to meet National Research Council (2001) protein recommendations, dairy cows consume an excess of many amino acids (AA) resulting in approximately 75% of dietary nitrogen (N) being lost to the environment as urine and feces. Reductions in environmental N release could be attained through an improvement of N efficiency in dairy cows. The objective of this study was to determine if the typical reduction in milk yield associated with feeding a low protein diet to lactating dairy cows could be avoided by dietary supplementation with one or more ruminally protected (RP) AA. Fourteen multiparous and 10 primiparous Holstein cows and 24 multiparous Holstein × Jersey crossbred cows were used in a Youden square design consisting of 8 treatments and 3 periods. The 8 dietary treatments were 1) a standard diet containing 17% crude protein (CP) (+Con), 2) a 14% CP diet (-Con), 3) -Con plus RP methionine (+Met, 16g/d), 4) -Con plus RP lysine (+Lys, 47g/d), 5) -Con plus RP leucine (+Leu, 181g/d), 6) -Con

plus RP methionine and lysine (+Met+Lys), 7) -Con plus RP methionine and leucine (+Met+Leu), and 8) -Con plus RP methionine, lysine, and leucine (+Met+Lys+Leu). Cows given the -Con and +Met+Lys+Leu diets had significantly lower milk production and milk protein yield than the +Con cows. The yield of milk and milk protein for all other AA treatments were not different from either the -Con or +Con treatments. Dry matter intake decreased for cows given the +Met+Leu diet, but all other treatments were not different from the +Con treatment. Milk urea N was significantly decreased for all diets compared with the +Con indicating N efficiency was improved for the low protein diets. Plasma isoleucine and valine were significantly reduced when CP was reduced. Leucine concentrations increased for the +Met+Leu treatment compared with -Con. All other AA were unchanged. In conclusion, supplementation of the individual AA or combinations of 2 AA, but not a combination of all 3 prevented a reduction in milk yield when dietary protein levels were reduced to 14% of dietary dry matter.

Key words: nitrogen efficiency, rumen-protected amino acids, milk production

M369 The effect of direct-fed microbial supplementation on reproductive and production performance of primiparous Holstein heifers. M. B. Cattell[1], A. J. Nelson[1], J. E. Nocek[2], and L. C. Solórzano*[3], *[1]Dairy Research and Technology LLC, Windsor, CO, [2]Spruce Haven Farm and Research Center, Union Springs, NY, [3]Chr. Hansen Inc., Milwaukee, WI.*

The effects of supplementing a direct-fed microbial (DFM) to primiparous dairy cows during the transition period were evaluated. Approximately 2 hundred Holstein primiparous cows were group housed and fed close-up and lactating diets without or with 2 g/cow/d of DFM. Direct-fed microbial supplementation contained approximately 5×10^9 cfu of bacteria (2 specific *Enterococcus faecium* strains) and 2×10^9 cfu of live viable yeast (*Saccharomyces cerevisiae*) incorporated into a limestone carrier. Supplemented cows were fed the DFM at least 7 d before calving and continued through 60 d postpartum. Statistical analyses were conducted by SAS JMP utilizing split-plot-in-time ANOVA for repeated measures. A Wilcoxon test was used to test treatment effects. Although no significant ($P > 0.1$) reproductive responses were observed, cows supplemented with DFM had 5 less days open than non-supplemented cows (140 vs. 145 d) and a lower incidence of retained placentas (2 vs. 5.3%). In addition, cows supplemented with DFM had a numerical ($P > 0.1$) decrease in the incidence of displaced abomasums (2 vs. 6.4%). Cows supplemented with DFM produced milk containing a higher ($P < 0.05$) percentage of milk fat (3.58 vs. 3.49%) and milk protein (3.04 vs. 2.99%), and a higher ($P < 0.1$) milkfat yield than nonsupplemented cows (1.01 vs. 0.98 kg/cow/d). Data suggests that DFM supplementation improves the transitional health of primiparous cows and their subsequent lactational performance.

Key words: direct-fed microbial, reproduction, production

M370 Rumination behavior and its relationship to feeding behavior in Holstein dairy cows prepartum. K. Schirmann*[1,2], N. Chapinal[1], D. M. Weary[1], W. Heuwieser[2], and M. A. G. von Keyserlingk[1], *[1]Animal Welfare Program, Faculty of Land and Food Systems, The University of British Columbia, Vancouver, BC, Canada, [2]Clinic for Animal Reproduction, Faculty of Veterinary Medicine, Freie Universität Berlin, Berlin, Germany.*

The objective of this study was to describe the rumination behavior, feeding behavior and feed intake in dairy cows. Rumination was monitored electronically using Vocal Tags and feeding behavior and intake were monitored using Insentec feed bins, by 2-h period, for 42 multiparous Holstein cows for a minimum of 9 d in the early dry period. Pearson correlations used to test the association, within cow, among 2-h periods, first examining the relationship within a single period, and then modeling how this relationship changes with a lag of 2, 4 or 6 h. We then investigated if daily rumination times were associated with feeding time and DMI among cows. Periods when cows spent more time ruminating were associated with lower feeding times and lower DMI ($r = -0.71$, $P < 0.001$, and $r = -0.72$, $P < 0.001$, respectively), likely because cows were unable to feed and ruminate simultaneously. The correlations with rumination time changed from negative to positive when lags of 2, 4 and 6 h were modeled ($r = -0.09$, 0.24, 0.15, $P < 0.01$, and $r = -0.16$, 0.23, 0.17, $P < 0.001$ for feeding time and DMI at lags of 2, 4, and 6 h, respectively). The results indicate that following periods of high feeding times and intakes cows spent more time ruminating, and that this relationship peaks at approximately 4 h after feeding. Among cows, animals that spent more time spend ruminating per day, spent less time feeding ($r = -0.34$, $P = 0.03$) with no effect on DMI ($r = 0.11$, $P = 0.48$). Overall these data indicate that rumination time can be used to estimate within cow variation in DMI, but that the use of daily summaries of rumination behavior to estimate DMI should be viewed with caution.

Key words: feeding time, dry matter intake, welfare

M371 Performance of dairy calves offered alternative preweaning feeding programs. S. L. Gelsinger*, P. C. Hoffman, and D. K. Combs, *University of Wisconsin, Madison.*

Sixty Holstein or Holstein × Jersey heifers were randomly assigned at birth to one of 3 milk feeding programs: (1) Control - calves fed 3.8 L/d whole pasteurized milk (WPM) and ad libitum complete calf starter from 3 d to 6 wk of age (2) Limit starter - calves offered a maximum of 115 g DM/d of calf starter from 3 d of age until 3 d before weaning and 3.8 L/d WPM during wk 1, 5.7 L/d WPM during wk 2 and 3, and 7.6 L/d WPM during wk 4, 5 and 6, and (3) Hay - calves offered alfalfa hay, but no calf starter until 3 d before weaning and fed WPM similarly to Limit starter calves. For 3 d before weaning, calves were fed 0.9 L WPM per feeding and provided ad libitum calf starter. Dry hay was replaced by calf starter for Hay treatment calves. The study was from November, 2010 to February, 2011. Calves were in individual calf hutches and fed milk twice daily and provided water. Body weight, body measurements and starter intake were recorded. Data was analyzed as a completely randomized design by the proc mixed procedure in SAS with treatment a fixed effect and calf the random effect. Calves assigned to the 3 treatments had similar (mean +/− SE) body weight, heart girth, hip height and body length at birth (39.5 kg +/− 0.9, 80.6 cm +/− 0.8, 77.6 cm +/− 0.9, and 69.9 cm +/− 1.1, respectively). At 6 weeks of age, weaning weights of calves fed Control (68.2 kg) and Limit (70.5 kg) were similar, but greater ($P < 0.05$) than calves on Hay (65.5 kg). Limit starter calves had higher ($P < 0.05$) 6wk hip height (93.7 cm) than Control calves (90.9 cm) and hip height of Hay calves (89.5 cm) was less ($P < 0.05$) than either other treatment. Total starter consumption during the first 5 weeks was 11.6, 3.6 and 0 kg per calf on Control, Limit and Hay, respectively. Starter consumption during the week of weaning was highest ($P < 0.01$) for Control (6.7kg/7 d), intermediate for limit (1.9 kg/7d) and least (1.1 kg/7d) for Hay. Calves on the Limited starter treatment protocol performed similarly to calves limit fed milk and calf starter ad libitum. Calves consuming no starter until 3 d before weaning were smaller, and consumed the least starter during the week of weaning.

Key words: calf, feeding, weaning

M372 Effect of *Origanum vulgare* L. leaves on production and milk fatty acid composition in lactating dairy cows. A. N. Hristov*[1], C. Lee[1], T. Cassidy[1], K. Heyler[1], J. A. Tekippe[1], G. A. Varga[1], and B. Corl[2], *[1]Pennsylvania State University, University Park, [2]Virginia Polytechnic Institute and State University, Blacksburg.*

This experiment investigated the effects of dietary supplementation with *Origanum vulgare* L. leaves (oregano; OL) on production and milk fatty acid (FA) composition in dairy cows. The experimental design was a replicated 4 × 4 Latin square with 8 ruminally-cannulated Holstein cows (DIM, 160 ± 38) and 20-d experimental periods. Treatments were: control (no OL supplementation), 250 g/cow/d OL (LOR), 500 g/d OL (MOR), and 750 g/d OL (HOR). The oregano leaves were supplemented to the basal TMR replacing an alfalfa-cottonseed hulls mix. The basal TMR (14.7% CP, 36.2% NDF) contained (DM basis) 58% forage (corn silage, alfalfa haylage, and a grass-straw mix). Oregano supplementation linearly decreased ($P = 0.02$; SEM = 1.80) DMI: 28.3, 28.3, 27.5, and 26.7 kg/d, control, LOR, MOR, and HOR, respectively. Milk yield tended to increase ($P = 0.07$; SEM = 7.43) quadratically with OL supplementation: 43.4, 45.2, 44.1, and 43.4 kg/d, respectively. As a result, feed efficiency was increased ($P < 0.001$) for all OL diets (1.59, 1.60, and 1.63, respectively) compared with the control (1.46). Milk protein and lactose concentrations and yields and FCM yield were not different among diets. Milk fat content tended to be increased ($P = 0.07$) by HOR compared with the control (3.57 vs. 3.26%, respectively), but OL tended to linearly reduce ($P = 0.07$) milk fat. Milk urea-N concentrations were lower ($P = 0.04$) for all OL diets (7.95 to 8.49 mg/dL) compared with the control (9.26 mg/dL). Rumen fermentation (pH, VFA, and ammonia concentrations) was not affected by treatment. Apparent total tract digestibility of nutrients was also not affected by OL, except NDF digestibility was slightly decreased ($P = 0.04$) by all OL diets compared with the control (49.3 vs. 51.3%, respectively). OL had no effect on milk FA composition. In this short-term study, oregano leaves fed at 250 to 750 g/d decreased linearly DMI and tended to quadratically increase milk yield in dairy cows. Feed efficiency was increased with all OL inclusion levels. Oregano leaves had no effect on ruminal fermentation and milk FA composition.

Key words: *Origanum vulgare*, feed efficiency, dairy cow

M373 Evaluation of algae as livestock feed. C. P. Payne*, J. E. Sawyer, and T. A. Wickersham, *Texas A&M University.*

Cultivation of algae for biofuel would result in the production of significant amounts of post-extraction algal residue (PEAR). The economic viability of algae as source of biofuel is dependent on deriving value from PEAR. Livestock feed is an attractive option for PEAR because of the successful utilization of other co-products by ruminants. While sufficient quantities of PEAR were not available for analysis, we evaluated 2 strains of algae that, based on their lipid content and growth characteristics, possess potential as a source of biofuel. Algae samples, unknown wild algae (WA) and *Neochloris oleoabundans* (NO), were analyzed for ash, crude protein, amino acid profile, total fat content (ether extract), fatty acid profile, fat soluble vitamins, macro- and micro-minerals, and heavy metals (n = 1). Samples were observed to have relatively high levels of ash, 30.5 and 43.2% for WA and NO, respectively. As expected, Na content of each sample was high, 10.3 (WA) and 10.8% (NO). The Ca and P contents were 0.67 and 0.43% for WA and 1.02 and 0.26% for NO, accordingly. Algae samples WA and NO contained 34.2 and 48.6 ppm Cu, 848 and 756 ppm Fe, and 20.1 and 62.3 ppm Zn, respectively. WA and NO contained significant quantities of aluminum at 840 and 858 ppm, accordingly. Analysis of algal CP content, 17.4 WA and 20.6% NO, indicates that PEAR may serve as a source of N in ruminant diets. Samples contained similar amounts of methionine (0.31 and 0.32%; WA and NO, respectively) and lysine (1.00 and 1.18%; WA and NO, respectively). Total fat content was 9.1 and 11.8% WA and NO, respectively. Fatty acids (% total fat) were profiled for WA and NO, correspondingly: Palmitic, 21.3 and 32.0; Oleic, 34.1 and 15.6; Trans-vaccenic, 7.7 and 5.6; Linoleic, 11.3 and 19.8; α-Linolenic, 16.3 and15.4%. Vitamin A content was high for both samples, with WA measuring 6614 and 5203 IU/kg for NO. Vitamin E content was 56.5 for WA and 87.7 IU/kg for NO. Future nutritive evaluations of algae and the resulting PEAR should focus on its value as a source of N in ruminant diets.

Key words: algae, coproduct

M374 Hourly changes in fatty acid profile of ruminal contents in continuous cultures as soybean oil is added and removed from the diet. C. M. Klein*, S. K. Thurmond, P. H. Morris, and T. C. Jenkins, *Clemson University, Clemson, SC.*

The objective of this experiment was to determine how quickly biohydrogenation patterns change in ruminal contents in response to the addition and removal of unsaturated fat from the diet. Four dual-flow continuous fermenters were fed 60 g/d of 1:1 forage (alfalfa hay) to concentrate mix in 2 equal portions at 0800 and 1600 h. Diets were fed to flasks for 4 12-d periods each divided into 3 phases; 1) a control diet for d 1–4 (CON1), 2) a diet with 4% added soybean oil for d 5–8 (SBO), and 3) the control diet for d 9–12(CON2). Samples of culture contents were taken at 0 (just before feeding), 2, and 4 h after the morning feeding on all days except d 5 and d 9. On d 5 and d 9, samples were taken hourly for 12 h starting just before the morning feeding. Results are expressed as g fatty acid/100 g total fatty acids. Differences among sampling times were declared if $P < 0.05$ and determined in SAS using single degree of freedom contrasts. During the CON1 phase, changes in fatty acid profile occurred daily after each feeding that were characterized by increased ($P < 0.05$) proportions of C18:2 and *cis*-9, *trans*-11 CLA, and decreased ($P < 0.05$) proportions of stearic acid, *trans*-10 C18:1 and *trans*-10, *cis*-12 CLA. Linoleic acid averaged 11.5 ± 1.4% during CON1 and peaked at 33.3 ± 1.1% immediately after the addition of soybean oil (d4h1). Linoleic acid averaged 26.1 ± 1.1% and 16.4 ± 2.6% during SBO and CON2 phases, respectively. Stearic acid showed little change from SBO to CON2 phases (averaging 9.6 ± 1.7 and 9.5 ± 1.9%, respectively). *Trans*-10, *cis*-12 CLA proportions averaged 0.61 ± 0.08% during CON1, increased gradually over the SBO phase, and peaked at 5.38 ± 1.51% at the start of CON2 (d 8h 0). *Trans*-10 C18:1 averaged 0.62 ± 0.12% over CON1 and peaked at 6.12 ± 1.62% during CON2 (d9h0). The results of this study show that the introduction of soybean oil into the diet causes an immediate increase in linoleic acid concentration in ruminal contents that is accompanied by little change in stearic acid and slow-developing increases in *trans*-10, *cis*-12 CLA and *trans*-10 C18:1.

Key words: biohydrogenation, soybean oil, conjugated linoleic acid

M375 Effects of tannin extracts on in vitro growth of selected food-borne pathogenic bacteria. B. J. Min[1], B. R. Min[1], J. M. Sieg[2], J.-S. Eun*[2], D. R. ZoBell[2], and D. C. Tice[1], [1]*Department of Agricultural and Environmental Sciences, Tuskegee University, Tuskegee, AL,* [2]*Department of Animal, Dairy, and Veterinary Sciences, Utah State University, Logan.*

An in vitro study was conducted to assess the growth inhibition of tannin extracts (TE) against *Escherichia coli* O157:H7, *Salmonella typhimurium*, *Listeria monocytogenes*, and *Staphylococcus aureus* in pure culture. Commercially available quebracho (QT; mainly condensed tannins), chestnut (CNT; containing 80% hydrolysable tannins), and mimosa tannins (MT; containing about 70% condensed tannins) (Chemtan, Exter, NH) were tested. An agar diffusion assay was used to evaluate the antimicrobial activity of TE at 1 mg TE/4 mL ethanol solution (1:5 dilution) and 1 mg TE/49 mL ethanol solution (1:50 dilution) against the bacteria. The in vitro experiment was performed in a 3 (source of TE) × 4 (pathogenic bacteria) × 2 (dilution rate) factorial design (n = 3). An aliquot of 10 mL hard tryptic soy broth was used to inoculate *E. coli* O157:H7 and *S. typhimurium*, whereas 10 mL hard brain heart infusion broth was used to inoculate *L. monocytogenes* and *S. aureus* at $10^{5–6}$ cfu/mL. Plates were incubated at 37°C for 48 h, and the disc with ethanol only was used as a control. After incubation, the diameter of inhibition zones was measured at least 3 cross-section points, and mean value was used for inhibition zone. At 1:5 dilution, CNT depicted the most inhibitory response (2.05 mm) followed by MT (1.44 mm) ($P < 0.05$). The CNT elicited an inhibitory effect across all pathogenic bacteria (*E. coli* O157:H7 = *S. typhimurium* > *L. monocytogenes* > *S. aureus*) ($P < 0.05$). Mimosa tannins had less inhibitory effects compared with CNT, while QT did not affect bacterial growth. At 1:50 dilution, only the CNT inhibited bacterial growth (*E. coli* O157:H7 = *S. typhimurium* > *L. momcytogenes*), but the overall response was lower than that in 1:5 dilution (1.10 vs. 2.05 mm). Results from this in vitro experiment showed that the CNT exerted a greater inhibition of pathogenic bacterial growth than the MT and the QT.

Key words: pathogenic bacteria, tannin extracts, growth inhibition

M376 Tannin extracts decrease in vitro growth of ruminal acidosis-causing bacteria in pure culture. J.-S. Eun*[1], B. R. Min[2], J. M. Sieg[1], D. R. ZoBell[1], and A. J. Young[1], [1]*Department of Animal, Dairy, and Veterinary Sciences, Utah State University, Logan,* [2]*Department*

of Agricultural and Environmental Sciences, Tuskegee University, Tuskegee, AL.

Antimicrobial activity of tannins has been well documented. However, there is lack of detailed knowledge to explore potential effects of tannin extracts (TE) on the growth of ruminal acidosis-causing bacteria (RACB) in beef steers. Two strains of RACB were used in a 2 (strain of RACB) × 4 (source of TE) factorial designed experiment (n = 3) to determine the effects of sources of TE on growth of RACB. Two strains of RACB, *Selenomonas ruminantium* JY35 (SR) and *Streptococcus bovis* S81 A Xy2 (SB), were tested in pure culture, as the 2 bacteria have been considered as main microbes causing ruminal acidosis in finishing beef steers. The bacterial growth was measured by OD_{550} readings during 24-h incubation at 39°C in Hungate tubes under CO_2 with a typical beef steer finishing TMR extracted using an artificial saliva in the growth medium containing soluble protein and carbohydrate. Commercially available quebracho (QT; mainly condensed tannins), chestnut (CNT; containing 80% hydrolysable tannins), and mimosa tannins (MT; containing about 70% condensed tannins) (Chemtan, Exter, NH) were used as sources of TE. Overall growth pattern of the RACB differed in response to TE ($P < 0.05$ for RACB × TE interactions). Adding TE decreased growth of SR starting at 2 h, and CNT was most effective to decrease growth of SR at 12 and 24 h followed by MT and QT ($P < 0.05$). At 24 h, the CNT decreased growth of SR at 48%. Growth of SB was inhibited by adding TE beginning at 4 h. At 12 and 24 h, the CNT elicited the least growth of SB followed by the MT and the QT ($P < 0.05$). The CNT decreased growth of SB at 73% at 24 h. Results of this study indicate that supplementing TE in a beef steer finishing diet decreased in vitro growth of SR and SB, and the CNT was the most effective in inhibiting the growth of RACB.

Key words: ruminal acidosis-causing bacteria, tannin extracts, bacterial growth

M377 Effects of wheat dried distillers grains with solubles (DDGS) and cinnamaldehyde (CIN) on fermentation and protein degradation in Rusitec. Y. L. Li[1,2], M. L. He[1], K. A. Beauchemin[1], and W. Z. Yang*[1], *[1]Research Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, Canada, [2]Feed Research Institute, Chinese Academy of Agricultural Sciences, Beijing, China.*

A study was conducted to evaluate the effect of wheat DDGS and CIN on in vitro fermentation using the Rusitec. The experiment was designed as a completely randomized block with a 2x2 factorial arrangement of treatment with 4 replications in each treatment. The control diet (10% barley silage, 90% barley concentrate, DM basis) and wheat DDGS diet (10% silage, 60% barley concentrate, and 30% wheat DDGS) were combined with 0 and 300 mg CIN/L of culture fluid. Experiment consisted of 10 d of adaptation and 7 d of data collection. Interactions of DDGS with CIN on fermentation and nutrient disappearances were not significant. Replaced barley grain with DDGS increased the concentration of total VFA (45 vs. 38 mM; $P < 0.04$), and molar proportions of acetate (46 vs. 41%; $P < 0.01$), propionate (19 vs. 17%; $P < 0.02$), and NH_3-N (15 vs. 10 mg/100 mL; $P < 0.01$) without altering ratio of acetate to propionate and CH_4. Disappearance of DM (48 vs. 45%; $P < 0.03$) and bacterial protein production (72 vs. 51 g; $P < 0.01$) were greater, whereas the disappearances of CP (46 vs. 50%) and NDF (17 vs. 24%) were less ($P < 0.01$) with DDGS than with control diet. With addition of CIN, concentration of total VFA decreased (33 vs. 49 mM; $P < 0.01$) and fermentation pattern changed to greater ($P < 0.01$) acetate and less ($P < 0.01$) propionate molar proportions. Supplementation of CIN overall reduced ($P < 0.05$) the nutrient disappearance by 10 to 15% depending on the nutrient studied. Consequently, the production of bacterial N reduced ($P < 0.01$) by 14%. The results indicate that substitution of wheat DDGS for barley grain or supplementation of CIN in finishing diet potentially increased protein in the intestine as a result of increased CP supply and RUP. However, decreased NDF disappearance with DDGS or CIN may reduce feeding value of the diet especially DDGS is high in NDF.

Key words: cinnamaldehyde, fermentation, wheat DDGS

M378 In vitro digestion and gas production of wheat grain varying processing. W. Z. Yang*[1], T. A. McAllister[1], and M. Oba[2], *[1]Research Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, Canada, [2]Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada.*

Rapid starch digestion in the rumen may lower rumen pH, depress fiber digestion and cause digestive disturbances. The rate and extent of DM digestion varies among wheat sources and with the extent of processing, but seldom have both of these properties been studied in the same experiment. Eight wheat samples collected from various location in Alberta were either ground (1-mm) or dry-rolled, and fermentability was assessed by measuring in vitro gas production (GP) and DM disappearances (DMD) at 0, 4, 8, 14, 24 and 48 h of incubation. The DMD increased ($P < 0.01$) from 21 to 81%, and from 12 to 53%, respectively, for ground and rolled wheat with increasing incubation time from 4 to 48 h. There was no interaction between wheat source and processing on GP and DMD at 24 h of incubation, whereas it was significant ($P < 0.01$) at 48 h of incubation. Variations in GP and DMD among wheat samples were substantial. The GP (ml/g OM) varied from 226 to 311 for ground wheat and from 95 to 194 for rolled wheat, and the DMD ranged from 60 to 81% for ground wheat, and from 30 to 50% for rolled wheat. As expected, GP and DMD were greater ($P < 0.01$) for ground wheat (279 and 64%) than for rolled wheat (141 and 34%) after 24 h of incubation. Similarly, VFA concentration in the culture fluid was higher ($P < 0.01$) for ground (102 m*M*) than for rolled wheat (90 mM). However, ratio of acetate to propionate was lower ($P < 0.01$) for ground (2.3) than for rolled wheat (3.4), indicate that more starch is available to be fermented for ground wheat. This work demonstrates that there is substantial variation in the digestive value of commercially available wheat grain and emphasize the need to have an accurate and rapid means of quality assessment at the point of sale.

Key words: wheat grain, DM digestion, batch culture

M379 The effect of DDGS when replacing corn or soybean meal on rumen microbial growth in vitro as measured using real-time PCR. E. Castillo-Lopez* and P. J. Kononoff, *University of Nebraska-Lincoln, Lincoln.*

Ethanol byproducts are a good source of energy and protein in ruminant diets. The aims were to evaluate the effect of dried distillers grains and solubles (DDGS) and in vitro fermentation time on the growth of rumen bacteria and protozoa, and to measure the contribution of yeast originating from DDGS to total microbial crude protein (MCP). Treatments were: 1) CONT, control with no DDGS, but with alfalfa hay, corn silage (CS), ground corn (GC) and soybean meal (SBM) included at 25% (DM basis); 2) RC, 20% (DM Basis) DDGS replacing GC; 3) RS, 20% (DM basis) DDGS replacing SBM; 4) RCS, 20% DDGS replacing 10% GC and 10% SBM (DM basis). For each treatment, 1 g of substrate was incubated in vitro in 100 mL of inoculum in duplicate. At 0, 4, 16, 32, 48 and 96 h of fermentation DNA was extracted from

each treatment and MCP was measured by real-time PCR. Microbial markers used are from the 16S rRNA gene, 18S rRNA gene and the II chromosome; for bacteria, protozoa and yeast, respectively. Data were analyzed as a completely randomized design with repeated measures to test the effects of treatments and fermentation time. Treatment did not affect ($P = 0.18$) mean bacterial CP which was observed to be 157.22 ± 16.53 mg/g DM across treatment. However, a treatment by time interaction was observed ($P < 0.05$). Specifically, at 16 h the RCS diet yielded higher ($P < 0.01$) bacterial CP than CONT (306.32 and 141.37 ± 49.97 mg/g DM for RCS and CONT respectively). However, at 32 h only the RS yielded higher ($P < 0.01$) bacterial CP than the CONT (393.08 and 251.15 ± 49.97 mg/g DM for RS and CONT respectively). In addition, compared with the CONT, bacterial CP of RCS tended ($P = 0.07$) to increase (343.67 and 251.15 ± 49.97 mg/g DM for RCS and CONT respectively). At 32 h the RS and RCS diet yielded higher ($P < 0.01$) protozoa CP when compared with the CONT (209.31, 165.38 and 117.64 ± 15.01 mg/g DM for RS, RCS and CONT respectively). Treatment did not affect ($P = 0.51$) yeast CP and averaged 0.03 ± 0.02 mg/g DM. Overall, bacterial and protozoal growth was improved when DDGS replaced SBM and it was maintained when DDGS replaced GC.

Key words: DDGS, microbial crude protein, real-time PCR

M380 Effects of semi-arid medicinal herb essential oils on growth of pure culture of *Butyrivibrio fibrisolvens* SH13. H. Jahani-Azizabadi*[1], M. Danesh Mesgaran[1], A. R. Vakili[1], and K. Rezayazdi[2], *[1]Dept. of Animal Science, Excellence Center for Animal Science, Faculty of Agriculture, Ferdowsi University of Mashhad, Mashhad, Khorasan Razavi, Iran, [2]Dept. of Animal Science, Faculty of Agriculture, University of Tehran, Karaj, Tehran, Iran.*

The objective of the present study was to investigate the effect of some semi-arid medicinal herb essential oils (EO) on Butyrivibrio fibrisolvens SH13 growth characteristics. The liquid version of Hobson's M2 medium (Hobson, 1969) in Hungate tubes was used to estimate sensitivity of *Butyrivibrio fibrisolvens* SH13 to semi-arid native cinnamon, thyme and coriander essential oils. *Butyrivibrio fibrisolvens* SH13 stock culture was grown anaerobically in M2 medium in 125-mL bottles for 16 h at 38.6°C before testing. *Butyrivibrio fibrisolvens* SH13 was obtained from the Rowett Research Institute (Aberdeen, UK) culture collection. After the medium was autoclaved, each essential oil was applied to give a concentration ranging from 0.0 (as control) to 10, 20, 40, 80, 120, 180, 240, and 360 ppm (4replicates). Essential oils were previously dissolved in equal volume of ethanol. All cultures were grown anaerobically at 38.6°C using an inoculum from stationary phase of stock culture (5% of v/v) for 24 h. The concentration of a EO at which the *Butyrivibrio fibrisolvens* SH13 growth was half of that measured in the control (IC50) was recorded during 24 h of incubation. *Butyrivibrio fibrisolvens* SH13 growth was measured by hourly reading optical density of the medium at 650 nm (OD650). As presented in Table 1, when each EO applied to the culture medium inhibited the growth of *Butyrivibrio fibrisolvens* SH13 at the concentration of higher than 240 ppm. An increase in the concentration of coriander EO (UP to 240 ppm) led to increase *Butyrivibrio fibrisolvens* SH13 OD650 compared with those of the control ($P < 0.05$). Results of the present study demonstrated that the essential oils might alter growth pattern of *Butyrivibrio fibrisolvens* SH13.

Table 1. The concentration of semi-arid medicinal plant essential oils at which the *Butyrivibrio fibrisolvens* SH13 growth was half of that measured in the control (IC50) during 24 h of incubation

	IC50 of EO (ppm)
Cinnamon	≥360
Coriander	>360
Thyme	≥240

Key words: *Butyrivibrio fibrisolvens*, coriander, essential oil

M381 Effects of microbial contamination on in situ estimates of ruminal degradability of fiber fractions. J. M. Arroyo, J. Guevara-González, F. Díaz-Royon*, and J. González, *Universidad Politécnica de Madrid, Madrid, Spain.*

Measures of ruminal digestibility of fiber constituents are usually considered as truly estimates. However, vegetable feeds are subjected, during its rumen residence, to a microbial contamination, which is especially high in rich fibrous feeds. Therefore, errors may occur if the fiber determination methods are not able to remove this contamination, as it is normally assumed. The microbial contamination of the neutral and acid detergent fractions (NDF and ADF) and of their N components (NDIN and ADIN, respectively) of in situ incubated residues of a fibrous Italian ryegrass (*Lolium multiflorum*) hay was determined as well as the associated effects on the ruminal degradation estimates. Hay samples (ground to pass a 2-mm screen) were incubated for 72 h in nylon bags (46 μm pore size) on 3 ruminally cannulated wethers fed with 75 g /$Kg^{0.75}$ of a 40:60 Italian ryegrass hay to concentrate diet. Incubations were performed in stable conditions of ^{15}N infusion (30 mg ^{15}N per day) and solid-associated bacteria were isolated and used as reference sample to control contamination. Analyses of NDF, ADF, as well as of N and ^{15}N abundance of both fiber fractions were performed. Effects of microbial contamination were determined by one-way variance analysis. Microbial contribution to NDF, ADF, NDIN and ADIN in the tested sample was 4.14, 0.45, 65.1 and 15.9%, respectively. The lack of contamination correction led to underevaluations of ruminal degradation: 22.4% (89.8 vs. 69.7%) for NDIN, 4.7% (79.4 vs. 75.7%) for ADIN, 2.3% (65.0 vs. 63.5%) for NDF and 0.3% (63.6 vs. 63.4%) for ADF ($P < 0.001$). The procedures of fiber fractioning with detergent solutions do not promote the total detachment of microorganisms adhered to fiber residues of rumen incubated samples leading to large errors for the concentration and degradation of NDIN and ADIN. The associated errors are moderate for NDF and very low for ADF.

Key words: fiber, microbial contamination, ruminal degradation

M382 Measurement of dry matter degradation of sugar cane molasses in rumen of bovine using nylon bag technique. J. J. Lomeli*[1], L. R. Flores[1], R. H. Ley[1], J. E. Guerra[2], I. Quintero[1], J. E. Borbolla[1], and R. Barajas[1], *[1]FMVZ-Universidad Autonóma de Sinaloa, Culiacán, Sinaloa, México, [2]FA-Universidad Autónoma de Sinaloa, Culiacán, Sinaloa, México.*

With the objective of determine the degradation of dry matter of sugar cane molasses in the rumen of bovine using nylon bag technique 2 experiments were performed. Two cows fitted with 10 cm ID cannula and fed a 70% concentrate diet (14.7% CP; NEm 1.73 Mcal/kg) containing 10% of sugar cane molasses were used. Exp. 1: Nylon bags (10 x15 cm) were filled with a combination of ground corn and rewashed oven-dried river-sand in proportions of 100, 90, 80, 70, 60, 50, 40, 30,

20, 10, and 0% of corn and complete to 100% with sand. Bags were incubated during 24 h in rumen. Compared by orthogonal contrasts, corn-DM disappearance was not affected (P = 0.98) by sand level, with values of 61.7% vs. 61.1% for only corn, and all other levels, respectively. Exp 2: Ground corn and cane molasses were mixed in proportion of 0, 20, 40, 60, and 100% molasses. To prevent the outflow of molasses from the bags, it was blend with dried river-sand. Nylon bags (10 x15 cm) bags were filled to contain the equivalent of 5 g of sample once discounted river-sand. Then were placed in rumen during 3, 6, 9, 12, 18 or 24 h. Data of rumen DM degradation for treatments containing from 0 to 60% of molasses at each time were used to calculate by linear regression the corresponding DM of molasses as 100% of DM. Calculated values were contrasted by regression against observed DM disappearance of 100% molasses treatment. The kinetics of degradation of molasses-DM was calculated by exponential regression. Molasses DM solubility was 69% and calculated by regression was 72%. Molasses DM effectively degraded in rumen was 98.5% at degradation rate of 84%/h (r = 0.97; $P < 0.0001$), and requires proximately 2 h. Predicted by regression and observed values shown a highly linear relationship (r = 0.99; $P < 0.01$). It is concluded that almost totality of molasses DM is degraded in rumen in the first 2 h after feeding

Key words: cane molasses, ruminal degradation, nylon bag

M383 Ruminal degradation of the dry matter of the sugar cane silage. J. A. Reyes-Gutierez[1,2], O. D. Montañez-Valdez*[1], R. Rodríguez Macías[2], E. Salcedo Pérez[2], M. A. Ruiz López[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, Zapopan, Jalisco, México, [3]Instituto Nacional de Investigaciones Agricolas y Pecuarias, Tecomán, Colima,México.*

The objetive of this work was to study the rumen degradability of dry matter (DM) of sugarcane (*Saccharum officinarum*) in 2 forms for use in ruminant nutrition: T1) fresh sugar cane (FSC) and T2) sugar cane silage (SCS). The digestibility was determined in situ using the technique of nylon bag with 4 Holstein cows fitted with ruminal cannula, which were fed only with each, FSC or SCS and supplemented with 1 kg of commercial dairy concentrate. Five grams of ground sample of FSC and SCS were incubated in nylon bags for periods of 0, 8, 12, 24, 36, 48, 72 and 96 h. Treatments were distributed in a completely randomized design with 6 replicates per treatment. It was found that in situ digestibility of dry matter was higher ($P \leq 0.05$) for FSC in most incubation periods with respect to SCS, except at 24 h of incubation ($P \geq 0.05$, Table 1). Ruminal pH showed no significant differences ($P \geq 0.05$) between treatments. We hypothesized that the degradation of the DM and OM in SCS was higher by the additive and inoculum use, although FSC showed the higher values on this study, the major problem is the daily harvest, sugarcane sours rapidly and becomes unpalatable if left unattended after chopping. Ensiling of sugarcane may solve these problems. However, knowledge on the feeding value of ensiled sugarcane is limited and most studies have been conducted with this forage.

Table 1. Coefficients of digestibility in situ of experimental materials (%)

Component	FSC	SCS	EE
Dry Matter			
96[1]	61.93[a]	56.60[b]	1.15
72	60.75[a]	52.29[b]	0.89
48	56.80[a]	51.45[b]	1.08
36	47.21[a]	44.08[b]	0.66
Organic Matter			
96	57.88[a]	47.43[b]	2.35
72	56.66[a]	54.66[a]	0.90
48	50.70[a]	45.87[b]	1.50
36	52.29[a]	47.50[b]	1.06
Ruminal pH			
Average	7.02	7.15	0.14

[a,b]Different letters in the same row differ ($P \leq 0.05$). [1]Hours of incubation.

Key words: degradation, sugar cane, ruminant

M384 A novel method to measure rumen stability of three rumen protected products. M. Sakkers*[1], P. H. Robinson[2], L. J. Erasmus[1], J. Garrett[3], and R. Meeske[4], *[1]University of Pretoria, Pretoria, South Africa, [2]University of California, Davis, Davis, [3]Quali Tech Inc., Chaska, MN, [4]Western Cape Department of Agriculture, Western Cape, South Africa.*

There are currently a large number of rumen protected products (RPP) on the market, designed to achieve precision delivery of key nutrients post-ruminally. There is however no method to assess the quantitative stability of these products in the rumen. The objective was to determine the stability of 3 RPP using a novel in vivo dual fluid phase marker technique. Three RPP were evaluated, being ascorbic acid, lysine (L) and niacin, composed of 62.3% nutrient (51.87% for L), 8.9% Co-EDTA (8.65% for L) and 28.8% fat matrix (39.48% for L) (specific gravity approximately 1.21). Four ruminally cannulated Jersey cows were fed a common total mixed ration composed of chopped lucerne hay, maize stover, maize meal, soybean oilcake, hominy chop, molasses, urea, Megalac and a vitamin/mineral premix containing 18% CP, 31.7% NDF and 21.3% starch on a dry matter basis. The experiment was a 4 × 4 Latin Square design with 4 14-d periods. Cows were ruminally dosed on d 11 with Cr-EDTA and one of the 3 RPP to deliver 2.4 g of Co and 2.4 g of Cr. Rumen fluid samples were collected before dosing, at 2 h intervals through 25 h, and then every 4 h until 49 h post-dosing. These samples were analyzed for Co, Cr and pH. Ruminal pH was unaffected by treatment and averaged 5.88, with diurnal variation between 5.65 and 6.40. Animal performance was unaffected by treatment with average milk production of 24.6 L/day, milk fat of 4.18% and milk protein of 3.56%. The stability of the RPP within the rumen was measured as the proportion of the area under the curve of rumen clearance of Co (in the RPP as Co-EDTA) relative to the clearance of the Cr (as free Cr-EDTA). The rumen stability of RP Niacin was the highest (P = 0.06) at 66.7% relative to RP Lysine at 55.0%, but only tended (P = 0.14) to differ from RP Ascorbic acid at 58.7%. Simultaneous in sacco incubations of the RPP showed that the appropriate incubation time to estimate the in vivo rumen stability was approximately 24 h. Results show that this in vivo method can be utilized to quantitate rumen stability of RPP, and indicate the most appropriate rumen in sacco incubation time to reflect that measurement.

Key words: area under curve, clearance rate, stability

M385 Biohydrogenation of docosahexaenoic acid into unsaturated 22-carbon fatty acid intermediates in ruminal batch cultures. C. M. Klein*, W. C. Bridges, and T. C. Jenkins, *Clemson University, Clemson, SC.*

Docosahexaenoic acid (DHA) disappears from the rumen indicating that it is converted into other compounds; however, there is limited information on what these compounds are. In this study batch cultures of mixed ruminal microorganisms were injected with 0, 0.5, or 1% DHA and incubated for 0, 6, 24, or 48h to determine if pathways similar to linoleic acid biohydrogenation are responsible for the decrease in DHA. Triplicate cultures were lyophilized and fatty acids were analyzed by GC. Molecular weights were determined by GC/MS using chemical ionization. Statistical analysis was completed using SAS 9.2. A LSmeans ANOVA in proc GLM was used to test time and treatment effects, and proc GLIMMIX was used to test changes in fatty acid profile. At 48h, trans-11 18:1 increased with increasing DHA supplementation with levels of 0.85, 1.59, and 1.86mg for 0, 0.5, and 1% DHA ($P < 0.05$). Stearic acid levels at 48h decreased when DHA was supplemented from 7.91mg with 0% DHA to 4.26 and 4.23mg at 0.5 and 1% DHA ($P < 0.05$). By 48h, 95 and 92% of DHA had disappeared from cultures for the 0.5 and 1% treatment groups respectively indicating biohydrogenation of DHA was occurring as seen in vivo. At 48h, ketostearate increased from 0.10mg with 0% DHA to 0.50 and 0.54mg at 0.5, and 1% DHA respectively ($P < 0.05$). In cultures supplemented with 0.5, 1, 2, or 3% U-13C DHA there was no label in ketostearate at 48h indicating that although ketostearate increases with DHA supplementation it is not produced from DHA ($P > 0.05$). In DHA cultures, up to 5 isomers of C22:5, 6 isomers of C22:4, 5 isomers of C22:3, and 5 isomers of C22:1 were isolated in 6, 24 or 48h cultures. No unsaturated 22 carbon fatty acids were isolated from cultures when DHA was not added. Over time, the isotope profiles changed from 55% C22:5 and 23% C22:4 at 6h to 35% C22:3 and 29% 22:1 at 48h ($P < 0.05$). The time course appearance of unsaturated 22 carbon fatty acids indicates that biohydrogenation of DHA in ruminal batch cultures occurs by pathways of isomerization and hydrogenation resulting in a variety of unsaturated 22 carbon intermediates.

Key words: rumen, docosahexaenoic acid (DHA), biohydrogenation

M386 Effect of a handmade inoculum and additive on in vitro dry matter digestibility of sugar cane silage. O. D. Montañez-Valdez*[1], J. A. Reyes-Gutierrez[1], G. Rocha-Chavez[1], J. M. Tapia-Gonzalez[1], J. A. Martinez-Ibarra[1], C. E. Guerra-Medina[2], J. J. Tinajero-Martinez[4], J. H. Avellaneda-Cevallos[3], and R. Santibañez-Escobar[1], *[1]Centro Universitario del Sur, Ciudad Guzmán, Jalisco, México., [2]Centro Universitario del la Costa Sur, Autlán de la Grana, Jalsico, México., [3]Universidad Técnica Estatal de Quevedo, Los Ríos, Ecuador., [4]Facultad de Ciencias Agrícolas, Universidad Autónoma de Chiapas, México.*

The objective of this study was to evaluate the effect of adding inoculum and an additive handmade in sugar cane silage (SCS) on the in vitro digestibility of DM and OM. The treatments were: T1) sugar cane silage with 1% inoculum and 1% additive; T2) sugar cane silage with 3% inoculum and 3% additive were incubated for 48 h incubations. Data were analyzed by mean comparison using a T Student test. The inoculum consists of 10% molasses, 1.0% of yogurt, 5.0% chicken manure, 0.5% urea and 83.0% water and the additive was formulated with 1.0% urea, 0.1% ammonium sulfate and 0.25% phosphorus on DM basis. There were differences ($P \leq 0.05$) between treatments on the in vitro digestibility of DM. T1 shows higher percentages of DM (41.93 ± 0.024 vs. 35.06 ± 0.030), but we do not found change in OM (84.18 ± 0.48 vs. 85.28 ± 0.39); these in vitro results were not reflected improved of inclusion of higher levels of inoculum and additive in sugar cane silage. These results possibly demonstrate that although the primary objective of the addition of inoculums and additives to the sugar cane silages is for avoiding an alcoholic fermentation, these additives can affect negatively the ruminal environment and decrease the animal production.

Key words: additive, inoculum, sugar cane

M387 Effects of dietary probiotics on growth performance, nutrient digestibility, blood profiles, fecal gas emission, fecal microflora and diarrhea index in weanling pigs. S. M. Hong*[1], T. X. Zhou[1], I. H. Kim[1], and Y. H. Park[2], *[1]Dankook University, Cheonan, Choongnam, South Korea, [2]Yeungnam university, Daedong, Gyeongsang, South Korea.*

This study was conducted to investigate the effects of dietary probiotics on growth performance, nutrient digestibility, blood profiles, fecal gas emission, fecal microflora and diarrhea index in weanling pigs. A total of 140 weanling pigs (7.90 ± 0.92kg, initial body weight) were used for 4 weeks. Dietary treatments included: 1) NC (free antibiotics diet), 2) PC (free antibiotics diet + 0.01% tyromix), 3) P1 (NC + 0.1% probiotics), and 4) P2 (NC + 0.2% probiotics). Each treatment had 7 replicates of 5 pigs per pen in a randomized complete block design. From 0 to 2 weeks, the ADG was higher ($P < 0.05$) in PC treatment than NC treatment. PC and P1 treatments were higher than NC treatment in ADG through the entire experiment period.PC treatment was higher than other treatments in nitrogen digestibility ($P < 0.05$) and P1 treatment was higher than NC treatment in gross energy digestibility ($P < 0.05$) at the end of 2 weeks. At the end of 4 weeks, nitrogen digestibility was higher in PC, P1 and P2 treatments ($P < 0.05$) than those in NC treatment. And gross digestibility was higher ($P < 0.05$) in P1 and P2 treatments than NC and PC treatments. P1 treatment had a higher blood lymphocyte percentage than NC treatment. IgG concentration was higher in PC, P1 and P2 treatments than NC treatment ($P < 0.05$). Dietary probiotics supplementation decreased ammonia, total mercaptan and hydrogen sulfide of fecal gas emission ($P < 0.05$). Lactobacillus of fecal microflora was higher in P1 treatment than those in NC and PC treatments ($P < 0.05$) No significant difference was noted in *Escherichia coli* among treatments ($P > 0.05$). Diarrhea index was lower in P1 treatment than that in NC treatment ($P < 0.05$). In conclusion, dietary probiotics supplementation can improve growth performance, nutrient digestibility, blood profiles, fecal gas emission, Lactobacillus in fecal microflora and prevent diarrhea.

Key words: growth performance, nutrient digestibility, probiotics

M388 The response of urea-N^{15} in ruminal content influenced by essential oils. S. Zhao, J. Wang*, D. Bu, and Y. Zhang, *State Key Laboratory of Animal Nutrition, Institute of Animal Sciences, Chinese Academy of Agriculture Sciences, Beijing, China.*

Urea-N is an important and cost-less nitrogen source for ruminant, because rumen microorganisms have the ability to hydrolyze urea to ammonia which is used for microbial protein synthesis. Essential oils were found that they regulated nitrogen metabolism and fermentation in rumen. However the effect of essential oils on urea-N metabolism in rumen is limited. The purpose of this study is to reveal the distribution of urea-N in rumen and its changes influenced by the essential oils in vitro. Garlic oil, tea tree oil, and eucalyptus oil were added

into different serum bottles (containing 1.5 g TMR diet, 100 mL McDougall′s buffer, 50 mL strained ruminal fluid and 0.015 g urea-N^{15}) to the final concentrations of 300 mg/L respectively. All bottles were inoculated in a 39°C shaking water bath. Blanks without essential oils were included. All treatments were incubated in triplicate. The content of each bottle was collected at 0, 6, 12 and 24 h of incubation. The microorganisms were isolated by differential centrifugation, and the abundance of N^{15} was analyzed by mass spectrometer. The results showed that the abundance of urea-N^{15} in fermentation fluid decreased following the incubation time, but which in solid-associated and liquid-associated microorganisms increased with time. The 3 kinds of essential oils had no significant effect on urea-N^{15} distribution in solid-associated and liquid-associated microorganisms from 0 to 12 h. However, the abundance of urea-N^{15} from garlic oil treatment decreased significantly compared with tea tree and eucalyptus oil treatment in solid-associated and liquid-associated microorganisms, at 24 h. The concentration of ammonia nitrogen from garlic oil treatment in fermentation fluid decreased significantly at 24 h. DGGE revealed that bacterial population can be changed by 3 kinds of essential oils. The Shannon′s diversity index of bacteria was 2.86, 3.66, 3.82 and 2.78 for blank, garlic oil, tea tree oil and eucalyptus oil treatment. In conclusion, urea-N is accumulated by microorganism and can be influenced by garlic oil with the increase of incubation time.

Key words: essential oils, urea-N^{15}, rumen

M389 Effects of polyclonal antibody against urease on ruminal fermentation and microbiota diversity in vitro. S. Zhao, J. Wang*, D. Bu, and Y. Zhang, *State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China.*

Microbial urease plays an important role in the nitrogen metabolism in rumen for ruminants. However the problem is the hydrolysis rate of urea exceeds the utilization of ammonia. Therefore, many nutritionists are eager to look for inhibitors of urea hydrolysis in the rumen. The purpose of this study is to evaluate the effect of urease antibody on ruminal fermentation and bacterial diversity. Urease gene was linked to pET-30 vector and expressed in *E.coli* BL21 (DE3). The purified urease protein was injected into rabbits to prepare antibody against urease from blood. Rabbit antibodies were dosed (0, 0.5 and 1 mL/bottle) into serum bottles containing 0.25 g TMR diet, 20 mL McDougall′s buffer, 10 mL strained ruminal fluid, 30 mg urea and inoculated at 39°C. The contents of each bottle were collected at 0, 1, 2, 4, 8 and 12 h of incubation. The total microbial DNA in content was extracted by the method of Repeated Bead Beating Plus Column (RBB+C), and analyzed by DGGE to reveal bacterial diversity. The results showed that about 10 mg purified urease protein was obtained. The titer of polyclonal antibody against urease was about 1: 51200 by ELISA analysis. Antibody had a significant effect on the concentration of urea and ammonia. Compared with that of 0 mL/bottle of antibodies, the rates of urea disappearance and subsequent ammonia formation from 1 mL/bottle of antibodies descended 70.3% and 17.9% respectively ($P < 0.05$). In addition, there were 10.9%, 9.4%, 11.8%, 6.5%, 21.4%, 45.2% increases in total VFA, acetate, propionate, butyrate, valerate, isovalerate between 0 and 1 mL/bottle of antibodies ($P < 0.05$). DGGE revealed that the microbial spices were changed, with 51% identity, after added with antibody. Shannon diversity index in 0.5 mL/bottle of antibodies (3.04) and 1 mL/bottle of antibodies (2.92) differed significantly from non-addition of antibody (3.24). In conclusion, antibody against urease could slow down the rate of urea hydrolysis, which may be caused by changes of microorganism.

Key words: microbiota diversity, rumen, urease

M390 Effects of nitrate on microbial communities and rumen fermentation characteristic by using consecutive culture system. Z. Zhou*[1], Z. Yu[2], and Q. Meng[1], *[1]College of Animal Science and Technology and State Key Laboratory of Animal Nutrition, China Agricultural University, Beijing, 100193, China, [2]The MAPLE Research Initiative, Department of Animal Sciences, The Ohio State University, Columbus.*

The primary objective of the study was to investigate the effect of sodium nitrate on population shift of methanogen and 3 cellulolytic species (*Ruminococcus albus*, *Fibrobacter succinogenes*, and *Ruminococcus flavefaciens*), methane production and fermentative characteristic in consecutive culture system. The effects of nitrate on rumen fermentation were compared during 6 24 h consecutive cultures of ruminal microbes. When consecutive culture inoculated with 12 mM nitrate, the cumulative CH_4 production was drastically increased ($P > 0.05$) in the 3rd and 4th series culture, and decreased in the 5th and 6th series culture. Analysis of volatile fatty acids at the end of the consecutive incubation revealed no ($P > 0.05$) or minor effects of nitrate treatment on acetate accumulations, no effect ($P > 0.05$) on propionate accumulations and ratio of acetate/propionate. Real-time polymerase chain reaction (PCR) was used to quantify for mean values of relative population size (RPS, the percent of bacterial 16S rRNA copy number) of methanogens and 3 cellulolytic species. In the consecutive bath culture, methanogens distinctly decrease (RPS > 88.08%) was shown from the 2nd incubation series. The abundance of *R. flavefaciens* was also decreased to nearly undetermined level from the 2nd incubation series. The mean RPS values of *R. albus* were not significantly decreased by nitrate addition consecutive incubation series. *F. succinogens* showed a general trend to increase in the consecutive culture. These data suggest that nitrate inhibited ruminal methane production in our in vitro system but their effects on fermentation differed. Nitrate inhibit populations of methanogens, *F. succinogenes* and *R. flavefaciens*, but have hardly effect on total bacteria and *R. albus*.

Key words: cellulolytic species, methanogene, nitrate

M391 Effects of lipid sources on performance and carcass traits of beef cattle finished at pasture. T. T. Berchielli*[1,2], I. P. C. Carvalho[1,2], G. Fiorentini[1,2], and J. F. Lage[1,2], *[1]São Paulo State University, Jaboticabal, São Paulo, Brazil, [2]FAPESP– Fundação de Amparo á Pesquisa do Estado de São Paulo, São Paulo, SÃo Paulo, Brazil.*

This study was carried out to evaluate the effects of lipid sources added to protein-energy supplements on performance and carcass traits of finishing beef steers kept at pasture. Forty-five Nellore steers (initial average body weight of 440 ± 14 kg) were assigned to 5 treatments of a completely randomized design. The animals were divided in to 10 paddocks (2 paddocks per treatment) of *Brachiaria brizantha* 'Xaraés'. The lipid sources: linseed oil, palm oil, soybean grain and by-pass fat (Lactoplus) were added to a supplement offered to the animals once a day (amount of 1,0% of the body weight) trying to complete 6% of ether extract on the total diet. The control treatment was composed of an energy-protein supplement with no additional fat. The supplements were based on corn and soybean meal. All the concentrate containing 20% CP and 10% EE (except the control supplement, which contained 3% EE). The experimental period was 90 d and the animals were weighed every 28 d and slaughtered at 495.6 kg. The treatments were compared by analyzing variables using the GLM procedure (SAS

9.1, SAS Institute, Inc., Cary, NC). Average daily gain (ADG) was not affected ($P > 0.05$) by the lipid sources, with mean of 0.601 kg/d. The hot carcass yield (HCY), hindquarter yield (HY), spare ribs yield (SRY) and forequarter yield (FY) were also not affected ($P > 0.05$) by the lipid source on the supplement (57.0, 48.3, 12.1 and 39.7% respectively). There was no effect ($P > 0.05$) on fat thickness, loin eye area (LEA) and LEA/100 kg of BW. The average values obtained for these traits were 7.78mm, 73.40 cm^2 and 14.83 cm^2 respectively. These results suggest that the addition of lipid sources on supplements for grazing beef cattle do not influence the performance and carcass traits when the fat level on the total diet is above 6% of ether extract.

Key words: carcass yield, fat thickness, loin eye area

M392 Effect of the different lipid sources on the carcass traits of the steers finished in a feedlot. T. T. Berchielli*[1,2], G. Fiorentini[1,2], I. P. C. Carvalho[1,2], J. F. Lage[1,2], and R. C. Canesin[1,2], *[1]São Paulo State University, Jaboticabal, São Paulo, Brazil, [2]FAPESP– Fundação de Amparo á Pesquisa do Estado de São Paulo, São Paulo, São Paulo, Brazil.*

The objective of this study was to evaluate the effect of the different lipidic sources on the carcass traits of the steers finished in feedlot. Forty-five Nellore steers (average initial body weight of 423 ± 15 kg, 16 mo of age) were fed with 60% of roughage basis of corn silage and 40% concentrate, with 7.0% of ether extract level. The fat sources were: soybean grain, protected fat (Lactoplus), linseed oil and palm oil plus a control, without additional fat. The supplements were based on corn and soybean meal. The animals were housed in individual stalls, for 90 d and slaughtered at 497.96 kg. The study was in a completely randomized design, with 5 treatments and 9 replications, and the averages were compared by the Tukey test at 5%. The carcass traits were evaluated: weight at slaughter (WS, kg), hot carcass yield (HCY, %), cold carcass yield (CCY, %), forequarter yield (FY, %), special hindquarter yield (SHY, %), spare rib performance (SRP, %), pH (24 h post slaughter), loin eye area (LEA, cm^2) and fat thickness (FT, mm). No effects of diets were observed ($P > 0.05$) in relationship to FY, SRP, pH, LEA and FT, with mean of 36.75, 9.39, 5.77, 82.41 and 6.48 respectively. However the other traits were different between treatments ($P < 0.05$) the WS was lower in animals that received the palm oil than the animals fed with linseed oil, protected fat, soybean grain and control (436.44, 494.57, 523.56, 510.22 and 522.67, respectively). Consequently the HCY and CCY were also affected and animals receiving the diet with protected fat had a greater yield than the animals fed with palm oil. The palm oil diet showed an increase of SHY compared with diet control (55.19% versus 53.31%, respectively). These results suggest that the addition of lipid sources at the level of 7.0% in diet influence the carcass traits of feedlot steers.

Key words: fat thickness, loin eye area, protected fat

M393 Blood biochemical constituents in growing lambs fed on orange pulp ensiled with exogenous enzymes. A. Z. M. Salem*[1,4], H. M. Gado[2], N. E. Odongo[3], and B. E. Borhami[1], *[1]Department of Animal Production, Faculty of Agriculture (El-Shatby), Alexandria University, Alexandria, Egypt, [2]Department of Animal Production, Faculty of Agriculture, Ain Shams University, Cairo, Egypt, [3]Animal Production and Health Section, Joint FAO/IAEA Division of Nuclear Techniques in Food and Agriculture, International Atomic Energy Agency, Vienna, Austria, [4]Centro Universitario UAEM-Temascaltepec, Universidad Autónoma del Estado de México, Estado de México, México.*

Twenty-four Ossimi male lambs were used to evaluate effects of feeding ensiled orange pulp (EOP) in lamb diets either with or without addition of exogenous enzymes (ZADO of anaerobic bacterium origin-ENZ) on blood protein (g/100 mL), globulin (g/100 mL), albumin (g/100 mL), cholesterol (mg/100 mL), urea (mg/100 mL), serum glutamic-oxaloacetic transaminase (GPT, units/ml) and glutamic-pyruvic transaminase (GOT, units/ml) concentrations. Lambs (21.1 ± 1.01 kg of BW) were assigned to one of 3 groups of 8 animals/group in a randomized complete block design being: Control (0 g/kg EOP), EOP (Control with 150 g/kg EOP without enzymes) or EOP+ENZ (EOP with 5 g/kg of ZADO®). Feeding lambs with EOP diet did not affect blood protein, albumin, urea, GPT and GOT concentrations (Table 1), whereas addition of ENZ during ensilage of orange pulp increased blood globulin concentration ($P = 0.048$) and reduced cholesterol level ($P = 0.043$). Data suggested that addition of enzymes to the EOP could improve the animal immunity and health.

Table 1. Blood biochemical constituents of lambs fed diets containing ensiled orange pulp (EOP) in the presence (EOP+ENZ) or absence (EOP) of an exogenous enzymes mixture

	Diets				
	Control	EOP	EOP+ENZ	SEM	*P*-value
Protein	7.2	7.1	7.4	0.61	0.26
Globulin	52.5[b]	54.6[ab]	60.8[a]	5.82	0.048
Albumin	3.8	4.0	3.9	0.32	0.34
Cholesterol	109.1[a]	103.7[a]	94.5[b]	11.41	0.043
Urea	33.6	34.2	35.9	10.62	0.28
GPT	40.3	43.4	47.2	6.23	0.23
GOT	24.5	25.3	24.8	4.36	0.36

[a,b]Means in the same row with different letters differ significantly ($P < 0.05$).

Key words: lambs, orange pulp, silage

M394 Effect of propionate on urea and glucose kinetics in sheep. U. Agarwal*, K. Somers, K. Bailey, Q. Hu, and B. J. Bequette, *University of Maryland, College Park.*

Feeding and post-ruminal infusion of propionate is known to increase N retention in growing ruminants, possibly through increasing urea recycling and/or gluconeogenesis. The aim of this study was to determine whether ruminal propionate increases urea recycling, gluconeogenesis or both in growing sheep. Wether sheep (n = 6, 32.5 kg BW), fitted with a rumen cannula, were fed to 1.8 × maintenance energy intake a pelleted ration (130 g CP/kg, 9.3 MJ ME/kg) and infused into the rumen with isoenergetic (1 MJ/d) solutions of either Na-Acetate (control) or Na-Propionate for 10-d periods in a balanced crossover design. [$^{15}N_2$]Urea was continuously infused i.v. for the last 5 d, and all urine and feces collected, and subsampled. Over the last 12 h, [$^{13}C_6$] glucose was infused i.v. and hourly blood samples collected during the last 5 h. Compared with background (no infusion), Acetate infusion increased ($P = 0.07$) rumen acetate but decreased ($P = 0.07$) butyrate, whereas Propionate infusion increased ($P < 0.05$) rumen propionate. Dietary DM digestibility was not different (70%). Propionate infusion increased ($P < 0.05$) plasma urea concentration (4.1 vs. 3.4 m*M*). Urea synthesis (14.2 vs. 14.3 g urea-N/d), urinary urea excretion (10.2 vs. 9.5 g urea-N/d) and urea recycled to the gastrointestinal tract (4.3 vs. 4.6 g urea-N/d) were not different between Propionate and Acetate (control) infusions. Propionate infusion increased plasma glucose entry rate (3.7 vs. 4.4 g/kg BW/d, $P < 0.01$) and gluconeogenesis (2.44 vs. 3.1 g/kg BW/d, $P < 0.01$) but did not affect glucose (Cori) recycling. Under the dietary conditions of this study, infusion of propionate into the rumen did not affect urea synthesis and recycling compared with the isoenergetic control (Acetate), despite the fact that plasma urea concentration was higher with Propionate infusion. The increase in gluconeogenesis with Propionate infusion increased the supply of glucose for peripheral tissue metabolism and likely spared amino acids for protein synthesis.

Key words: isoenergetic, gluconeogenesis, urea kinetics

M395 Duodenal flow of nitrogenous compounds by wethers fed a fresh ryegrass-based diet intraruminally infused with *Acacia mearnsii* tannins. F. Hentz*[1], C. J. Härter[2], G. V. Kozloski[1], M. P. Mezzomo[1], and A. C. Fluck[1], *[1]Universidade Federal de Santa Maria, Santa Maria, RS, Brazil, [2]Universidade Estadual Paulista, Jaboticabal, SP, Brazil.*

Four Polwarth × Texel wethers (30 ± 4.8 kg BW) fitted with chronic rumen catheter and duodenal cannula, housed in metabolic cages and offered fresh ryegrass (*Lolium multiflorum*) ad libitum (10% refusals) were used in a 4 × 4 Latin Square design experiment to evaluate the effects of ruminal infusion of *Acacia mearnsii* tannin extract (0.625 g/g of condensed tannins) on duodenal flow of N compounds and efficiency of microbial protein synthesis (EMPS). Treatments consisted of no tannin (0) or intraruminal infusion of 20, 40 or 60 g tannin extract/kg of DMI, according to the DMI of the previous day. Experimental periods lasted for 15 d (10 d adaptation, 5 d collection periods). Feed, orts, feces and urine output were recorded daily on d 10 to 15 and samples collected and composited within animal and period. On d 15, duodenal digesta samples (100 mL) were collected at 3 h intervals over a 24 h period and composited within animal and period. Duodenal flow of N compounds (g/d) was calculated by multiplying their concentrations in duodenal digesta (g/kg of DM) by duodenal flow of DM (g/d). Duodenal microbial N flow was estimated from urinary excretion of purine derivatives. Data were analyzed using the MIXED procedures of SAS. When the treatment effect by ANOVA was significant ($P < 0.05$) or tended to be significant ($0.05 < P \leq 0.10$), linear and quadratic effects of treatments were tested by regression analysis. Duodenal flow of total N ($P = 0.108$), α-amino N ($P = 0.305$) and ammonial N were not affected ($P = 0.568$) by tannins. There was a linear reduction ($P = 0.020$) in duodenal microbial N flow (from 6.2 to 2.9 g/d) whereas the EMPS was not affected linear ($P = 0.298$) or quadratically ($P = 0.143$) by the increasing levels of tannin infusion. In conclusion, although dietary inclusion of tannin extract from *Acacia meanrsii* in concentrations up to 60 g/kg of DMI significantly reduced microbial N flow,

it does not affect the amount of duodenal α-amino N supply and the EMPS in wethers fed a temperate grass-based diet.

Key words: condensed tannins, microbial N, sheep

M396 Effect of germinated and ensiling sorghum grain on digestion and ruminal fermentation by sheep. D. García[1], F. Castrejón[1], G. Mendoza[2], and L. Corona*[1], *[1]Universidad Nacional Autónoma de México, Cd. Universitaria, DF, México, [2]Universidad Autónoma Metropolitana, Xochimilco, DF, México.*

To evaluate the influence of sorghum grain germinated and ensiling on nutrient digestion and ruminal fermentation of sheep, 5 Pelibuey lambs (38 ± 2.84 kg BW) with cannulas in the rumen and proximal duodenum were used, in a Latin square 5 × 5. Treatments consisted of a basal finished diet containing 72% sorghum grain (% DM basis) as: 1)dry whole sorghum (DWS); 2) zero days germinated sorghum and ensiled for 42d, (GSE (G0); 3) 1d GSE (G1); 4) 3d GSE (G3); 5) 5d GSE (G5). G1, G3 and G5 showed higher ruminal OM digestion ($P < 0.01$, 25.6%), ruminal starch digestion, RSD ($P < 0.01$, 25.6%) and ruminal NDF digestion, RNDFD ($P = 0.17$, 4.31%) but smaller protein efficiency, PE ($P < 0.05$, 18.65%) and postruminal OMD($P < 0.05$, 9.88%) compared with DWS (percentages are the differences between treatments). G1, G3 and G5 had higher RNDFD ($P < 0.05$, 14.63%), but smaller RSD ($P < 0.10$, 5.20%) and PE ($P < 0.05$, 18.04%), compared with SG0E. The treatments G1, G3 and G5 showed bigger total digestion of OM ($P < 0.05$, 3.42%), total starch digestion, TSD ($P = 0.18$, 2.12%) and total nitrogen digestion, TND ($P < 0.10$, 3.65%) compared with DWS and this higher TOMD ($P = 0.11$, 2.61%), total NDF digestion, TNDFD ($P < 0.10$, 24.79%) regarding SG0E. The TSD ($P = 0.13$, 2.9%) was higher for G0 and TNDFD was lower ($P < 0.05$, 27.62%) compared with DWS. The increasing of germinated days, decrease (lineal effect, $P < 0.05$) TSD. The digestible energy DE (Mcal/kg) values were higher for G1, G3 and G5 ($P < 0.05$, 4.39%) compared with DWS. The ruminal pH was bigger ($P < 0.05$, 5.78%) for G1, G3 and G5 compared with DWS. The germination days increased (lineal effect, $P < 0.01$) acetate and reduced propionate (lineal effect, $P < 0.01$). Germination days increased (lineal effect, $P < 0.05$) methane production. It was concludes that the treatments with germinated sorghum and ensiled presented higher total digestion of OM, starch, N, DE and ruminal pH compared with whole sorghum grain, due mainly to an increment of the ruminal digestion. When increasing the days of germination decrease the starch digestion. The best treatment in terms of digestion of starch, ruminal pH and energy value was G1.

Key words: digestion, germinated sorghum, lambs

M397 Concentration of some elements in blood serum of nonlactating goats in a subtropical region of Southwest of México State. A. Olmedo, R. Rojo, A. Z. M. Salem, J. Cedillo-Monrroy*, J. Morales-Diaz, J. L. Tinoco-Jaramillo, J. L. Martínez-Benitez, and F. Vázquez-Armijo, *Centro Universitario UAEM-Temascaltepec, Universidad Autónoma del Estado de México, Temascaltepec, Estado de México, México.*

A study was conducted to determinate the P, Ca, Mg, K, Na, Cu and Zn nutritional status of grazing nonlactating goats during 2 different season (dry and rainy of 2008) in 4 localities (Tejupilco, Amatepec, Luvianos and Tlatlaya) at south-western of México State. Eighty-four nonlactating goats (>2 calving, BW 39 ± 8), were sampled before morning feeding. Blood mineral concentration were assayed and data were analyzed using one way ANOVA test; significant differences between means were tested by Tukey. Amatepec region registered the higher ($P < 0.01$) P concentration (4.79 mg/dL). Ca concentration was higher ($P < 0.01$) during rainy season (11.20 mg/dL), than dry period (9.54 mg/dL). There were no differences ($P > 0.05$) among season*localities. Luvianos showed the highest ($P < 0.01$) Na value during dry season (411.76 mg/dL) and Tejupilco presented the lowest values at the same season (322.0 mg/dL). K concentration was different ($P < 0.01$) during dry season. Tlatlaya showed the highest ($P < 0.01$) K value (29.50 mg/dL) and Tejupilco had the lowest (17.31 mg/dL). Tlatlaya recorded the highest ($P < 0.05$) serum Cu concentration during dry season compared with rainy season (0.192 vs. 0.080 mg/dL, respectively). The rest of regions, showed similar Cu concentration and ranged between 0.082 and 0.111 mg/dL. Zn concentration showed the same trend as most of minerals. The interaction season*localities, was highly significant ($P < 0.0004$), with Luvianos that showing higher concentration during dry season (0.117 mg/dL) versus rainy season (0.056 mg/dL), whereas for the rest of regions had a different concentration (from 0.059 to 0.096 mg/dL). P and Ca from the 4 regions in both seasons had low values, suggesting deficiency of these elements. K and in particular Na, were above normal levels reported in the literature. Based on results for Cu and Zn, nonlactating goats could be have reproductive problems due to the deficient or marginal levels in blood serum.

Key words: mineral status, blood serum, nonlactating goats

M398 Exogenous phytase effects on performance of weaned Dorper x Pelibuey lambs. G. Buendía-Rodríguez[1], S. S. González-Muñoz*[2], G. D. Mendoza-Martínez[3], L. Y. Bernal-Zamora[3], R. Basurto-Gutiérrez[1], M. M. Crosby-Galván[2], and J. J. A. Méndez-Romero[4], *[1]CENIDFyMA INIFAP, Ajuchitlán, Querétaro, México, [2]Colegio de Postgraduados, Montecillo, Estado de México, México, [3]Universidad Autónoma Metropolitana–Xochimilco, México DF, [4]Universidad La Salle Bajío, Guanajuato, 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 in vitro residual phosphorus concentration and performance of 30 weaned 3/4 Dorper × 1/4 Pelibuey lambs (12.12 ± 1.46 kg BW). In vitro treatments were: 0 and 0.12 mg phytase per g of sorghum, corn gluten meal (CGM), alfalfa hay and experimental diet (70% ground sorghum grain, 16.9% CGM, 12% alfalfa hay, 11% calcium carbonate). The experimental design was completely randomized and Tukey test ($P \leq 0.05$) was used to determine differences for residual P concentration (%) between 0 and 0.12 mg phytase: 1) at 24 h (incubation), 0.086^{a} and 0.050^{b} sorghum, 0.259^{a} and 0.119^{b} CGM, 0.365 and 0.240 alfalfa, 0.276^{a} and 0.240^{b} diet; 2) at 48 h, 0.054 and 0.048 sorghum, 0.178 and 0.161 CGM, 0.198^{a} and 0.131^{b} alfalfa, 0.237^{a} and 0.211^{b} diet. For the performance trial (60 d) lambs were fed the experimental diet and 0, 6 or 12 g/t phytase (treatments). The experimental design was completely randomized (10 lambs 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 ($P \leq 0.05$). Variables were average daily gain (ADG), dry matter intake (DMI), feed conversion (FC), apparent DM digestibility (DMD), plus P fecal excretion (PFE). Phytase did not change ($P \geq 0.05$) ADG (251, 294 and 266 g/d), DMI (905, 1119 and 975 g/d) or FC (4.06, 4.37 and 3.94). However, phytase addition increased ($P \leq 0.05$) DMD (72.34^{b}, 82.54^{a} and 82.57^{a} %) and PFE (1.01^{b}, 1.09^{ab} and 1.26^{a} g/d). Therefore, it may be concluded that apparent DM digestibility as well as phosphorus fecal excretion were affected when an exogenous phytase was added to a 70% sorghum grain diet, fed to weaned Dorper × Pelibuey lambs during 60 d.

Key words: phytase, weaned lambs, performance and fecal phosphorus

M399 Calcium propionate and grain level effects on performance, ruminal variables and plasma glucose of finishing lambs. H. A. Lee-Rangel[1], S. S. González-Muñoz*[1], G. D. Mendoza-Martínez[2], A. Hernández-Garay[1], and M. M. Crosby-Galván[1], *[1]Colegio de Postgraduados, Montecillo, Estado de México, México, [2]Universidad Autónoma Metropolitana–Xochimilco, México DF, México.*

The aim of this trial (42 d) was to evaluate the effect of calcium propionate and grain level on performance, ruminal variables and plasma glucose concentration in 32 finishing Criollo lambs (28.14 ± 2.34 kg initial BW). The experimental design was completely randomized with a factorial arrangement of treatments 2 × 2 (55 and 65% grain; 0 and 1% calcium propionate). Grain was a 50:50 mixture of corn and sorghum grain. Data collected over time were analyzed using MIXED procedure (SAS) and treatment means were compared with Tukey test ($P \leq 0.05$). There were no differences ($P \geq 0.05$) between treatments for DMI, ADG, feed conversion, rib eye area and ruminal pH. Carcass yield was increased ($P \leq 0.06$) in lambs fed 65% grain without calcium propionate (52.79 vs. 50.62%) and 55% grain with calcium propionate (52.48 vs. 50.06%). Ruminal concentration of propionate was increased ($P \leq 0.05$) in lambs fed 55 or 65% grain plus calcium propionate. However, concentration of acetate or butyrate in the rumen and plasma glucose did not change ($P \geq 0.05$). Therefore, it may be concluded that calcium propionate could partially replace the energy from the grain on diets for finishing lambs.

Key words: calcium propionate, finishing lambs, weight gain and carcass variables

M400 Effects of zilpaterol hydrochloride and genotype on performance of finishing lambs. F. Montoya[1], R. Castañeda[1], S. S. González-Muñoz*[2], G. Buendía-Rodríguez[1], R. Basurto[1], P. Partida[1], and H. Jiménez-Severiano[1], *[1]CENIDFyMA INIFAP, Ajuchitlán, Qerétaro, México, [2]Colegio de Postgraduados, Montecillo, Estado de México, México.*

Zilpaterol hydrochloride (zilpaterol), a β-adrenergic agonist, has been approved for finishing cattle, but few data are available for lambs. Therefore, the objective of this study was to determine the effects of zilpaterol and genotype on performance of 28 finishing lambs during 32 d. Genotypes were Pelibuey × Blackbelly and Pelibuey × Dorset, and lambs (32.7 ± 4.9 kg BW) were randomly assigned to experimental diets (16% CP and 2.75 Mcal ME/kg DM): Control (no zilpaterol); diet plus 6 ppm zilpaterol. Variables evaluated were ADG, DM intake (DMI), feed efficiency (FE; ADG/DMI) and final BW (FBW). The statistical model included zilpaterol and genotype effects and interaction; besides, initial BW was used as a covariable. Data collected over time was analyzed as repeated measurements using the MIXED option of SAS; and LS means are shown. Zilpaterol × genotype interactions were not significant ($P \geq 0.05$). There was no effect ($P \geq 0.05$) of zilpaterol on ADG (315 vs. 318 g/d; SEM = 0.012), DMI (1.57 vs. 1.55 kg/d; SEM = 0.031), FE (0.200 vs. 0.205; SEM = 0.007) and FBW (42.7 vs. 42.4 kg; SEM = 0.38) for control and zilpaterol diets, respectively. Regarding genotype, Pelibuey × Dorset lambs showed a higher ($P \leq 0.05$) ADG (0.336 vs. 0.284; SEM = 0.012), DMI (1.62 vs. 1.55; SEM = 0.031) and FBW (43.4 vs. 41.8 kg; SEM = 0.38) as compared with Pelibuey × Blackbelly. Therefore, the results of this trial suggest that addition of zilpaterol did not change performance of finishing lambs, but there were differences between lamb genotypes.

Key words: finishing lambs, genotype, zilpaterol

M401 Feed intake and performance by yearling Boer goat doelings consuming deep-stacked or ensiled broiler litter. A. L. Goetsch*, G. D. Detweiler, B. Bah, T. Sahlu, and J. Hayes, *American Institute for Goat Research, Langston University, Langston, OK.*

Boer goat doelings (48; 8 per treatment), 10.4 ± 0.13 mo of age and 27.1 ± 0.98 kg BW, were used in a 9-wk experiment to compare feeding value of deep-stacked (DS) and ensiled (EN) broiler litter. Broiler litter was processed for 82 d before feeding. Temperature in the upper area of the DS bay was 55–65°C for 2 wk and that in the lower area was 45–57°C for 10 wk; EN temperature ranged from 0 to 20°C. Treatments were feeding 1% BW (DM) of a 3:1 corn-soybean meal mixture and moderate to high-quality grass hay free-choice (Cont-Hay), 1% BW hay and concentrate mixture free-choice (Cont-Conc), 1% BW hay, 1.1% BW corn, and DS or EN free-choice (DS-L and EN-L, respectively), and 1% BW hay and DS or EN free-choice (DS-H and EN-H, respectively). Daily samples of DS and EN averaged 70.9 and 73.3% OM (DM basis), 21.8 and 23.2% CP, and 34.0 and 37.2% NDF, respectively. Total DM intake was less for H vs. L treatments, similar between DS-L and EN-L, and greater ($P < 0.05$) for EN-H than for DS-H (1.13, 1.28, 0.98, 1.13, 0.59, and 0.80 kg/d Cont-Hay, Cont-Conc, DS-L, EN-L, DS-H, and EN-H, respectively; SE = 0.072). There were similar differences in ADG (126, 234, 58, 75, −46, and −8 g; SE = 10.1) and the ratio of ADG:DM intake (118, 188, 60, 66, −84, and −11 g/kg for Cont-Hay, Cont-Conc, DS-L, EN-L, DS-H, and EN-H, respectively; SE = 12.7). There appeared to be more adaptation over time to EN-H than DS-H, with similar DM intake in wk 1–3 (0.48 and 0.64; SE = 0.082) but greater values in wk 4–6 (0.65 and 0.88; SE = 0.076) and 7–9 (0.64 and 0.87 kg/d for DS-H and EN-H, respectively; SE = 0.080). Likewise, ADG was similar between DS-H and EN-H treatments in periods 1 (−60 and −42 g; SE = 18.5) and 2 (6 and 27 g; SE = 12.5) and greater for EN-H in wk 7–9 (−83 and −9 g for DS-H and EN-H, respectively; SE = 22.2). In conclusion, feeding value of DS and EN for yearling meat goat doelings appears similar with moderate dietary levels, but with limited consumption of other feedstuffs, feeding value of EN may be greater.

Key words: goat, broiler litter, performance

M402 Effects of night-locking on intake, digestion, behavior, and energy use by meat goat does grazing grass/legume pasture. I. Tovar-Luna[1,2], R. Puchala*[1], T. A. Gipson[1], G. D. Detweiler[1], L. J. Dawson[3], T. Sahlu[1], A. Keli[4], and A. L. Goetsch[1], *[1]American Institute for Goat Research, Langston University, Langston, OK, [2]Universidad Autonoma Chapingo, Unidad Regional Universitaria de Zonas Aridas, Bermejillo, Durango, Mexico, [3]College of Veterinary Medicine, Oklahoma State University, Stillwater, [4]Department of Animal Production and Pastoralism, National School of Agriculture, Meknes, Morocco.*

Boer × Spanish does (24), 8 with ruminal cannula, were confined at night with access to grass/legume pasture from 0700 to 1900 h (R) or had continual access (C) in a completely randomized design with repeated measures. Data collection periods (15 d) were in late gestation (L-G; 137 d), early lactation (E-L; 43 d), late lactation (L-L; 97 d), the dry period (Dry), and early gestation (L-G; 65 d). Most does had a litter size of 2, and kids were weaned at 118 d. Pasture access treatment did not affect ingesta composition; CP (20, 13, 15, 13, and 20%) and NDF (51, 59, 63, 61, and 38% in L-G, E-L, L-L, Dry, and E-G, respectively) varied among periods. Kid ADG tended ($P < 0.08$) to be greater for C vs. R (138 vs. 118 g). Fat-corrected (4%) milk yield was greater ($P < 0.05$) for C vs. R in E-L but not L-L (2.04, 0.86, 3.27, and 1.23 kg/d for R/E-L, R/L-L, C/E-L, and C/L-L, respectively). Intake of ME was greater ($P < 0.05$) for R vs. C (823 vs. 735 kJ/kg $BW^{0.75}$). Treatment affected ($P < 0.05$) time lying (12.4 and 10.5), grazing (4.5 and 5.8), and resting (18.5 and 16.7 h for R and C, respectively). Energy expenditure (EE) was greater ($P < 0.05$) for C vs. R (754 vs. 687 kJ/kg $BW^{0.75}$) and recovered energy (RE) in tissue gain was similar between treatments. The RE of lactation (RE_l) from dietary ME was greater ($P < 0.05$) for C vs. R (244 vs. 194 kJ/kg $BW^{0.75}$); however, RE_l from mobilized tissue differed between treatments ($P < 0.05$) in E-L but not L-L (54, 15, 175, and 11 kJ/kg $BW^{0.75}$ in L-G, E-L, L-L, Dry, and E-G, respectively). The EE of activity tended to be greater ($P < 0.07$) for C vs. R (243 vs. 202 kJ/kg $BW^{0.75}$). In conclusion, R decreased activity EE to an extent less than it lessened ME intake, and greatest R impact was in E-L, with reduced RE_l and a tendency for lower kid ADG.

Key words: goat, grazing, energy

M403 Effects of replacing different levels of alfalfa hay and corn silage with sunflower residue silage on feed intake and nutrient digestibility in Mohabadi dairy goats. A. Gholami-Yangije[1], R. Pirmohammadi[1], J. Amini Jabal Kandi[2], and H. Khalilvandi-Behroozyar*[1,3], *[1]Department of Animal Science, Urmia University, Urmia, West Azerbahjan, I. R. Iran, [2]Department of Animal Science, West Azerbaijan Agriculture and Natural Resource Research Center, Urmia, West Azerbahjan, I. R. Iran, [3]Department of Animal Science, University of Tehran, Karaj, Tehran, I. R. Iran.*

Efficient inclusion of agricultural byproducts in ruminants diets is economically and environmentally beneficial. Annual production of sunflower residues in Iran reached 3 million tons in 2005. This study was conducted to determine digestibility of diets where alfalfa hay and corn silage are replaced with sunflower residue silage (SRS) at 4 rates: 0 (control, group 1), 30 (group 2), 60 (group 3) and 90% (group 4). Diets had similar NDF, ADF, CP, ME content and forage: concentrate ratio (81:19) in DM basis. Silages were made by addition of urea and dried whey (0.5% of DM from each) to chopped heads and stalks (3–5 cm, 60:40 ratio). Eight lactating dairy goats (BW = 60 ± 3) in second lactation, were divided into 4 groups of similar BW in 2 4 × 4 Latin square design, with lactation period considered as row block and goat as cloum block. Each Experimental period include 14 d for adaptation and 7 d for sample collection. Diets were formulated according to NRC 2007, prepared each day and provided in 2 equal meals (0800 and 1600h). Animals had ad-libitum access to water. Dry matter intake (DMI) and total fecal excretion of the goats was recorded daily and feed and fecal samples were withdrawn at regular intervals for chemical analysis. Nutrient intake was corrected with nutrient contents of the ort. Data were analyzed by GLM procedure of SAS 9.1 with reapeted Latin square design and duncan test ($P \leq 0.05$). DM intake decreased with increasing levels of SRS, that can be partly due to increased NDF contents in the rations and large particle size of the sunflower stalks. DM and OM digestibility decreased with increasing levels of SRS. Differences in CP and NDF digestibility were statistically significant and highest and lowest values were obtained in group 3 and 4, respectively. This experiment indicated that sunflower residue silage is an acceptable forage for dairy goat and can be replaced with forages up to 60 percent as an uncommon feedstuff in dairy goat rations.

Table 1. DMI and nutrient digestibility of experimental diets

Traits	Group 1	Group 2	Group 3	Group 4	SEM
DMI (kg/d)	1.43[a]	1.45[a]	1.37[a]	1.06[b]	0.06
DM digestibility (%)	75.51[a]	75.48[a]	72.83[a]	57.49[b]	1.86
CP digestibility (%)	76.97[a]	76.57[a]	78.55[a]	65.95[b]	1.62
OM digestibility (%)	77.17[a]	75.55[a]	74.96[a]	57.32[b]	1.89
NDF digestibility (%)	69.59[a]	70.87[a]	73.39[a]	46.18[b]	2.34

[a,b]Means within each row with different superscripts are significantly different ($P < 0.05$).

Key words: sunflower residue silage, dairy goat, feed intake

M404 Effects of inclusion of different levels of sunflower residue silage in dairy goat diets on milk production and composition. A. Gholami-Yangije[1], R. Pirmohammadi[1], J. Amini Jabal Kandi[2], and H. Khalilvandi-Behroozyar*[1,3], *[1]Department of Animal Science, Urmia University, Urmia, West Azerbahjan, I. R. Iran, [2]Department of Animal Science, West Azerbaijan Agriculture and Natural Resource Research Center, Urmia, West Azerbahjan, I. R. Iran, [3]Department of Animal Science, University of Tehran, Karaj, Tehran, I. R. Iran.*

Ruminant species occupy an important niche in modern agriculture because of their unique ability to digest certain feedstuffs, especially agricultural byproducts, efficiently. Sunflower residues is one of these materials that its annual production in Iran reached above 3 million tons. Present study was carried out to determine potential of sunflower residues silage (SRS) in support of lactation instead of alfalfa hay and corn silage at 4 rates: 0 (control, group 1), 30 (group 2), 60 (group 3) and 90 percent of dry matter (group 4). Diets had similar NDF, ADF, CP, ME content and forage:concentrate ratio (81:19) in DM. Silages were made by addition of urea and dried whey (0.5 percent of dry matter from each) to chopped heads and stalks (3–5 cm, 60:40 ratio). Eight lactating dairy goats (BW of 60 ± 3 kg) in second lactation, were divided into 4 groups of similar BW in 2 4 × 4 Latin square design, which lactation period considered as row block and goat as column block. Each experimental period consisted 14 d for adaptation and 7 d for sample collection. Diets were formulated by NRC 2007, prepared each day and provided in 2 equal meals (0800 and 1600), with ad libitum access to water. Goats were milked twice a day and milk production data were recorded and milk sampled daily and analyzed with milkoscan apparatus. DM intake was recorded daily. Data were analyzed by GLM procedure of SAS 9.1 with repeated Latin square design and Duncan test ($P \leq 0.05$). DM intake decreased with increasing levels of SRS. Milk yield decrease with increasing levels of SRS and differences were statistically significant with highest substitution level compared with control. Milk composition percentage was similar across diets but daily milk components production decreased with 60 and 90 percent SRS replacement. Also, there were a significant difference between morning and evening milk fat and total solid percentage. According to these results, sunflower residue silage is an acceptable feed for dairy goat and can be replaced with forages up to 30 percent without affecting milk production and composition.

Table 1. Milk yield and milk composition of sunflower residue silage consuming goats

Traits	Group 1	Group 2	Group 3	Group 4	SEM
Milk yield (kg/day)	1.126[a]	1.103[a]	0.902[ab]	0.763[b]	0.071
CP (kg/day)	0.038[a]	0.038[a]	0.030[ab]	0.025[b]	0.001
Fat (kg/day)	0.049[a]	0.053[a]	0.046[ab]	0.032[b]	0.002
Lactose (kg/day)	0.052[a]	0.050[a]	0.041[ab]	0.035[b]	0.001
TS (kg/day)	0.148[a]	0.151[a]	0.125[ab]	0.106[b]	0.011

[a,b]Means within each row with different superscripts are significantly different ($P < 0.05$).

Key words: sunflower residue silage, dairy goat, milk production

M405 Effect of protein restriction on body characteristics and fat storage in Awassi sheep. S. F. Abi Saab[1,2], F. T. Sleiman[3], F. Ayoub[2], and P. Y. Aad*[4], *[1]Lebanese University, Faculty of Agricultural & Veterinary Sci., Dekwaneh, Lebanon, [2]Holy Spirit University of Kaslik, Faculty of Agricutural Sci., Kaslik, Lebanon, [3]American University of Beirut, Faculty of Agricultural &Food Sci., Beirut, Lebanon, [4]Notre Dame University, Faculty of Natural & Applied Sci., Louaizeh, Lebanon.*

Awassi sheep, the predominant fat-tail breed in Lebanon, stores fat mainly in the tail, resulting in leaner meat. Little research exists on the importance of these fat reserves in compensating for arid rearing during the dry summer months. The objective of this study was to determine the effect of different dietary protein levels on BW, fat distribution and storage in Awassi sheep. Twenty-four rams (7–9 mo) weighing 53.7 ± 6.4 kg were distributed in 3 groups fed 12% (Control-C), 9% (moderately restricted-MR), and 6% (highly restricted-HR) protein diets. Body weight and girth, caudal volume and circumference, organ weights as well as fat distribution were measured over a period of 7 mo at the Agricultural Research and Education Center (AREC) of the American University of Beirut (AUB). Data were analyzed using MSTATC and presented as means ± SEM. Final BW of C (84.3 ± 5.35 kg) and MR (78.3 ± 6.68 kg) was higher ($P < 0.05$) than HR (65.3 ± 7.62 kg), whereas carcass weight was higher ($P < 0.05$) in C (38.0 ± 3.46 kg) than in MR (34.3 ± 1.91 kg) or HR (28.8 ± 3.42 kg). Girth measurement of C (98.6 ± 3.37 cm) and MR (97.7 ± 0.84 cm) was higher ($P < 0.05$) than HR (92.3 ± 4.24 cm). Both caudal volume and circumference were higher ($P < 0.05$) in C (10.5 ± 0.51 L; 58.1 ± 3.01 cm) and MR (9.3 ± 0.91 L; 54.5 ± 2.85 cm) than in HR (7.2 ± 1.63 L; 49.6 ± 4.28 cm), respectively. Abdominal and tail fat weight were greater ($P < 0.05$) in C (2.27 ± 1.05 and 7.94 ± 2.03 kg) and MR (2.0 ± 0.7 and 7.2 ± 1.2 kg) than in HR (0.9 ± 0.3 and 5.0 ± 1.4 kg) whereas organ weights (heart, kidneys, pancreas and testicles) did not vary ($P > 0.05$) among groups. Altogether, these results indicate that moderate protein restriction in diet of Awassi sheep does not greatly affect lean body composition except for the abdominal and tail fat deposition. However, a high restriction of dietary protein greatly depletes Awassi sheep fat reserves as well as significantly affects the carcass weight. We concluded that Awassi sheep uses the stored abdominal and tail fat to compensate for protein dietary restrictions without much decrease in carcass characteristics.

Key words: Awassi, abdominal and tail fat, body characteristics

M406 Nutrient intake and performance of lambs fed diets with different levels of inactive dry yeast. L. D. A. Rufino[1], O. G. Pereira*[1], K. G. Ribeiro[2], S. C. V. Filho[1], and L. L. Cardoso[1], *[1]Fed-*

eral University of Viçosa, Viçosa, Minas Gerais, Brazil, [2]Universidade Federal dos Vales do Jequitinhonha e Mucuri, Diamantina, Minas Gerais, Brazil.

Inactive dry yeast is a co-product obtained during the process of sugarcane alcoholic fermentation that is used as high protein ingredient for animal feed. The objective of this study was to evaluate the nutrient intakes and productive performance of Santa Ines lamb fed diets containing different levels of inactive dry yeast (0, 33, 67 and 100%, DM basis) in substitution of soybean meal. Diets consisted of 60% concentrate and 40% corn silage (DM basis), formulated to be isonitrogenous (15.5% CP, DM basis). Thirty-six lambs non-castrated, averaging 20 kg BW were allotted in a randomized blocks design with 9 replicates. The animals were kept in individual pens with protected feeders and waterers. The experiment lasted 78 d, divided in 3 periods of 21 d after 15 d of adaptation. Dry matter, organic matter, crude protein and ether extract intakes were not affected by yeast levels ($P > 0.05$), registering average values of 947, 905, 151 and 18 g/day, respectively. However, NDF intake decreased linearly ($P < 0.05$) as yeast levels increased in diets. The average daily gain, carcass daily gain, feed conversion and dressing percentage were not affected by yeast levels ($P > 0.05$), which were, on average, 203 g/day, 88 g/day, 4.74 and 44%, respectively. Our results suggest that inactive dry yeast can replace 100% of the soybean meal in diets of lamb. However, the utilization of this co-product depends on economic factors, because more than 90% of the Brazilian production of inactive dry yeast is traded for European countries. Financial support by CNPq and FAPEMIG.

Key words: average daily gain, crude protein, carcass dressing

M407 Effect of low and high oil corn distillers grain on rumen fermentation, growth performance and carcass characteristics of lambs. A. S. O'Hara*[1], A. V. Chaves[1], A. Tanner[2], T. A. McAllister[3,1], D. J. Gibb[3], F. van Herk[3], and R. D. Bush[1], *[1]Faculty of Veterinary Science, The University of Sydney, Sydney, NSW, Australia, [2]Faculty of Agriculture, Food and Natural Resources, University of Sydney, Sydney, NSW, Australia, [3]Agriculture and Agri-Food Canada, Lethbridge Research Centre, Lethbridge, Alberta, Canada.*

The objective of this study was to determine the effect of replacing a mixture of canola meal and barley grain in the diet with (low and high oil) corn distillers grains with solubles (DDGS) or wheat DDGS on rumen fermentation, feed intake, daily gain, feed conversion and hot carcass weight in lambs. Seventy Canadian Arcott lambs (24.7 ± 3.21 kg) were used in a completely randomized block design over a 14-week trial. Experimental diets were provided ad libitum as pelleted total mixed rations (TMR). In the treatment diets, canola meal and barley grain were replaced with 200 g/kg of dietary DM of either high oil corn DDGS, low oil corn DDGS or wheat DDGS. A positive control diet was added to match the lipid content of 39 g/kg DM of the high oil corn DDGS diet. Average daily gain (ADG) was determined by dividing weight gain by the number of trial days. Feed conversion was calculated as the ratio between DMI and ADG (g of DMI/g of LW gain. An in vitro rumen digestibility trial was conducted using ruminal fluid obtained from 3 nonlactating Holstein dairy cows. Rumen contents were also collected from each lamb at the time of slaughter for testing in vivo rumen fermentation. Data from both the in vivo and in vitro results were analyzed using the MIXED procedure of SAS. The in vitro incubations revealed both corn DDGS diets produced less microbial N and microbial DM than all other diets, however this difference was too minimal to affect growth performance. Similarly, there was no dietary effect on ($P > 0.05$) on in vivo ruminal fermentation or hot carcass weight ($P \geq 0.19$) of the lambs. Lambs fed low oil corn DDGS had lower average daily gains ($P < 0.03$) than those fed either high oil corn DDGS or wheat DDGS, however they did not differ from those fed the control. This research demonstrated that replacing canola meal and portions of barley grain with 200 g/kg DM of either high oil corn DDDGS, low oil corn DDGS or wheat DDGS in finishing lamb ratios could effectively maintain healthy rumen function, growth performance and hot carcass weight.

Key words: barley grain, ruminal fermentation, sheep supplementation

M408 Nutrient intake and performance of lambs fed diets containing different levels of rumen degradable protein. J. L. Silva[1], K. G. Ribeiro*[1], O. G. Pereira[2], S. C. V. Filho[2], D. S. Pina[3], and P. V. R. Paulino[2], *[1]Federal University of Jequitinhonha and Mucuri Valleys, Diamantina, Minas Gerais, Brazil, [2]Federal University of Viçosa, Viçosa, Minas Gerais, Brazil, [3]Federal University of Mato Grosso, Sinop, Mato Grosso, Brazil.*

The objective of this study was to evaluate the nutrient intake and productive performance of Santa Ines lambs in feedlot fed diets containing different levels of RDP. Thirty-one lambs non-castrated, averaging 22 ± 1.94 kg BW were allotted in a randomized blocks design with 8 replicates. The treatments consisted of diets with 40% corn silage and 60% concentrate formulated to contain 4 levels of RDP (9.15, 9.97, 10.79 and 11.61%, in DM basis), corresponding to 14.25, 15.50, 16.75 and 18.00% of CP. The animals were kept in individual cages with protected feeders and waterers. The experiment lasted 48 d, after 10 d of adaptation. The animals were weighed every 14 d until reaching the predetermined weight of 30 kg when they were slaughtered. The DM, EE, NDF and TDN intakes were not affected ($P > 0.05$) by RDP levels in diets, registering average values of 1,056.5, 34.7, 294.9 and 803.1 g/animal/day, respectively. However, CP, RDP and RUP intakes increased linearly ($P < 0.05$) with increasing levels of RDP in the diets. The daily weight gain was not affected ($P > 0.05$) by RDP levels which was, on average, 217 g/day. The carcass yield obtained in relation to empty body weight and feed conversion were not affected ($P > 0.05$) by RDP levels which were, on average 53.7% and 5.1, respectively. The conversion of protein (kg CP intake/kg gain in BW) increased linearly ($P < 0.05$) with increasing levels of RDP, according to the equation $Y = -0.1565 + 0.094*PDR$. In conclusion, the RDP levels evaluated did not change the lamb performance, being able to use the lowest level of RDP (9.15% DM with 14.25% CP), contributing to reduction of nitrogen excretion in environment and feeding costs. Financial support by CNPq and FAPEMIG.

Key words: average daily gain, carcass yield, crude protein

M409 Diet preference of lambs offered a choice of concentrate diets containing different proportions of wheat dried distillers grain with solubles. E. K. R. Charles, A. V. Chaves, E. Jonas, and A. S. O'Hara*, *Faculty of Veterinary Science, The University of Sydney, Sydney, NSW, Australia.*

This study determined if lambs showed an intake preference for diets, that differed in their grain component. The grain consisted of either 20% or 40% wheat dried distiller's grain with solubles (WDDGS) or 60% barley. The study used 36 lambs that were assigned at random to one of 3 groups at 105 d of age (live weight 33.5 ± 4.6kg). All diets were formulated with NRC requirements for growing lambs in mind. Each group was offered the choice of all 3 diets on an ad libitum basis

for a 45 d period with the groups randomly rotated between pens every 7 d to ensure all lambs had access to all pens and all feeders. Daily feed intake, eating patterns, live weight change and wool characteristics were measured. The automatic feeders allowed the evaluation of the total feed intake, total time spent in a feeder and total time eating in the feeder. This allowed the evaluation of an intake preference for a particular diet, accounting for particular behavior of single sheep. Intake preference data was analyzed as a completely randomized design using the proc MIXED procedure of SAS. Means for intake were compared using the LSMEANS/DIFF with treatment, week and the interaction of treatment × week as fixed terms; lambs nested within groups as a random block effect, and week as a repeated measure. Dietary intake preference (as measured by total intake and time spent eating) over the course of the trial varied on a weekly basis (interaction treatment by week $P < 0.001$). The final live weight (39.8 ± 1.88 kg) and wool production was the same for the 3 groups of lambs. There was a tendency for lambs to prefer diets supplemented with WDDGS when compared with the barley grain control diet. There are several possible explanations as to why the lambs may have preferred the WDDGS diets over the control, including the aspects of feed novelty, variety and palatability, as well as the higher crude protein (CP) content of the WDDGS diets.

Key words: wheat distillers, ethanol by-products, sheep

M410 Effect of inclusion of dried citrus pulp on in vitro ruminal fermentation kinetics of a total mixed ration for goats. J. Hernández*[1,2], R. Rojo[1], A. González[2], A. Z. M. Salem[1], F. Lucero[2], J. L. Tinoco[1], A. Carreón[2], and J. F. Vázquez[1], *[1]Centro Universitario UAEM-Temascaltepec, Universidad Autónoma del Estado de México, Temascaltepec, Estado de México, México, [2]Unidad Académica Multidisciplinaria AgronomÍa y Ciencias, Centro Universitario Victoria, Universidad Autónoma de Tamaulipas, Ciudad Victoria, Tamaulipas, México.*

A completely randomized design was used to evaluate the effect of different levels inclusions (0, 100, 200 and 300 g/kg DM) of dried citrus pulp (orange): Control (%): Sorghum grain: 25, Soybean meal: 9, Urea: 1, Molasses: 2, Mineral premix: 3, Buffel grass hay: 60, Dried citrus pulp: 0, T1 (%): Sorghum grain: 15, Soybean meal: 9, Urea: 1, Molasses: 2, Mineral premix: 3, Buffel grass hay: 60, Dried citrus pulp: 10, T2 (%): Sorghum grain: 10, Soybean meal: 9, Urea: 1, Molasses: 2, Mineral premix: 3, Buffel grass hay: 55, Dried citrus pulp: 20, T3 (%): Sorghum grain: 10, Soybean meal: 9, Urea: 1, Molasses: 2, Mineral premix: 3, Buffel grass hay: 45, Dried citrus pulp: 30, on in vitro ruminal fermentation kinetics of total mixed rations balanced for lactating goats (CP 15.5%). One ± 0.002 g of DM of each treatments was weighed in triplicate into 160-mL serum bottles and incubated with ruminal inoculums of 4 goats feeding with a forage (50):concentrate (50) diet. Cumulative gas production was taken at 2, 4, 6, 8, 10, 12, 15, 19, 24, 30, 36, 48, 72 and 96 h post incubation at 39°C. Data of in vitro rumen gas production profiles were analyzed using a completely randomized design and the difference among means the Tukey test was used. Gas production (GP) at 24, 48 and 96 h was higher ($P < 0.01$) in the T3, showing a linear effect ($P < 0.01$). Inclusion of dried citrus pulp in the diet increased (linear effect ($P < 0.0$) the gas production (b) (ml/g DM). Fractional rate of gas production was different among treatments, T1 and T2 had the highest values, control and T3 presented the same values (quadratic effect $P < 0.01$). Lag time (h) had linear effect ($P < 0.01$), control diet had the highest value respect to the others treatments. The inclusion of dried citrus pulp in the diet for goats improved the gas productions parameters, and then this subproduct could be considered as potential feed to ruminant nutrition.

Key words: dried citrus pulp, ruminal fermentation kinetics, goats

M411 The under-nourishment of the Alpine-French goats does not diminish reproductive outcomes, but does affect dynamics of the offspring-growth. R. Rivas-Muñoz[1], E. Carrillo[1], C. A. Meza-Herrera[2], C. Leyva[3], H. Zermeño-González[1], R. Rodríguez-Martínez[3], M. Mellado[3], F. G. Véliz[3], and G. Arellano-Rodriguez*[3], *[1]Instituto Tecnológico de Torreón, Torreón, Coahuila, México, [2]Universidad Autónoma Chapingo, Unidad Regional Universitaria de Zonas Áridas, Bermejillo, Durango, México, [3]Universidad Autónoma Agraria Antonio Narro, Torreón, Coahuila, México.*

The aim of this study was to determine whether under-nourishment decreased the sexual response of Alpine-French goats, as well as to characterize both litter size and offspring -growth dynamics at weaning. Since April 1, a group of females (n = 10) received an experimental diet to provide 70% of their maintenance requirements (T-70), while the other group (n = 10) received a diet to cover 100% of their maintenance requirements (T-100). On October 1, both weight (42.4 ± 1.6 kg) and body condition (3.6 ± 0.1 units) of T-100 were higher ($P < 0.05$) in the T-100 as compared with the T-70 group (28.7 ± 1.1 and 1.8 ± 0.2). On October 9, both groups of females were exposed to one males which was changed every 12 h. Males remained in contact with females during 16 d. The total proportion of females which depicted estrus behavior and kidding were compared by Fisher exact test. Prolificity between groups was compared with the Student *t*-test. Weight data of the offspring were subjected to an ANOVA with repeated measures on 2 factors (Group * Time). All tests were performed using the statistical package SYSTAT 10. The number of estrous females was 100% in both groups ($P > 0.05$). Most of the females kidded in both groups (100 and 90%, T-70 and T-100, respectively, $P > 0.05$). However, the prolificity was higher in the T-100 as compared with the T-70 group (1.8 ± 0.1 vs. 1.1 ± 0.1, respectively, $P < 0.01$). Body weight of offering at birth was similar (2.7 ± 0.1 vs. 2.4 ± 0.2, T-100 and T-70, respectively; $P > 0.05$), however, there was a time by group interaction ($P < 0.05$), final weight was also different (7.6 ± 0.4 vs. 6.1 ± 0.8, T-100 and T-70, respectively; $P > 0.05$).. These results suggest that, irrespective of nutritional level, reproductive outcomes of Alpine-French goats were similar. Nonetheless, both litter size and offspring-growth dynamics at weaning favored the well-nourished females goats.

Key words: goats, under-nourishment, sexual activity

M412 Evaluation of crude glycerin on performance and carcass characteristics of growing meat goats. K. B. Tuoho*[1], N. K. Gurung[1], S. G. Solaiman[1], B. R. Min[1], J.-S. Eun[2], and W. H. McElhenney[1], *[1]Tuskegee University, Tuskegee, AL, [2]Utah State University, Logan.*

Today's high feed costs especially corn price have forced many goat producers to seek alternative energy sources. Crude glycerin (CG), a byproduct of the biodiesel production, is becoming increasingly available in the US and has a potential to partially replace high-starch containing ingredients such as corn. Research has shown that glycerin is converted to propionate in the rumen and acts as a precursor for hepatic glucose synthesis. Therefore, objectives of this were to determine the effects of varying levels of CG inclusion on feed intake, growth performance, feed efficiency, and carcass characteristics in meat goats.

Twenty 4 Boer crossbred intact male goats (23.93 ± 0.98 kg initial BW and 4 to 5 mo of age) were randomly assigned to one of the 4 experimental diets (n = 6) containing 30% bermudagrass hay plus 70% concentrate mix with 0, 5, 10 or 15% CG in the diet on an as-is basis. Feed was offered once a day and water was provided at all times. Goats were weighed every 2 weeks. At the end of 84-d feeding, goats were harvested and carcass characteristics were determined. Feed intake, average daily gain, gain: feed ratio, and carcass data were analyzed as a completely randomized design. Initial BW ($P = 0.99$), final BW ($P = 0.98$), ADG ($P = 0.91$), DM intake ($P = 0.35$), and G:F ratio ($P = 0.32$) were not different among treatments. No differences were observed ($P > 0.05$) in HCW ($P = 0.33$), chilled carcass weight ($P = 0.37$), or kidney and pelvic fat ($P = 0.07$), backfat thickness ($P = 0.71$), body wall fat thickness ($P = 0.94$), LM area ($P = 0.30$) and dressing percent ($P = 0.17$) and shrinkage ($P = 0.98$) among treatments. Results suggest that CG is a viable feedstuff for meat goats and up to 15% of CG can be included in the diet on as-is basis, for growing goats without any compromise in DM intake, growth performance, and carcass quality.

Key words: goats, crude glycerin, growth, carcass characteristics

M413 A meta-analysis for comparing dry matter intake prediction models in dairy goats. G. Caja, X. Roca, A. K. K. Salama, and M. Rovai*, *G2R, Universitat Autònoma de Barcelona, Bellaterra, Barcelona, Spain.*

Intake prediction is a key factor in dairy goats due to its effects on goat performances and ration costs. Currently available models for dairy goats (INRA, 2007; NRC, 2007; Cannas and Pulina, 2008) estimate daily dry matter intake (DMI) depending on body weight (BW) and daily milk yield (MY). A direct comparison of these models for a similar BW (50 kg) showed marked differences (0.4 to 0.8 kg DM/d) in predicted DMI depending on MY (0 to 6 L/d) and breed type. A meta-analysis of the available data on dairy goat intake from articles published in scientific journals indexed in PubMed and Science Direct through December 2010 was performed to calculate the differences between actual and predicted values across studies. Data were extracted from 125 papers (335 data) from which 219 values obtained under controlled conditions and using conventional diets (i.e., forage:concentrate >30%) were finally retained. Milk yield was standardized to 3.5% milk fat ($MY_{3.5\%}$) and data were normally distributed. Goat performances were, on average, 51.3 ± 0.7 kg BW (29.0 to 85.5), 2.7 ± 0.4 $MY_{3.5\%}$ L/d (0.4 to 6.2) and 2.22 ± 0.04 kg DMI/d (0.8 to 3.5). A stepwise regression was performed to estimate DMI (kg DM/d) from $MY_{3.5\%}$ (L/d) and BW (kg). Prediction models were (±SEM; $P < 0.001$): DMI (± 0.099) = 1.233 (± 0.050) + 0.370 (± 0.017) × $MY_{3.5\%}$; $R^2 = 0.69$; DMI (± 0.075) = 0.553 (± 0.092) + 0.277 (± 0.018) × $MY_{3.5\%}$ + 0.018 (± 0.002) × BW; $R^2 = 0.76$. Comparison of actual data with the results obtained from the meta-analysis data model showed the lowest mean error of the prediction (–0.030 kg DM/d), being lower than the underestimation obtained with the Pulina and Cannas (2008; –0.092 kg DM/d) and INRA (2007; –0.101 kg DM/d) models. On the contrary, the NRC (2007) prediction overestimated DMI on average (+0.185 kg DM/d). Despite agreeing at the intercept (MY = 0) and at high milk yield (MY = 6), the greatest differences between INRA and NRC predictions were observed around the mean. The oposite was observed with the model of Cannas and Pulina (2008). In conclusion, the INRA (2007) model showed the greatest agreement with the results of the meta-analysis.

Key words: feed intake, dairy goat, meta-analysis

M414 Intake and digestibility of rations containing dry yeast in Saanen goats during peripartum. C. R. Alcalde*, B. S. L. Molina, L. R. Lima, L. C. Gomes, and R. Souza, *Universidade Estadual de Maringá, Maringá, Paraná, Brazil.*

The objective to evaluate the intake and digestibility of rations containing dry yeast (sugar cane) as a substitute of soybean meal in Saanen goats. Twenty-four Saanen goats (15 multiparous and 9 primiparous) were used during the peripartum period, distributed in a completely randomized design in factorial arrangement (2 parity order × 3 rations), analyzed in SAEG system. The rations, similar in crude protein (16% CP), were composed of: soybean meal (SB), soybean meal plus dry yeast (SBDY) or dry yeast (DY) as a protein source, and remaining ingredients: ground corn, corn silage, limestone and mineral mixture, and the roughage:concentrate was 40:60. The marker used to estimate the digestibility was the indigestible neutral detergent fiber. After an adaptation period of 10 d, data were collected during the 21 d before and after the partum. Were collected partial samples of feces in the rectum, during 6 d in both periods (prepartum and postpartum). The intake of dry matter and nutrients was higher ($P < 0.05$) for multiparous goats in both evaluated periods. Among the rations, the intake ether extract with the ration SB was higher ($P < 0.05$) than the others, just to the goats in postpartum. The digestibility of dry matter and nutrients were not modified by the parity order to the goats in prepartum. However, in the postpartum primiparous obtained the best digestibility coefficients to dry matter, organic matter, crude protein and total carbohydrate, which resulted in higher ($P < 0.05$) total digestible nutrients (79.77%) related to the multiparous (74.95%) in the same physiological period. Among the rations, the addition of dry yeast reduced the digestibility of ether extract in both evaluated periods, however, the SBDY ration resulted in higher total digestible nutrients (77.02% in prepartum and 78.26% in postpartum) compared with the others rations. Dry yeast can replace soybean meal in rations, providing good nutritional value to Saanen goats in peripartum.

Key words: ruminant, *Saccharomyces cerevisiae*, transition

M415 Net protein requirements for growth of female Saanen goat kids. F. O. M. Figueiredo*, I. A. M. A. Teixeira, K. T. Resende, T. T. Berchielli, L. D. Lima, O. Boaventura Neto, B. Biagioli, and A. R. Rivera, *UNESP - São Paulo State University, Jaboticabal, São Paulo, Brazil.*

The objective of this study was to determine net protein requirements for growth of female Saanen goat kids using comparative slaughter technique. A total of 30 female goats kids with initial body weight (BW) of 30 kg were used. Six animals were slaughtered at beginning of the experiment (baseline animals), another 6 animals were slaughtered when they reached 38 kg of body weight (intermediate slaughter). The remainder was randomly allocated into 6 groups of 3 animals (0%, 30% and 60% of feed restriction) and each group was considered a block. The animals of each group were slaughtered when the animal set in the 0% feed restriction reached 45 kg of body weight. Animals fed ad libitum (initial, intermediate and 0% of feed restriction) were used to estimate body composition and net protein requirements for gain. To estimate net protein maintenance requirements were used the animals subjected to feed restriction (0, 30 and 60% of feed restriction). Logarithmized allometric equations were used to calculate protein body composition through the relationships between protein content and empty body weight (EBW), based on the following equation: Log_10_Protein, g = 2.33 + 0.48 x Log_10_EBW, kg. The protein body composition ranged from 40.48 to 31.40 g/ kg EBW. Net

protein requirements for gain (NP_g_) ranged from 10.99 to 11.30 g/100 g of body weight gain. The net protein requirements for maintenance (NP_m_) was estimated through the equation Retained Protein, g/EBW0.75/d = −0.37 + 0.092 x CP intake, as NP_m_ = 2.03 g/kg0,75BW/day. The total net protein requirement for growth of female Saanen goat kids with body weight ranging from 30 to 45 kg can be estimated by the followed model: Total net protein, g/g of ADG/day = (2.03 xBW00.75) + (1.47 + 0.11 * ADG). (Fapesp project number 2009/06588–4).

Key words: comparative slaughter, gain, maintenance

M416 Net energy requirements for growth of female Saanen goat kids. F. O. M. Figueiredo*, I. A. M. A. Teixeira, K. T. Resende, T. T. Berchielli, C. J. Harter, A. N. Mendonça, S. F. Souza, R. A. Gomes, D. S. Castagnino, and T. F. V. Bompadre, *UNESP - São Paulo State University, Jaboticabal, São Paulo, Brazil.*

The objective of this study was to determine net energy requirements for growth of female Saanen goat kids using comparative slaughter technique. A total of 30 female goats kids with initial body weight (BW) of 30 kg were used. Six animals were slaughtered at beginning of the experiment (baseline animals), another 6 animals were slaughtered when they reached 38 kg of body weight (intermediate slaughter). The remainder was randomly allocated into 6 groups of 3 animals (0%, 30% and 60% of feed restriction) and each group was considered a block. The animals of each group were slaughtered when the animal set in the 0% feed restriction reached 45 kg of body weight. Animals fed ad libitum (initial, intermediate and 0% of feed restriction) were used to estimate body composition and net energy requirements for gain. To estimate net energy maintenance requirements were used the animals subjected to feed restriction (0, 30 and 60% of feed restriction). Logarithmized allometric equations were used to calculate energy body composition through the relationships between energy content and empty body weight (EBW), based on the following equation: log Energy, kcal = 2.60 + 1.59 Log EBW, kg. The energy body composition ranged from 2630.425 to 3508.741 kcal / kg EBW. Net energy requirements for gain (NEg) ranged from 346.61 e 503.62 kcal / 100 g of body weight gain. The net energy requirements for maintenance (NEm) was estimated through the equation Log Heat Production, kcal/EBW0.75/d = 2.02 + 0.00152*EM intake, as NEm = 88.74 kcal/kg0.75 BW0.75/day. The total net energy requirement for growth of female Saanen goat kids with body weight ranging from 30 to 45 kg can be estimated by the followed model: Total Net Energy, kcal/g of ADG/day = (88.84* BW0.75) + (10.78 + 4.84 * ADG) (Fapesp project number 2009/06588–4).

Key words: comparative slaughter, maintenance, gain

M417 Effect of Clinoptilolite (zeolite) substituting for corn-soybean meal on productive performance and carcass characteristics of Pelibuey sheep. A. Estrada-Angulo*, J. D. Urías-Estrada, J. A. Aguilar, J. L. Bolado, H. Davila-Ramos, J. J. Portillo, J. C. Robles, and F. G. Rios, *FMVZ-UAS, Culiacan, Sinaloa, Mexico.*

To determine the effect of 4 levels of clinoptilolite (Zeolite) substituting for corn-soybean meal on growth performance of sheep, 20 Pelibuey ram lambs (BW = 32.6 kg ± 2.2 kg) were fed for 42 d in a randomized block design (experiment). The animals were weighed and blocked by weight in individual form, placed into 20 (2 × 3 m) floor pens, and assigned to one of 4 (4) diets: 1) Control had 16.43% CP and 2.92 Mcal ME/kg, and contained 7.5% corn straw, 5% alfalfa hay, 62% cracked corn grain, 14% soybean meal, 9% sugarcane molasses, and 2.5% mineral premix; 2) similar (like) Control, (ZEO5) had 16.23% CP and 2.91 Mcal of ME/kg, but contained 0.5% zeolite, 61.75% cracked corn grain, and 13.75% soybean meal; 3) like Control, (ZEO10) had 16.03% CP and 2.89 Mcal of ME/kg, but contained 1.0% zeolite and 61.5% cracked corn grain and 13.5% soybean meal; and 4) like Control, (ZEO15) had 15.83% CP and 2.87 Mcal ME/kg, but contained 1.5% zeolite and 61.25% cracked corn grain. Feed was offered twice daily under free access conditions. In daily feed intake, zeolite treatments decreased 6% respect to Control treatment (1187 vs. 1116 g/d). In average daily gain zeolite treatments increased (14.3% than Control group (216 vs. 189 g/d). About feed conversion, zeolite treatments improved in 20.5% respect to Control group (5.21 vs. 6.28). Hot carcass weight, cold carcass weight and dressing percent tended to improve ($P < 0.08$) in zeolite treatments respect to Control group. Rib eye area, carcass characteristics, fat thickness and primary cuts were similar in all treatments ($P > 0.05$). It is concluded, that zeolite is an ingredient of low price and appropriate substitute for a mix of cracked corn grain and soybean meal in diets for Pelibuey sheep.

Key words: clinoptilolite, zeolite, Pelibuey sheep

M418 Effect of live yeast *Saccharomyces cerevisiae* (strain Sc 47) on fattening efficiency and blood parameters of growing Mehraban lambs. N. Baleghi[1], A. Taghizadeh[2], A. FarahAvar[3], and H. Khalilvandi-Behroozyar*[3,4], *[1]Islamic Azad University, Maragheh Branch, [2]Department of Animal Science,University of Tabriz, [3]Department of Animal Science, University of Tehran, [4]Department of Animal Science, Urmia University.*

Yeast (*Saccharomyces cerevisiae*) products may exert beneficial effects on ruminant productivity by either increasing fermentability of fiber and/or allowing rumen microbes to more effectively metabolize end products of ruminal starch fermentation. The objective was to evaluate the possible effects of live yeast on live weight gain and selected blood parameters of growing Mehraban lambs. Twelve male lambs (average BW 34+4.2 kg) randomly assigned to 3 groups: a) control, without additive b) 1 g/day/head and c) 1.5 g/day/ head *Saccharomyces cerevisiae* (strain Sc 47) with 8×10^9 cfu per gram. Additives supplemented via gelatin capsules to TMR ration (alfalfa hay, wheat straw, barley grain, canola meal, wheat bran, Mineral-vitamin mix, calcium carbonate and salt) formulated for 200 g/d weight gain using CNCPS-S. Animals fed experimental rations for a period of 60 d in 2 equal meals. Lambs were weighting after 2 week adaptation period and in weekly intervals after feed restriction. Blood samples withdrawn via heparinized vacuum venoject tubes through Jugular vein in last day of the experiment and analyzed for selected parameters via an autoanalyzer apparatus and commercial kits. Data were analyzed by GLM procedure of SAS 9.1 with CRD design and duncan test ($P \leq 0.05$). addition of 1.5 g/day/head of *Saccharomyces cerevisiae* caused significant increase in daily weight gain. Addition of different levels of *Saccharomyces cerevisiae* failed o induce a statistically significant difference in white and red blood cells, hemoglobin, hematocrit, mean cell volume, mean cell hemoglobin, platelet number, lymphocytes, lymphocytes and monocytes, but a tendency ($P \leq 0.1$) for reduction of white blood cells was determined and supplementation of 1 g/day/head was resulted in least value of white blood cells (70+6, 15.66 ± 2.13 and 32.66 ± 2.13, respectively for control, 1g/day/head and 1.5g/day/head group). These results indicated that supplementation of 1.5 g/day/head of yeast can be beneficial for maximizing live weight gain and improve health status.

Table 1. Characteristics of live weight gain in sheep fed *Saccharomyces cerevisiae*

Item	Group 1	Group 2	Group 3	SEM
Initial weight (kg)	35.36	35.55	36.71	3.15
Final weight (kg)	45.00	45.12	49.12	3.51
Average daily weight gain (g/day)	160.67^{b}	159.51^{b}	206.83^{a}	36.25

Means within a row that do not have a common superscript are different ($P < 0.05$), 1: control, 2: 1 g/day/head *Saccharomyces cerevisiae*, 3: 1.5 g/day/hd *Saccharomyces cerevisiae*.

Key words: *Saccharomyces cerevisiae*, blood parameters, Mehraban lambs

M419 Relationship of blood enzymes and metabolites to residual feed intake of lambs. F. A. Rodriguez-Almeida*, C. Arzola, J. A. Grado-Ahuir, A. Corral, P. I. Ochoa, and G. Jasso-Diaz, *Universidad Autonoma de Chihuahua, Chihuahua, Chihuahua, Mexico.*

The aim of this study was to identify blood enzymes and metabolites (BEM) that do relate to residual feed intake (RFI) as predictor of feed efficiency. A total of 111 F_1 lambs (males and females) weaned at 90 d (BW = 17 ± 3.7 kg), sired by Charollais, Dorper, Hampshire, Suffolk and Texel rams bred to estrus synchronized-Pelibuey and Blackbelly ewes, were utilized. Lambs were fed an ad libitum mixed ration and weighed every 14 d until they reached a minimum BW of 42 kg (81 ± 18 d) for males and 40 kg (110 ± 24 d) for females. At the onset of the feeding trial, blood was collected and creatinine, blood urea nitrogen (BUN), cholesterol, triglycerides, albumin, globulins, glutamate-oxaloacetate transaminase (GOT), glutamate-pyruvate transaminase (GPT), albumin/globulin, GOT/aspartate aminotransferase (AST), GPT/Alanine transaminase (ALT), alkaline phosphatase (ALP), lactate dehydrogenase (LDH), gamma-glutamyl transpeptidase (GGT), creatinine phosphokinase (CPK), BUN/creatinine, and AST/ALT were determined in serum. Residuals of the regression of standardized ADFI on ADG, mid term BW and back fat at slaughter were regarded as RFI (R^2 = 0.55). Animals were classified into 3 categories according to RFI: efficient (first quartile; n = 29), medium (second and third quartile; n = 54), and inefficient (fourth quartile; n = 28). A stepwise analysis was carried out to identify BEM to discriminate animals into feed efficiency groups at the beginning of the feeding period. Entering variables were then analyzed with PROC GLM of SAS, fitting a linear model that included class effects of efficiency group, breed of sire, breed of dam, sex, number weaned (1 or more), 2 way interactions and initial body weight as a covariate. Variables in the discriminant function were ALP, GPT/ALT, CPK, and albumin (R^2 = 0.24). When fat was taken out of the regression equation to predict RFI, the variables in the discriminant function were ALP, AST/ALT and LDH (R^2 = 0.13). It may be concluded that most related variables to feed efficiency groups as defined by RFI were ALP, GPT/ALT, CPK, AST/ALT and LDH.

Table 1. Least squares means for variables affected by growth efficiency groups as defined by RFI: efficient (1st. quartile), medium (2nd. and 3rd. quartile), and inefficient (4th. quartile)

Group	n	ALP ($P < 0.05$)	GPT/ALT ($P < 0.05$)	CPK ($P < 0.05$)	AST/ALT ($P < 0.08$)	LDH ($P < 0.07$)
Efficient	29	170 ± 12^{b}	10 ± 0.8^{b}	200 ± 39^{b}	9.9 ± 0.7^{a}	800 ± 24^{b}
Medium	54	207 ± 9^{a}	13 ± 0.6^{a}	232 ± 29^{b}	8.8 ± 0.5^{ab}	858 ± 17^{a}
Inefficient	28	179 ± 12^{b}	13 ± 0.8^{a}	345 ± 39^{a}	7.7 ± 0.7^{b}	873 ± 23^{a}

Key words: residual feed intake, blood enzymes, metabolites

M420 Nutritive value of *Vicia panonica* forage and its effect on ram Kurdish lamb performance. F. Fatahnia[1], M. Moeini[1], F. Moradi[1], R. Ebnabasi[1], and H. Mirzaei Alamouti*[2], *[1]Department of Animal Science, University of Ilam, Iran, [2]Department of Animal Science, University of Zanjan, Iran.*

This study was conducted to determine chemical composition of *Vicia panonica* forage and its effect on ram Kurdish lamb performance. Male lambs (n = 16; 29 ± 4.3 kg BW; 120 ± 5 d of age) were assigned randomly to one of 4 dietary treatments (7 lambs/dietary treatment). Experimental diets consisted of control diet (without *V. panonica* forage) and diets containing 15, 22.5 or 30% of *V. panonica* forage (DM basis). The experiment lasted for 100 d. Animals were housed in individual shaded pens and fed twice daily with diets (as total mixed ration). *V. panonica* forage used in this experiment had 94.04, 15.55, 1.2, 19.6, 9.5, 1.52 and 0.29% of DM, CP, ether extract, crude fiber, ash, calcium and phosphorus respectively. Data were analyzed using the MIXED procedure of SAS. Dry matter intake was not affected by experimental diets ($P > 0.05$). Average daily gain (ADG) was higher in lambs fed control or 15% *V. panonica* forage containing diets than others ($P < 0.05$). Feed conversion ratio (FCR) was higher ($P < 0.05$) for control and 15% *V. panonica* forage containing diets. Average final weight was similar among all treatment diets. These data indicate that feeding Kurdish lambs diets containing up to 15% *V. panonica* forage did not affect growth performance.

Key words: lambs, nutrition, *Vicia panonica*

M421 Daily supplementation of *Saccharomyces cerevisiae* (strain Sc 47) can cause reduction of blood cholesterol. N. Baleghi[1], A. Taghizadeh[2], A. FarahAvar[3], and H. Khalilvandi-Behroozyar*[3,4], *[1]Islamic Azad University, Maragheh Branch, [2]Department of Animal Science,University of Tabriz, [3]Department of Animal Science, University of Tehran, [4]Department of Animal Science, Urmia University.*

east (*Saccharomyces cerevisiae*) products may exert beneficial effects on ruminant productivity by either increasing fermentability of fiber and/or allowing rumen microbes to more effectively metabolize end products of ruminal starch fermentation. The objective was to evaluate the possible effects of live yeast on live weight gain and selected blood parameters of growing Mehraban lambs. Twelve male lambs (average BW 34+4.2 kg) randomly assigned to 3 groups: a) control, without additive b) 1 g/day/head and c) 1.5 g/day/ head *Saccharomyces cerevisiae* (strain Sc 47) cfu 8 × 102. Additives supplemented via gelatin capsules to TMR ration (alfalfa hay, wheat straw, barley grain, canola meal, wheat bran, Mineral-vitamin mix, calcium carbonate and salt) formulated for 200 g/d weight gain using CNCPS-S. Animals fed experimental rations for a period of 60 d in 2 equal meals. Lambs were weighting after 2 week adaptation period and in weekly intervals after feed restriction. Blood samples withdrawn via heparinized vacuum venoject tubes through Jugular vein in last day of the experiment and analyzed for selected parameters via an autoanalyzer apparatus and commercial kits. Data were analyzed by GLM procedure of SAS 9.1 with CRD design and Duncan test ($P \leq 0.05$). dietary treatments were failed to exert any statistically significant differences in blood urea, glucose, creatinine, albumin, total protein, TG, SGPT and alkaline phosphatase, but there was a trend ($P \leq 0.1$) for increase in blood alkaline phosphates levels. Daily supplementation of *Saccharomyces cerevisiae* was resulted in lower blood cholesterol levels (69.5 ± 4.06, 62.00 ± 4.06 and 51.75 ± 4.06, respectively for control, 1 and 1.5 g/day/head supplementation groups). Also, *Saccharomyces cerevisiae* increased aspartate aminotransferase levels from 102 ± 6.48 to

130 ± 6.48 IU/L in control and 1 g/day/ head supplementation groups, respectively.

Key words: *Saccharomyces cerevisiae*, cholesterol, Mehraban lambs

M422 Cull pinto bean as a supplement to pregnant-lactating hair ewes. F. Castillo*, G. Villalobos, D. Dominguez, J. E. Cruz, A. Anchondo, and J. A. Ortega, *Facultad de Zootecnia y Ecología. Universidad Autonoma de Chihuahua., Chihuahua, Chihuahua, México.*

Cull pinto bean (CPB; *Phaseolus vulgaris*) is a feeding option for sheep producers in northern Mexico. The objective was to evaluate the effect of 3 CPB levels (0, 25 and 50% of concentrate DM) on performance of ewes in late pregnancy (LP) and lactation (L). One-hundred 60 8 pelibuey ewes, 105 multiparous (M), and 63 primiparous (P), were randomly allotted to 1 of 24 pens (8 replications per treatment). Treatments were: 1) Control (C; 0% CPB) Low CPB (L; 25% CPB), and High CPB (H; 50% CPB). Supplements (LP: 0.45 kg; 2.8 Mcal/ Kg DM ME; 15.4% CP; L: 0.95 kg; 2.8 Mcal/Kg DM ME; 21.8% CP) and forage (ad libitum) were offered daily. Ewes were weighed 8 d before calving and each 14 d after it; dry matter intake (DMI) was measured daily; body condition score (BCS) was measured at the end of pregnancy and lactation. Lambs were weighed at birth and each 14 d until weaning. Data for pregnancy DMI (PDMI), lactation DMI (LDMI), pregnancy body weight (PBW), start of lactation body weight (SLBW), end of lactation body weight (ELBW), pregnancy BCS (PBCS) and lactation BCS (LBCS) was analyzed with PROC GLM in a completely randomized design; data for lamb average daily gain (LADG) was analyzed by PROC MIXED in a completely randomized design with repeated measures in the time. Models included treatment and kind of ewe as main effects and their interaction. Interaction effect was not found in any variable ($P > 0.05$). Data for PDMI (C: 1.7, L: 1.7, and H: 1.6 kg), LDMI (C: 2.4, L: 2.3, and H: 2.4 kg), PBW (C: 44, L: 42.7, and H: 42.8 kg), SLBW (C: 41.9, L: 39.6, and H: 40.2 kg), ELBW (C: 39.3, L: 39.2, and H: 38.8 kg), PBCS (C: 2.7, L: 2.6, and H: 2.7) and LBCS (C: 2.8, L: 2.8, and H: 2.8) was not different among treatments ($P > 0.05$). Differences among kind of ewe for PBW (M: 49.5; P: 36.8 kg), SLBW (M: 45.9; P: 35.2 kg), and ELBW (M: 45.1; P: 33.1 kg), were found ($P < 0.05$). No differences ($P > 0.05$) among treatments were found for LADG, lsmeans (kg) were (C: 0.21, L: 0.23, and H: 0.22). Due to the cost of CPB, and equal ewe performance to treatments, CPB use is a recommendable alternative in hair ewe feeding for these productive stages.

Key words: Cull pinto bean, hair ewes, pregnancy-lactation

M423 Effect of different sources of lipid on blood parameters of sheep. E. H. C. B. van Cleef*, D. A. V. Silva, A. C. Homem Júnior, and J. M. B. Ezequiel, *São Paulo State University, Jaboticabal, São Paulo, Brazil.*

Twenty crossbred sheep (19.5 ± 2.9 kg BW) were used to evaluate the effect of different lipid sources on hemogram and serum concentrations of AST, GGT, triglycerides, cholesterol, glucose and urea. The animals were confined for 80 d, in individual pens and received 5 experimental diets containing sunflower grain (SG), peanuts grain (PG), peanut oil (PO) or protected fat (PF) and a control diet without added lipid (CON), formulated in roughage: concentrate ratio of 40: 60, with corn silage as roughage and concentrate composed of corn, soybean meal, citrus pulp and mineral supplement. The blood samples were taken when the animals reached 37 kg BW, 3 h before and after feeding by jugular vein puncture. The statistical design was a completely randomized and the contrasts among treatments and control × lipid sources were analyzed. The lipid sources did not alter ($P > 0.05$) the serum concentrations of GGT triglycerides and urea, comparing to the control diet. Although some contrasts show significant differences ($P < 0.05$) in blood parameters studied, the results are within normal ranges as suggested by the literature. However, it is emphasized that the animals that received PO diet showed increases ($P < 0.05$) in cholesterol value and decrease in erythrocyte and hemoglobin, comparing to grain diets studied (PG and SG), which may indicate damage to animal health and consequent production decrease. The protected fat caused decrease ($P < 0.05$) in erythrocyte count and hemoglobin concentration. All the parameters analyzed showed minimum variations in serum concentrations when compared with normal indicated by the literature. The increase serum levels of AST and cholesterol in pure oil diets ($P < 0.05$) can indicate possible liver alterations. It was concluded that the inclusion of lipids from oil seeds is better for animal health than oil, and that the control diet conducted to more favorable results of serum AST and cholesterol.

Key words: blood, feedlot, ruminant

M424 Use of ionophores in Santa Inês lambs diet for meat production. P. M. França[1], J. R. O. Pérez[1], V. A. A. Reis[1], I. F. Furuscho-Garcia*[1], R. F. Leite[2], F. Oliveira[3], S. P. Greca[1], and I. Leopoldino Junior[1], *[1]Universidade Federal de Lavras, Lavras, Minas Gerais, Brasil, [2]Universidade Paulista Júlio de Mesquita Filho, Jaboticabal, São Paulo, Brasil, [3]Universidade Paulista Júlio de Mesquita Filho, Botucatu, São Paulo, Brasil.*

The experiment was carried out at the Sheep Production Sector of Federal University of Lavras (UFLA), Brazil, to evaluate the effect of adding ionophores (monensin and lasalocid) in the diet on performance, digestibility, carcass and meat quality characteristics in lambs on feedlot. Eighteen lambs were used in a Completely Randomized Design and the animals were allotted to 3 treatments (control diet, diet plus monensin, diet plus lasalocid), with 6 replicates per treatment. The ionophore dose was based on the rumen content using the equation: y = −0.0014 x2 + 0.2034 × −0.8376, that is obtained through a compilation of data on rumen content (kg) relative to body weight (kg) from several experiments conducted in the Department of Sheep Production, (UFLA). A reference dose of 14.85 mg per kg of rumen contents was given. The lambs were slaughtered at 45 kg live weight. Data were analyzed using GLM procedure of SAS and the means compared using the *t*-test. The use of ionophores, monensin and lasalocid increased the average daily weight gain of lambs, but did not affect consumption. In the digestibility trial, the intake and the dry matter, crude protein, neutral detergent fiber and acid detergent fiber digestibility were not influenced by additives. Initial and final pH, color, tenderness, cooking loss, and chemical composition of meat were not affected by ionophores. The concentration of the fatty acid C18:2 C9T11 (CLA) in Longissimus lumborum muscle increased with the use of monensin and lasalocid, which may be a promising tool to further improve the nutritional value of meat and an important strategy to promote this product. In conclusion, the use of ionophores in the diet of confinement lambs can produce favorable results if used properly.

Key words: carcass, meat quality, sheep

M425 Evaluation of behavior and apparent dry matter intake of sheep in tropical pasture. F. P. Portilho*[1,2], J. M. S. Diogo[1], and S.

L. S. Cabral Filho[1], [1]*University of Brasilia, Brasilia, DF, Brazil,* [2]*Agrodefesa, Rio Verde, GO, Brazil.*

The aim of this study was to evaluate the ingestive behavior (size of bite, bite rate and grazing time) and apparent dry matter intake in sheep grazing *Cynodon dactylon* 'Coastcross' and *Panicum maximum* 'Aruana'. For the evaluation of feeding behavior, adult male, crossbred Santa Inês (n = 3; 42 kg) were used (one animal per plot). Data were collected on the DM content (%), canopy height (cm), the availability of dry matter (kg DM / ha), the percentage of leaves (%), the percentage of stem (%) and the percentage of dead material (%), leaf: stem and leaf, dead material. The data were analyzed using the T TEST procedure in SAS, and correlations were generated through excel. The plots of Aruana (2,113 and 2,121 kg DM / ha) and Coastcross (1,545 and 2,619 kg DM / ha; February and June cuts, respectively) did not differ ($P > 0.05$). In February there were no differences ($P > 0.05$) among the grasses or the average percentage of leaf, stem and dead material. However, there were differences ($P < 0.05$) in average canopy height and average content of dry matter. The canopy height was higher ($P < 0.05$) in Aruana compared with Coastcross, 68cm and 35cm, respectively. The DM content was higher in Coastcross (42%) compared with Aruana (36%). In June there were no differences ($P > 0.05$) among the forages in average canopy height, average content of dry matter and mean percentage of dead material. In this period differences in mean percentage of leaves and average percentage of stems were observed ($P < 0.05$). On the other hand, no significant difference was observed related to the intake behavior of sheep in both forages, in those evaluation periods. The plots of both forages did not differ ($P > 0.05$) in the size of bite between the evaluation periods. The correlation between apparent consumption and bite size of the Aruana (0.92) and Coastcross (0.86) were positive. The *Panicum maximum* and *Cynodon dactylon* were similar regarding the pattern of intake behavior and apparent consumption of sheep, regardless of the evaluation period. The dry matter content influenced positively the grazing time and bite rate of sheep, in both forages.

Key words: forage, sheep, Santa Inês

M426 Palatability of sainfoin (*Onobrychis viciifolia* Scop.) in sheep. H. Khalilvandi-Behroozyar*[1,2], M. Dehghan-Banadaky[1], and K. Rezayazdi[1], [1]*Department of Animal Science, University of Tehran, Karaj, Tehran, Iran,* [2]*Department of Animal Science, University of Urmia, Urmia, West Azerbaijan, Iran.*

Sainfoin is a tanniferous legume forage. Reports about sainfoin CT contents and effects are very variable. Along with possible beneficial effects of tannins, adverse effects on palatability could be demonstrated. An experiment was carried out to evaluate palatability of sainfoin hay compared with control forage (alfalfa), using 6 nonlactating Zandi ewes (45 ± 5 kg BW). Diets were formulated to meet 110% of maintenance energy requirements, using CNCPS-S software and fed 2 equal meals per day at 0800 and 2000 h. Sainfoin and alfalfa provided exactly half of ME. The experiment started with the morning feeding on the first day and finished after the morning feeding on the tenth day. First 3 d were considered as preliminary period. The allocation of the 2 forages was switched between troughs for evening meals, to avoid association of place, forage type, and time of day by the animals. To evaluate the palatability of the sainfoin in comparison with alfalfa, intakes of 2 diets were measured by weighing the boxes at a fixed time (t). Based on preliminary tests, t was set to 10 min after feeding, that was approximately equivalent to the time needed to consume about half of the total feed. Palatability index (PI) was calculated according to Ben Salem et al. (1994) as amount of test forage consumed compared with control forage following the equation: PI (t) = [ITT (t)/ICtr (t)].100, where ITT (t) equals intake of sainfoin after time t per total intake after half a day, and ICtr (t) equals intake of control (alfalfa) eaten after time t per total intake after half a day. Total phenolic, total tannin and condensed tannin contents of sainfoin were 39.4, 38.5 and 21.3 g/ kg of DM, respectively. Palatability index of sainfoin compared with alfalfa, was 274%. Sainfoin CT was reported to have a different monomeric constitution and a higher degree of polymerization than others, that can be responsible for this result. It can be concluded that the chemical properties of CT may be important than the CT content in determining palatability.

Key words: sainfoin, palatability, sheep

M427 Effect of feeding tannin-containing pine bark on fecal bacterial population and methane gas production in Kiko-cross goats. B. R. Min*, S. Solaiman, R. Shange, and R. Ankumah, *Tuskegee University, Tuskegee, AL.*

Eighteen Kiko-cross meat goats (33.4 ± 0.98 kg; n = 6) were used to determine DM intake, fecal DM output, fecal bacterial and in vitro methane gas production. Animals were fed condensed tannins (CT)-containing pine bark (PB) for 83 d and total fecal was collected for 7 d with 2 periods. Experimental treatments included: the control diet – 0% PB and 30% wheat straw (WS; 0.17% CT DM); 15% PB and 15% WS (1.6% CT DM) and 30% PB and 0% WS (3.2% CT DM) as fed. Freshly dried PB and WS were finely (1.5–3 mm) ground and incorporated in the grain mix to provide 0, 16, and 32 g CT/kg DM in 0, 15, and 30% PB diets, respectively. Fecal bacterial populations were measured using a 16S-based pyrosequencing technique to characterize and elucidate changes in bacterial diversity among the diets. Fecal samples collected from each goat were pulled for each treatment for sequencing analysis. In vitro methane gas production was measured as plunger displacement (mL) at 0 to 24 h incubation periods with fecal inoculants that were obtained from experimental animals. Total methane gas production was estimated from total fecal DM output and in vitro methane gas production per unit of fecal material. Fecal DM output was linearly increased ($P < 0.04$) with PB supplementation (375, 386, and 460 g DM/animal for 0, 15 and 30% PB diets respectively), but estimated methane gas (291, 158, and 51 mL/goat per d; $P < 0.01$) and in vitro methane (0.77, 0.42, and 0.11 mL/g of feces) gas production decreased (linear; $P < 0.001$) as the level of PB increased in the diet. Predominant fecal genera were Flavobacteriaceae (up to 18%), Oscillibacter (up to 15%), and Oscillibacter spp. (up to 17%) of microbial population in 0, 15 and 30% PB diets, respectively. The proportion of Flavobacteriaceae (25, 4.5, and 3%), Acinetobacter (4.6, 3.1, 4.1%), Acinetobacter-baumannii (4.9, 3.0, and 5.8%), Moraxellaceae (4.4, 1.1, 1.2%), and *E. coli* (6.3, 2.1, and 2.1%) population decreased as the level of PB supplement increased in the diet. These results indicated that feeding PB reduced methane gas and *E. coli* population and modified fecal bacterial population.

Key words: fecal bacteria, methane gas, pine bark

Animal Behavior and Well-Being Symposium: Novel Techniques for Euthanasia

8 Euthanasia—An overview of the AVMA's criteria and recommendations. G. C. Golab*, *American Veterinary Medical Association, Schaumburg, IL.*

Since 1963 the AVMA has convened a Panel on Euthanasia to evaluate methods and potential methods of euthanasia for the purpose of creating guidelines for veterinarians who carry out or oversee the euthanasia of animals. More than 70 individuals, including veterinarians and non-veterinarians with expertise across a range of disciplines and species, were engaged to research and create the 2011 update to the Panel′s report (its eighth edition) titled the *AVMA Guidelines on Euthanasia*. Euthanasia techniques should result in rapid loss of consciousness followed by cardiac or respiratory arrest and the ultimate loss of brain function. In evaluating methods of euthanasia, the Panel used the following criteria: (1) ability to induce loss of consciousness and death with a minimum of pain distress, anxiety or apprehension; (2) time required to induce loss of consciousness; (3) reliability; (4) safety of personnel; (5) irreversibility; (6) compatibility with requirement and purpose; (7) emotional effect on observers or operators; (8) compatibility with subsequent evaluation, examination, or use of tissue; (9) drug availability and human abuse potential; (10) compatibility with species, age, and health status; (11) ability to maintain equipment in proper working order; (12) safety for predators/scavengers should the carcass be consumed; (13) legal requirements; and (14) environmental impacts of methods or carcass disposition. The various sections of the Guidelines address particular euthanasia techniques (e.g., inhalant agents, non-inhalant pharmaceutical agents, and physical methods) and the application of those techniques to various animal types, species, and uses (e.g., companion animals, food animals, laboratory animals, wildlife, aquatics). This edition of the Guidelines has been expanded and includes more detail about the techniques, covers more species, and more comprehensively considers the special needs and challenges posed by the range of environments and conditions under which euthanasia is conducted. This presentation will summarize the creation and content of the 2011 version of the *AVMA Guidelines on Euthanasia*.

Key words: euthanasia, *AVMA Guidelines on Euthanasia*

9 Euthanasia of livestock: Public perception and influence. S. R. Niekamp*, *National Pork Board, Clive, IA.*

While livestock producers strive to maintain good health of all animals in their care, it is inevitable that an animal will become ill or injured. Euthanasia may be the best option for the animal′s well-being in situations where ill or injured animals cannot be successfully treated. As the US population has become more urbanized, the contemporary consumer has become less familiar with the practices associated with raising livestock. There is currently a trend in the marketplace for certain consumer demographics to proactively learn more about the source of their food and how it was produced. Additionally, consumers have unlimited access to internet resources that depict livestock production practices. These resources often depict the production practice being performed incorrectly which raises more questions than they answer. While surveys indicate that customers do not hold retailers responsible for how animals are raised, consumers often look to their preferred food retailer for assurances and answers to their questions about how animals are treated on the farm. In effort to provide these assurances, retail and foodservice customers turn to their suppliers for answers regarding on-farm practices. The euthanasia process has increasingly become a topic of interest for customers and consumers. Specifically, their questions focus on the timely application of euthanasia, the effectiveness and the aesthetics of the method used, and the attitude of the caretaker euthanizing the animal. Scientific validation of current methods of euthanasia, identifying and validating new and novel methods that account for aesthetics are 2 key aspects needed to effectively answer customer and consumer questions. Caretaker training is another key aspect as caretakers must know when it is appropriate to euthanize an animal that is ill or injured and how to properly apply the method so to minimize pain and suffering. The ability of livestock producers to effectively answer questions about euthanasia and other on-farm practices will help to build consumer trust in today′s food system.

Key words: euthanasia, consumer, perception

10 The signs of unconsciousness and death: How can we recognize them on the farm? T. M. Widowski*[1], T. M. Casey-Trott[1], and M. A. Erasmus[2], *[1]Campbell Centre for the Study of Animal Welfare, University of Guelph, Guelph, Ontario, Canada, [2]Michigan State University, Lansing.*

All methods for euthanasia should begin with rapid loss of consciousness followed by full loss of brain function, respiratory failure and cardiac arrest. To ensure that death occurs without pain or distress, animals must be monitored for signs of unconsciousness until cardiac arrest is confirmed. The brainstem and cortex are primary brain regions associated with consciousness and arousal; therefore brainstem and nociceptive reflexes, similar to those used to determine effective stunning at slaughter or depth of anesthesia during surgery, are practical measures for determining loss of consciousness on the farm. Brainstem reflexes include corneal, palpebral, and pupilary light reflexes and the nictitating membrane reflex in birds. Unconscious animals do not blink in response to touching the eyelid or cornea and their pupils remain fixed and dilated when exposed to light. However, ocular reflexes are not always reliable indicators of anesthesia (pigs), and corneal reflexes can be observed during unconsciousness even after damage to the cerebral cortex if the brain stem remains intact (e.g., head only electrical stunning). Therefore, using a combination of measures including nociceptive reflexes, such as the pedal and anal reflexes (withdrawal response to a sharp pinch or prick) is most useful. If the animal is not paralyzed and is able to show a motor response, absence of withdrawal responses to painful stimuli indicates that the animal no longer perceives pain. In addition to the sensory reflexes, several types of behavioral observations can be used for assessing effectiveness of euthanasia. These include absence of rhythmic breathing and absence of vocalizations. Collapse and loss of muscle tone occurs with the onset of unconsciousness and a limp jaw or tongue is a reliable indicator of insensibility in pigs and cattle. Clonic muscle spasms (seizures), characterized by kicking, wing flapping or paddling, and tonic muscle spasms, characterized by rigid extension of the limbs, are associated with some euthanasia techniques. These neuromuscular spasms are involuntary, and should not be confused with deliberate movements or escape attempts.

Key words: euthanasia, unconsciousness, reflexes

11 Novel euthanasia technologies for the pig. S. T. Millman*, *Veterinary Diagnostic & Production Animal Medicine, Iowa State University, Ames.*

In a systematic review of the scientific literature, there are relatively few studies providing empirical data about on-farm swine euthanasia. Recently, specific calls for research proposals have been issued for swine euthanasia, and several novel technologies are emerging. Furthermore, researchers are refining techniques to measure the aversiveness and efficacy of euthanasia methods. Mechanical methods of euthanasia, including penetrating and non-penetrating captive bolt technologies, are based on disruption of brain function resulting from impact of a solid object with the skull. Postmortem examinations indicate that head injuries are likely to be fatal when there is hemorrhage within the brain stem. The AVMA Guidelines for Euthanasia (2007) states "non-penetrating captive bolt must not be used as a sole method of euthanasia," but recent research results indicate new devices are capable of inducing death without risk of return to consciousness for some weight classes of pig. In the OIE Terrestrial Code, it is recommended that penetrating captive bolt be followed by pithing or bleeding when used for swine, but a new generation of captive bolt device has been shown to be an effective single step euthanasia method for all but the largest weight class of pig. Euthanasia using gases such as carbon dioxide and argon have been developed for the suckling and market weight pig, and present some advantages over mechanical methods. Novel gas delivery systems for on-farm use may provide opportunities to refine flow rates and gas mixtures for more humane induction of insensibility. Novel electrical methods have been explored for suckling pigs and breeding stock. Since all euthanasia techniques have trade offs, there is no Gold Standard for on-farm swine euthanasia and considerations for animal welfare, worker health, carcass disposal and public health must be weighed in each situation. Further research is needed to address challenges associated with swine euthanasia including reliable techniques for the mature sow and boar, methods of restraint, tools for decision making about humane endpoints, safeguards for safety and psychosocial effects imposed on those performing this task.

Key words: animal welfare, euthanasia, swine

12 Euthanasia techniques for dairy and beef cattle. J. K. Shearer*[1], J. P. Reynolds[2], D. D. Griffin[3], and G. Johnson[4], *[1]Iowa State University, Ames, [2]Western Veterinary College, Pomona, CA, [3]University of Nebraska, Lincoln, [4]Reedsburg, Wisconsin.*

The physical methods for conducting euthanasia in cattle include gunshot and captive bolt. Euthanasia may also be accomplished by the parenteral administration of an anesthetic in an amount capable of causing death. This latter method requires a veterinarian to administer the drug and creates residue problems that limit carcass disposal options. There are few methods as humane as gunshot or penetrating captive bolt combined with a secondary step to ensure death such as exsanguination, the rapid intravenous injection of a saturated solution of potassium chloride or possibly pithing of the brain and upper spinal cord. When properly performed, both gunshot and captive bolt meet the objectives of inducing immediate loss of consciousness and rapid death without pain or distress to the animal. In most circumstances on the farm or ranch, gunshot is the most practical method of euthanasia. A 0.22 long rifle solid point bullet fired from either a pistol or rifle is sufficient for young animals. Higher caliber firearms are required for consistent results with adult animals. Proper placement of the bullet is essential and best achieved by holding the firearm within 12 to 24 inches of the intended target. Firearms should never be held flush with the skull. On the other hand, when penetrating captive bolt is used, the device must be held flush over the intended anatomical site. The preferred anatomical site is on the intersection of 2 lines each drawn from the rear corner of the eye to the base of the opposite horn.

Key words: euthanasia, euthanasia techniques, cattle euthanasia

13 Weaning management of newly received beef calves with or without continuous exposure to a persistently infected bovine viral diarrhea virus pen mate: Effects on rectal temperature, peripheral blood leukocytes and serum proinflammatory cytokine concentrations. J. T. Richeson*[1], E. B. Kegley[1], J. G. Powell[1], R. G. Schaut[2], R. E. Sacco[3], and J. F. Ridpath[3], *[1]University of Arkansas, Fayetteville, [2]Iowa State University, Ames, [3]USDA-ARS, National Animal Disease Center, Ames, IA.*

Exposure to animals persistently infected (PI) with bovine viral diarrhea virus (BVDV) results in immunomodulation in cohorts. It is hypothesized that the extent of modulation differs for preconditioned (PC) vs. auction market (AM) cattle. Our objective was to compare immune responses of PC or AM calves in presence (PI) or absence (CON) of a PI-BVDV pen mate using a 2 × 2 factorial arrangement. Crossbred PC steers (n = 27) from a single ranch-origin were selected randomly, weaned, dewormed, vaccinated, tested for PI-BVDV, and kept on the ranch for 61 d. Subsequently, PC steers were transported to a stocker receiving unit (RU), weighed (282 ± 1.6 kg), stratified by d −1 BW, and assigned randomly to treatment (PCPI or PCCON) with no additional processing. Simultaneously, crossbred AM calves (n = 27) were assembled from regional auction markets and delivered to the RU 24 h before PC arrival. The AM calves were weighed (268 ± 2.3 kg), stratified by gender and d −1 BW, processed under the same regimen used for PC steers at their origin ranch except bull calves were castrated, then assigned randomly to treatment (AMPI or AMCON). Treatment pens (50 m × 15 m) were arranged spatially so that PI did not have fence-line contact with CON. For cytokine and hemagram analyses, serum or whole blood was analyzed from d 0, 1, 3, 5 (hemagram only), 7, and 14. In AM calves, RT increased ($P < 0.001$) sharply on d 1. Exposure to PI cohort decreased ($P = 0.01$) the percentage of neutrophils, and increased ($P = 0.02$) percentage lymphocytes resulting in a tendency ($P = 0.07$) for a decreased neutrophil:lymphocyte ratio. Serum concentrations of TNF-α tended to increase ($P = 0.09$) for PI cohort. Interferon-γ concentrations on d 7 and 14, IL-6 concentrations on d 14, and platelets on d 7 were greatest for AMPI ($P \leq 0.05$). Results indicate weaning management and PI exposure alter the immune status of newly received calves. These effects may be additive because alterations were greatest for AMPI.

Key words: bovine viral diarrhea virus, cytokine

14 Effect of oral meloxicam on performance and health of stocker calves after castration. J. F. Coetzee*[1], L. N. Edwards[1], R. A. Mosher[1], A. M. O'Connor[2], B. Wang[2], B. KuKanich[1], and D. A. Blasi[1], *[1]Kansas State University, Department of Animal Science and Industry, Manhattan, [2]Iowa State University, Ames.*

Castration of weaned calves affects profitability by reducing ADG and increasing susceptibility to disease. This study investigated the effect of meloxicam on performance and health of stocker calves after surgical castration. British × Continental calves (n = 258; BW = 193 – 285 kg) were transported for 12 h in 3 truckloads (d −1), weighed and randomly treated with either lactose placebo (CONT; 1 mg/kg) or meloxicam (MEL; 1 mg/kg). Doses were suspended in water and administered per os 24 h before castration. On d 0, bulls were surgically castrated (CAST) and steers were submitted to simulated castration (SHAM). Plasma meloxicam concentrations at the time of castration (d 0) were determined by LC-MS. DMI and ADG determined using BW obtained on d 14 and d 28 were analyzed using PROC GLIMMIX in SAS. Animals were classified as sick based on a depression score of ≥2 on a 5-point scale and a rectal temperature of ≥39.78°C. Relative risk of disease was calculated using PROC NLMIXED in SAS and cumulative pull rate, crude morbidity and BRD morbidity were compared using Kaplan-Meier survival analysis and log-rank tests. On d 0, 1 and 14, calf temperament in the squeeze chute was evaluated using a 4-point scale. Plasma meloxicam concentrations at the time of castration were not significantly different ($P = 0.87$). Castration was found to reduce ADG and DMI over the first 14 d after surgery ($P < 0.001$) but meloxicam administration did not significantly improve performance parameters compared with placebo-treated control calves ($P = 0.48$). Meloxicam treatment significantly reduced the first pull rate in castrated calves ($P = 0.04$) and tended to reduce the BRD morbidity rate ($P = 0.14$). Also, more CONT-CAST calves were pulled ($P = 0.016$) and treated for BRD ($P = 0.023$) over time than MEL-CAST calves. There were a greater percentage of CAST calves with a temperament score ≥2 as compared with SHAM calves. These findings suggest that meloxicam administration before castration in post-weaning calves may reduce the number of animals identified as requiring treatment by feedlot personnel and may extend the time to first treatment for BRD.

Key words: castration, NSAID, performance

15 Characterization and antibiotic susceptibility of *Mycoplasma* isolates from mastitic buffaloes. I. Hussain*[1], S. ur Rahman[2], F. A. Atif[1], and M. Arif[1], *[1]University College of Agriculture, University of Sargodha., Sargodha, Punjab, Pakistan, [2]University of Agriculture Faisalabad, Faisalabad, Punjab, Pakistan.*

The objective of the study was isolation and identification of *Mycoplasma* isolates from mastitic buffaloes and to evaluate the antibiotic resistance of *Mycoplasma bovis* in Faisalabad, Pakistan. A total of 235 buffalo milk samples were collected from 4 private small holder dairy farms located around Faisalabad district of Pakistan. Clinical samples were identified through visual changes and sub-clinical samples with surf field mastitis test. The overall occurrence of mastitis was 40.42% (95/235). The incidence of clinical and sub clinical mastitis was 24.21% (23/95) and 75.78% (72/95) respectively. Mastitic samples were subjected to various passages for the purification of *Mycoplasma* species. *Mycoplasma* species were identified based on colony characteristics and biochemical tests. A total of 19 isolates belonged to 2 species i.e., *Mycoplasma bovis* (18) and *Mycoplasma dispar* (1) were isolated. *Mycoplasma bovis* and *M. dispar* were prevalent in 8.33 and 1.67 % respectively. Highest antibiotic resistance was observed for Tylosin (MIC50 = 8µg/ml) followed by Tetracycline (MIC50 = 7µg/ml), Spiromicin (MIC50 = 4µg/ml) and Gentamicin (MIC50 = 3µg/ml). The results of the study suggested that there should be testing for *Mycoplasma* in routine bacterial examination, while considering other causes of mastitis.

Key words: mastitis, *Mycoplasma*, antibiotic

16 Development of detecting kit for bovine myeloperoxidase using enzyme-linked immunosorbent assay. J. Shi, Q.-Z. Li*, Y. Yang, Y. Lv, and X.-J. Gao, *Key Laboratory of Dairy Science of Ministry of Education, Northeast Agricultural University, P.R. China.*

Myeloperoxidase (MPO) is a heme glucoprotein found in the primary granules of mammalian neutrophils. At the site of infection, MPO is

released extracellularly or into phagocytic vacuoles. It has shown that MPO is abundant in milk taken from mammary glands of cows with mastitis and that the amount of MPO in milk is well correlated with the somatic cell count in mastitis milk. To evaluate the potential of using MPO in the diagnosis of mastitis in cows, this study developed a specific enzyme immunoassay for MPO in milk. Bovine MPO was isolated and purified from bovine whole blood by Sephadex G-200 chromatography and ConA-Sephrose 4B affinity chromatography. Antiserum against bovine MPO were produced using the purified MPO with conA as a coated "antibody," and mouse anti-bovine antiserum against MPO as a second detection antibody, and chicken HRP-labeled polyclonal antibody as a anti-antibody, a special sandwich ELISA for MPO was established. ELISA kit was developed. Evaluating kit by methodology showed good specificity, reproducibility (variant coefficient: 1.09% ~7.2% in batch and 1.47% ~6.7% between batches), and the detection limit was 1.1ug/mL. The experiment certified that this kit could maintain over one year and the detection time of the kit was about 3.5h.

Key words: bovine myeloperoxidase, purification, ELISA kit

17 The identification of candidate genes and candidate gene structural variation for bovine spongiform encephalopathy. J. Thomson*, V. Bowles, J. Choi, P. Stothard, and S. Moore, *University of Alberta, Edmonton, AB, Canada.*

Previous work in our lab identified several regions throughout the bovine genome associated with classical BSE in European cattle. There are a total of 64 regions found to be associated with BSE incidence ($P < 0.05$). All of the genes under those regions were analyzed using gene ontology information as well as current literature findings and 100 candidate genes were identified. Data from 10 mRNA sequence libraries and 2 whole genome sequences, created using the SOLiD next generation sequencing system from Applied Biosystems, was interrogated to identify structural variation in these candidate genes. mRNA seq libraries including liver, adipose, hypothalamus, muscle, duodenum, kidney, lung, peyers patch, cortex, and blood were used for single nucleotide polymorphism identification. Whole genome re-sequencing was performed on both a Holstein and a Black Angus bull. Utilizing both the mRNA-sequence libraries and the whole genome re-sequencing, structural variation was found in 98 of the 100 candidate genes identified as positional candidates for BSE susceptibility. This structural variation included 107 non-synonymous mutations, 18 synonymous mutations, 111 intronic mutations, and 19 3′and 5′ UTR region mutations. The identified polymorphisms will be tested in a family based data set of 302 BSE affected and 179 unaffected half-sib Holsteins from 6 sire families. The results of this research will give indicators of the gene pathways underlying BSE disease progression and enhance our understanding of the disease in its host species.

Key words: BSE, single nucleotide polymorphisms, animal health

18 Genomic regions associated with incidence of disease in cattle using DNA pooling and a high-density single nucleotide polymorphism array. E. Casas*, L. A. Kuehn, T. G. McDaneld, T. P. L. Smith, and J. W. Keele, *USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE.*

Genomic regions associated with general disease (respiratory disease, foot rot, and pinkeye) in beef cattle were identified using treatment records on 2,849 animals. General disease cases included animals treated for bovine respiratory disease, foot rot, or pinkeye. Untreated cohorts, matched on breed composition and contemporary group, for cases were included as controls. Fifteen pools of DNA with 102 cases/pool and 13 pools with an average of 101 controls/pool were genotyped using 777,000 single nucleotide polymorphisms (SNP). Mixed model methods were used to estimate differences in allele frequency between cases and controls while accounting for technical variation (specific to SNP array platform), binomial sampling and pool construction error. Hidden population structure unaccounted by the matching procedure was considered statistically using eigenvectors of the correlation among pools across all SNP. Single nucleotide polymorphisms residing on chromosomes 3, 6, 7, 20, 23, and X were highly significant (nominal $P < 0.00001$). Three of these SNPs reside on chromosome 3 between 25 megabase (Mb) and 26 Mb. Fourteen additional SNPs were also significant ($P < 0.001$) in this chromosomal region. On chromosome 6, one highly significant SNP ($P < 0.00001$) is located between 63 and 64 Mb. In this genomic region, 10 additional SNPs were also significant ($P < 0.001$). Two SNPs were highly significant ($P < 0.00001$) on chromosome 7. One resides on Mb 56, while the other resides on the telomeric end of the chromosome. One SNP was highly significant ($P < 0.00001$) on chromosome 20 (on 55 Mb), and one on chromosome 23 (on 20 Mb). Three SNPs on chromosome X were highly significant ($P < 0.00001$). These SNPs reside at 12, 21, and 94 Mb. Results from this study, combined with future studies in a meta-analysis, should provide strong evidence for these genomic regions as harboring genes associated with defense mechanisms against pathogens.

Key words: cattle, diseases, DNA pooling

19 In vitro and in vivo anthelmintic activity of *Amomum subulatum* Roxb. seeds. Z. Iqbal*, N. Badar, M. Khan, and Z. Sindhu, *Department of Parasitology, University of Agriculture, Faisalabad, Punjab-Pakistan.*

This study was carried out to validate the anthelmintic activity of *Amomum subulatum* seeds used in traditional veterinary medicine in Pakistan. Crude aqueous methanol extract (CAME) and its different solvent fractions were tested in vitro employing adult motility assay and egg hatch tests using mature *Haemonchus contortus* and its eggs, respectively. In vivo, CAME and crude powder (CP) were tested employing fecal egg count reduction test in sheep naturally parasitized with gastrointestinal nematodes. In adult motility assays, 73.3% mature H. contortus exposed to CAME @ 50 mg/ml were found dead compared with no mortality in the worms kept in PBS by 10 h post-exposure. There was 100% mortality of worms exposed to the standard drug (levamisole) @ 0.5 mg/ml. Ethyle acetate fraction of CAME was the most effective resulting in 100% mortality of worms @ 50 mg/ml followed by chloroform (76.7%), aqueous (50%) and petroleum spirit (46.7%) fractions. In egg hatch test, CAME was found an effective ovicidal with LC_{50} 13.1872 µg/ml. Chloroform and ethyle acetate fractions had comparable LC_{50} values (18.1413 and 18.6102 µg/ml, respectively) which followed in increasing order by aqueous (20.4178 µg/ml) and petroleum spirit (253.9106 µg/ml) fractions. The LC_{50} values of plant extracts were, however, far greater than that of standard drug, albendazole (0.0345 µg/ml). The maximum reduction (74.45%) in eggs per gram of feces (EPG) was recorded in sheep treated with CAME @ 3 g/kg body weight on d 12 post-treatment (PT). CP was less effective as maximum reduction in EPG was recorded as 57.45% @ 3 g/kg body weight on d 12 PT. There was 100% reduction in EPG by d 8 PT in sheep treated with standard drug, levamisole. Therefore, use of *A. subulatum* seeds in traditional veterinary medicine as an anthel-

mintic is valid. Large-scale control studies, however, are suggested to identify the active principles in the plant material tested in this study.

Key words: *Amomum subulatum*, anthelmintic, sheep

20 Lentisk (*Pistacia lentiscus* L.) browse prevents gastro-intestinal nematode infection in goats. S. Y. Landau*[1], A. H. Azaizeh[2], H. Muklada[1], T. A. Glasser[3], E. D. Ungar[1], and A. Marcovics[4], *[1]Agricultural Research Organization, the Volcani Center, Department of Agronomy and Natural Resources, Bet Dagan, Israel, [2]Institute of Applied Research, The Galilee Society (Affiliated with University of Haifa), Shefa-Amr, Israel, [3]The Ramat Hanadiv Nature Park, Zikhron Ya'akov, Israel, [4]Department of Parasitology, Kimron Veterinary Institute, Bet Dagan, Israel.*

Gastro-enteritis caused by infection with gastro-intestinal nematodes (GIN) is widespread among goats in the Middle-East. It is characterized by extreme emaciation, diarrhea, and mortality. In a 2-year survey, we observed that the Damascus and Mamber breeds of goats that graze on brushland rich in lentisk (*Pistacia lentiscus* L.) had very low fecal egg counts (FEC). Lentisk contains 20% polyethylene glycol (PEG, MW 4,000)-binding tannins on a dry matter basis. We tested possible mechanisms of protection against GIN. In a series of in vitro experiments, we showed that ethanol 70% and, to a less extent, water and ethanol 100% extracts of lentisk prevent exsheathment of L3 larvae, thus impairing nematode maturation to the egg-producing adult stage. In addition, we showed that feeding lentisk foliage to young goats infected with mixed GIN species resulted in a drastic decrease in FEC (241 vs. 1293, $P < 0.001$; n = 14). When goats were administered daily 20 g of PEG (which binds to and thereby neutralizes the tannins), the effect of lentisk on FEC was approximately halved to 705 epg. This suggests that tannins are not the only anthelmintic moiety in lentisk. The daily intake of tannins needed to eliminate fecal egg excretion was 1 g·kg BW^{-1} d^{-1}. After lentisk feeding was stopped, FEC returned to the control level, implying that the effect of lentisk on GIN was suppressive but not lethal. Our data suggest that daily ingestion of lentisk—5 to 15% of DM ingested—prevents egg formation and possibly larval maturation all year-round, resulting in effective control of GIN populations. This seems to be a passive mechanism, and not an active mechanism of adaptive feeding behavior to a worm challenge.

Key words: tannin, browse, self-medication

21 Withdrawn

22 Occurrence of paratuberculosis in the hilly regions of Himachal Pradesh, India. J. S. Sohal*, S. V. Singh, P. K. Singh, and A. V. Singh, *Central Institute for Research on Goats, Mathura, UP, India.*

In India paratuberculosis has been studied widely in the plain regions, however, to our knowledge there have been no reports from hilly regions. Present study was attempted to study the occurrence of paratuberculosis in hilly regions of northern parts of country. A total of 4 flocks (sheep and goat) belonging to Chamba District of Himachal Pradesh, India were studied in the present investigation. These flocks usually come to plain regions of the state in search of fodder in the winter season. A total of 52 animals were sampled for feces from these flocks. In total 12 (8- sheep, 4- goats), 15 (10- sheep, 5- goats), 9 (7- sheep and 2- goats) and 16 (12- sheep, 4- goats) animals belong to flock 1, 2, 3 and 4, respectively. Animals were tested for direct fecal examination, fecal DNA PCR and culture for the presence of MAP. The positive PCR samples were subjected to IS1311 PCR-REA to know the genotype of infecting strain.

Key words: paratuberculosis, hilly regions, genotyping

23 Status of *Mycobacterium avium* subspecies *paratuberculosis* Infection in the Cow Shelters (Goshalas/Pinjarapoles) in India. S. V. Singh*[1], A. V. Singh[1], P. K. Singh[1], B. Singh[1], A. Kumar[1], B. S. Chandel[3], A. Srivastav[2], S. Gupta[1], H. Singh[1], A. Mittal[1], and S. Yadav[2], *[1]Central Institute for Research on Goats, Mathura, Uttar Pradesh, India, [2]College of Veterinary Sciences, Mathura, Uttar Pradesh, India, [3]College of Veterinary Science, Dantiwada, Gujarat, India.*

India possesses huge population (>480 million) of domestic livestock, however, per animal productivity remains poor. Due to poor per animal productivity, large number of low or unproductive goats, sheep and buffaloes go for early slaughter. Slaughtering of cows (even those suffering from incurable diseases) is banned in India. Such cows are either let off or sent to Cow Shelters by farmers. Cow shelters (or Goshalas in North India and Pinjarapoles in Western India) provide shelters for un-productive and homeless cows. Number of these cow shelters is very large in country and depend on charity money. Cows in these shelters survive on low plane of nutrition and are in poor health and suffer from varieties of health problems and are rarely screened for diseases including Johne's disease. Mycobacterium avium subspecies paratuberculosis (MAP), the cause of JD, is responsible for huge losses in production and is endemic in farm and farmer's herds. Study estimated status of MAP in 4 Goshalas in Mathura, UP (region A) and 3 in Dantiwada, Gujarat (region B) using microscopy, indigenous ELISA kit and Blood PCR. 211, 143 and 183 cows were screened by microscopic examination (feces), ELISA (serum) and PCR (blood), respectively. Whereas, of the 3 Goshalas in region B, 37 and 135 cows were screened by microscopy (fecal) and ELISA (serum), respectively. In region A, 57.4 and 55.9 and 36.1% cows were positive in microscopy, ELISA and PCR, respectively. In region B, 48.6 and 62.2% cows were positive by microscopy and ELISA, respectively. Load of MAP infection was high in cow shelters and serve as reservoir and need special attention for the control of MAP at National level.

Key words: Johne's disease, ruminants, prevalence

24 Finishing performance and carcass traits of heifers previously managed with three respiratory disease protocols. J. L. Wahrmund*[1], D. B. Burken[1], B. K. Wilson[1], S. J. Terrill[1], C. R. Krehbiel[1], D. L. Step[2], S. M. Trost[3], C. L. Goad[4], and C. J. Richards[1], *[1]Oklahoma State University, Department of Animal Sciences, Stillwater, [2]Oklahoma State University, Department of Veterinary Clinical Sciences, Stillwater, [3]Strategic Solutions International, Stillwater, OK, [4]Oklahoma State University, Department of Statistics, Stillwater.*

This experiment evaluated the finishing performance and carcass traits of 331 heifers (BW = 351 ± 51 kg) previously managed for 56 d with 3 bovine respiratory disease (BRD) health management protocols. The protocols were: visual monitoring (CON), visual and ruminal temperature monitoring (TEMP), or visual monitoring following a d 0 metaphylactic treatment (MET). Heifers were blocked by BW and randomly allotted to 24 pens for the receiving phase. At finishing, 169 heifers from 12 pens were blocked by BW and reallocated to 30 pens based on receiving treatment, and all heifers were adapted to a 94% concentrate diet. Percentage of heifers receiving 0, 1 or 2 treatments for BRD were 57, 37 and 8% for CON; 26, 49 and 25% for TEMP;

and 81, 10 and 9% for MET; respectively. Heifers treated twice for BRD began the finishing phase weighing 16.9 kg less ($P < 0.01$) than all other heifers. Interactions were observed between health protocol and number of times treated for final BW and overall ADG ($P \leq 0.02$). Final BW of CON heifers treated twice was 32.2 kg less ($P \leq 0.04$) than other CON heifers, while number of times treated did not affect ($P \geq 0.13$) final BW of TEMP and MET heifers. CON heifers treated twice gained 0.16 kg/d less ($P = 0.01$) than other CON heifers. TEMP heifers treated twice gained 0.11 kg/d more ($P = 0.03$) than those never treated and MET heifers' ADG was unaffected ($P \geq 0.12$) by times treated. Heifers treated twice for BRD had 11.4 kg lighter ($P \leq 0.04$) HCW than those receiving 0 or 1 treatment. Heifers not treated for BRD had 1.1% greater dressing percent ($P < 0.01$), 7.6% greater marbling score ($P \leq 0.04$) and 0.25 cm greater fat thickness ($P \leq 0.02$) compared with those treated once or twice. Carcass value showed a health protocol × number of times treated interaction ($P = 0.04$). Carcasses from CON heifers treated twice were valued at $91.48 less ($P \leq 0.02$) than those from other CON heifers, while carcass value of TEMP and MET heifers was not affected ($P \geq 0.27$) by number of times treated. Results indicate that metaphylaxis and remote temperature monitoring may spare some of the detrimental effects of BRD on performance and carcass value.

Key words: respiratory disease, performance, carcass

Beef Species and Ruminant Nutrition Joint Symposium: Cow Size, Genetics, Management and The Beef Industry

25 Management and genetic factors affecting efficiency of cattle in a grazing environment. A. J. Roberts*, J. T. Mulliniks, R. C. Waterman, T. W. Geary, L. J. Alexander, M. K. Petersen, and M. D. MacNeil, *USDA-ARS, Fort Keogh Livestock and Range Research Laboratory, Miles City, MT.*

Much of current efforts to improve efficiency in cattle use measures of individual feed intake in combination with weight gain as an indication of efficiency. This approach provides pertinent information concerning efficiency during the growing phase, but the relationship to cow efficiency remains to be determined. Efficiency in grazing cows is much more complex, especially when considering input and output traits associated with efficiency as functions of genetics and environmental factors, and interactions of these factors. The most critical output influencing efficiency of beef cattle production is reproductive rate, which is a cumulative process requiring years to establish. Nutrition and management components of environment are more complex in range settings and subject to greater seasonal and annual variation than in confined settings relying solely on harvested feed with greater homogeneity. Methodology to measure feed intake while grazing under range conditions are lacking. Seasonal and annual variations in quantity and quality of forage can result in greater distinctions between biological and economic efficiency in the cow-calf phase compared with other segments. For example, cows that consume more calories during the growing season and gain sufficient weight to exist on less harvested feed inputs during winter may require less total economic input than cows with greater biological efficiency that consumes less during the growing season, but require more calories from harvested feed later. Efficiency of beef cattle production requires a balance between nutritional inputs and prolonged optimal output. A provocative question to consider is whether traditional approaches of providing sufficient feed to a herd of cows to achieve a relative high rate of reproduction results in improved efficiency or not? Is this analogous to selecting a type of cattle and managing the environment to sustain the type? What happens when cattle are managed corresponding to restriction imposed by a limited environment and provided relatively minimal inputs rather than feed for a desired level of production associated with a resource rich environment?

Key words: genetics, management, efficiency

26 Genetics of postweaning performance of beef cattle on forage. M. A. Brown*[1], J. W. Holloway[2], D. L. Lalman[3], C. Dobbs[3], and S. M. Clifton[4], *[1]USDA-ARS, Grazinglands Research Laboratory, El Reno, OK, [2]Texas AgriLife Research, San Angelo, [3]Oklahoma State University, Stillwater, [4]Redlands Community College, El Reno, OK.*

Increases in the costs of feed grains have revived interest in increasing use of forages to either market as forage-finished beef or to produce heavy calves that will finish on less grain. However, little is known about the interactions of animal genetics and grazing environment that allows the most efficient use of resources and has the best potential to be economically efficient. Determination of the optimal combination of animal genetics and production environment requires that the target end-points of production are well-defined and it requires knowledge about available animal genetics and the intended production environment. Animal genetics is loosely defined by rate of maturing, milk production potential, and level of tropical adaptation. In addition, knowledge of breed combination, gender, and genetic merit is helpful. Environmental effects that must be considered include nutritional value of the forage, climate, geography, time, and management. With this information, robust systems can be developed considering the interactions of environmental effects, interactions of genetic effects, and the interactions of genetic and environmental effects. Not only do these systems need to appropriately match genetics and environment, they need to be low-capital systems that are simple to implement . Attributes of animal genetics that might be desirable include efficiency of forage utilization, adaptation not only heat and cold conditions but also adaptable to rapid changes in climate. To fit within the current commodity beef system, it is desirable that cattle in these systems marble early with respect to their mature weight, and that they have sufficient growth to produce acceptable carcass weights by 18 to 24 mo of age. It seems reasonable that selection of appropriate genetics will match frame size to forage quality with lower quality forages requiring more moderate frame size. The use of crossbreeding in these systems will require a closer evaluation of genetic effects. The incorporation of tropical adaptation into efficient forage-based beef production systems will be dependent on forage quality, climate, and pressure from external parasites.

Key words: beef cattle, forage, genotype x environment

27 A historical perspective on the influence of the beef industry on mature cow size. B. McMurry*, *Cargill Animal Nutrition, Minneapolis, MN.*

Between 1975 and 2005 efficiency as measured by pounds of beef produced per beef cow increased dramatically. Driven by technological advancements in nutrition, health, reproduction, growth physiology, breeding and genetics, weight gain increases were realized in every industry segment, Calves weaned heavier, stocker and background cattle gained more rapidly, average daily gain and feed conversion in feedlots improved than previous to 1975. During the 30-year period carcass weights of steers and heifers increased 144 and 194 pounds, respectively. The average steer and heifer carcass weights in 1975 were 673 and 556 pounds, by 2005 they had reached 817 and 750 pounds, respectively. Calculated live weights increased for steers and heifers, respectively from 1068 and 869 pounds in 1975 to 1297 and 1172 pounds in 2005. Genetics of European breeds and the advent of EPDs underpinned growth and carcass weight increases. The introduction of faster-growing, later maturing breeds and heavy selection pressure toward growth also had an impact on the US beef cow herd. Selection criteria favored higher growth rates and EPDs for yearling weight, which are highly correlated with mature weight. Consequently, from 1975 to 2005 carcass weights of bulls and cows increased 223 and 146 pounds, respectively. Average bull and cow carcass weights in 1975 were 682 and 475 pounds, by 2005 they had reached 905 and 621 pounds, respectively. Calculated live weights at harvest increased for bulls and cows respectively from 1047 and 1340 pounds in 1975 to 1350 and 1769 pounds in 2005. Additionally during this period, to improve weaning weights, cow/calf producers selected for increased milk production, and, along with increased mature weight, raised the average beef cow's forage dry matter requirements by approximately 25%. During this same 3year period the producing beef cow population declined 13.4 million head or 28.6%, however total DM required to support the US cowherd only declined 6% (from 186 million to 174

million tons); the impact of increasing mature size and milk production. Consequently, limited forage resources constitute a significant barrier for increasing beef cow inventories and domestic beef supplies.

Key words: mature size, beef cattle, efficiency

28 Conclusion: Cow size and keeping perspective. R. H. Pritchard*, *South Dakota State University, Brookings.*

There are enumerable considerations to be accounted when idealizing mature cow weight (MW). Some inputs such as bulls, vaccines, labor are fixed per cow, regardless of MW and cannot be overlooked. Oftentimes we evaluate cow size by creating 2 component production ratios that are considered efficiencies. We express WW per cow or WW per cow BW and get different rankings. Divide these ratios by calving interval and rankings change again, depending on a production environment. Rankings created by using efficiency ratios to identify optimum MW will vary with the nutritional environment, management inputs, and climatic stressors. Alternatively we could work backward from a desirable carcass weight to determine an appropriate cow size. If 385 kg is an appropriate carcass weight, then the cow MW weight may be 580 kg. This average may not be ideal or justifiable in all production situations and includes many assumptions. It is subject to correction (lower) for the use of anabolics; higher for high growth genetics used in an accelerated production system; or lower for progeny reared in a deferred production system. Declining cow numbers have led to lighter and especially younger feeder cattle placements in feedlots. This has created pressures that ultimately increase cow MW. How the feedlot industry responds to greater competition for corn may elicit new influences on the direction of cow size.

Key words: beef, cow, size

Breeding and Genetics: Genomic Selection and Whole-Genome Association I

29 Effect of different genomic relationship matrices on accuracy and scale. I. Misztal*[1], C. Y. Chen[2], I. Aguilar[5], Z. G. Vitezica[3], A. Legarra[3], and W. M. Muir[4], *[1]University of Georgia, Athens, [2]Newsham Choice Genetics, Chesterfield, MO, [3]INRA, Castanet-Tolosan, France, [4]Purdue University, West Lafayette, IN, [5]INIA, Las Brujas, Uruguay.*

Phenotypic data on body weight (BW) and breast meat area (BM) were available on up to 287,614 broilers. A total of 4,113 animals were genotyped for 57,636 SNP. The records were analyzed by a single step genomic BLUP (ssGBLUP), which accounts for all phenotypic, pedigree and genomic information. The genomic relationship matrix (G) in ssGBLUP was constructed using either equal (0.5; GE) or current (GC) allele frequencies, and with either all SNP or SNP with minor allele frequencies (MAF) below multiple thresholds (0.1, 0.2, 0.3, and 0.4) ignored. Additionally, a pedigree based relationship matrix for genotyped animals (A_{22}) was available. The matrices and their inverses were compared with regard to average diagonal (AvgD) and off-diagonal (AvgOff) elements. In A_{22}, AvgD was 1.00 and AvgOff was 0.01. In GE, both averages decreased with the increasing thresholds for MAF; AvgD decreasing from 1.37 to 1.02 and AvgOff decreasing from 0.72 to 0.03. In GC, AvgD was around 1.01 and AvgOff was 0.00 for all MAF. For inverses of relationship matrices, all AvgOff were close to 0; AvgD was 2.4 in A_{22}, varied from 11.6 to 13.0 for GE, and increased from 8.7 to 12.9 for GC as the threshold for MAF increased. Predictive abilities with all GE and GC were similar. Compared with BLUP, EBVs of genotyped animals in ssGBLUP were, on average, biased up to 1 additive SD higher with GE and down by 2 additive SD with GC. The bias was eliminated by adding constant 0.014 (equal to AvgOff in A_{22}) to GC. This constant is equivalent to twice the mean relationship between gametes in the genotyped and ungenotyped populations. Reduction of SNP with low MAF has a low effect on the realized accuracy. Unbiased evaluation in ssGBLUP may be obtained with GC scaled for compatibility with A_{22}.

Key words: genomic selection, single step, bias

30 Comparisons of numerator and genomic and relationship matrices. H. Wang* and I. Misztal, *University of Georgia, Athens.*

The objective of this study was to quantify differences between the numerator (A) and genomic (G) relationship matrices for possible application in detection of pedigree and genotyping errors. Data were obtained from Cobb-Vantress, including 2422 individuals in 3 generations from the same line and genotyped for 57,636 SNP. The A matrix was constructed using pedigrees for 3 generations. The G matrix was constructed using current allele frequencies and scaled for identical means of diagonal and off-diagonal elements of A for the common animals. In A (G), the mean diagonal (AvgD) element was 1.01 ± 0.015, ranging from 1.00 to 1.09 (1.01 ± 0.07, ranging from 0.48 to 1.86). The mean of the off-diagonal elements (AvgOff) was 0.031 ± 0.051, ranging from 0 to 0.062 (0.031 ± 0.055, ranging from −0.13 to 0.69). For G–A, AvgD was 0 ± 0.073, ranging from −0.52 to 0.86, and AvgOff was 0 ± 0.032, ranging from −0.50 to 0.52. The distribution of AvgOff for G–A was approximately normal with long tails, with only 0.53% elements outside the range from −0.10 to 0.10. The SD of the off diagonal elements of G–A increased from 0.03 where aij < 0.01 to 0.04 where aij > 0.10. Visually, matrix A contained blocks with elements close to 0 and blocks with higher correlations. Similar blocks occurred in G; however, the blocks with elements close to 0 were smaller. Moreover, G–A showed several rows and columns with high values. After removing animals with the average relationship to other animals >0.030, the differences between G and A decreased. When A is obtained with long generation pedigrees and G is scaled for compatibility with A, differences between G and A are very small. Larger differences may indicate pedigree errors, genotyping errors, or mixing of lines/breeds.

Key words: genomic selection, genomic relationship matrix, errors

31 A recursive method of approximation of the inverse of genomic relationships matrix. P. Faux*[1], N. Gengler[1,2], and I. Misztal[3], *[1]University of Liege, Gembloux Agro-Bio Tech, Animal Science Unit, Gembloux, Belgium, [2]National Fund for Scientific Research, Brussels, Belgium, [3]University of Georgia, Animal and Dairy Science Department, Athens.*

Genomic evaluations by some procedures such as genomic BLUP (GBLUP) or single-step GBLUP (ssGBLUP) use the inverse of the genomic relationship matrix (G). The cost to create such an inverse is cubic and becomes prohibitively expensive after 30–100k genotypes. The purpose of this study was to develop methodologies, which eventually could compute a good approximation of G^{-1} at reduced cost. A recursive approximation of the inverse is based on a decomposition similar to that for the pedigree-based relationship: $G^{-1} = (T^{-1})'D^{-1}T^{-1}$, where T is a triangular and D a diagonal matrix. In the first step, animals are processed from the oldest to the youngest. For each animal, a subset of ancestors is selected with coefficients of genomic relationship to that animal greater than a threshold. A system of equations is created where the coefficients of G for the selected ancestors are in the left hand side and the coefficients of G for the given animal corresponding to the ancestors are the right hand side. The solution to that system of equation is stored in one line of T. Then, D is computed as diagonal elements of $T^{-1}G(T^{-1})'$. If off-diagonals of D are too large, the approximation to G can be improved by repeated applications of $G^{-1} = (T^{-1})'D^{-1}T^{-1}$ and $D = T^{-1}G(T^{-1})'$. After n rounds, the approximation of G inverse is a product of 2n triangular matrices and one diagonal matrix. This recursive method has been assessed on a sample of 1,718 genotyped dairy bulls. The correlation between GEBV using the complete or approximated G were 0.54 in the first round, 0.96 in the second, and 0.99 in the third. The cost of the proposed method depends on the population structure. It is likely to be high for closely related animals but lower for populations where few animals are strongly related. Additional research is needed to identify near-sparsity in T and D to eliminate unimportant operations.

Key words: genomic prediction, computing methods, dense matrix inversion

32 Adapting Bayesian mixture model algorithms to estimate hyperparameters that characterize genetic architecture in genomic selection models. R. J. Tempelman*[1], W. Yang[1], J. P. Steibel[1], and N. M. Bello[2], *[1]Michigan State University, East Lansing, [2]Kansas State University, Manhattan.*

Various genomic selection models (e.g., BLUP, BayesA, BayesB) have been formally compared with each other with the understanding that different traits are better fit by one model versus another. However, it has been generally underappreciated that BLUP and BayesA are

merely special cases of BayesB; that is, certain key hyperparameters can be estimated rather than arbitrarily specified. These key hyperparameters are: 1) the proportion (π) of single nucleotide polymorphism (SNP) markers that are directly associated with causal variants, 2) the scale parameter that determines the typical genetic variance for each non-null SNP marker, and 3) a degrees of freedom parameter that determines how much heterogeneity there exists in this genetic variability across SNPs. We demonstrate the use of fundamental Bayesian mixture model algorithms for estimating these key hyperparameters from the data, highlighting, in particular, methods based on slab and spike priors as well as the stochastic search and variable selection algorithm. We use simulation studies to demonstrate the properties of these methods on estimates of these 3 key hyperparameters. First, we consider simulated populations assuming linkage equilibrium between all markers with a proportion π of the markers being synonymous with causative variants. These simulations provide a positive control for which the model for both data generation and analysis are in near agreement; we subsequently demonstrate that inferences were in good agreement with the true values specified for each hyperparameter. We then consider more extensive comparisons between the various methods under more realistic linkage disequilibrium situations between SNP markers with different levels of marker density ($0.15 < r^2 < 0.30$). In general, estimates of all 3 hyperparameters decreased as marker density increased, thereby further highlighting the need to infer upon these hyperparameters rather than arbitrarily specifying them.

Key words: genetic architecture, genomic selection, mixture models

33 Improving accuracy of genomic selection by hierarchical Bayesian modeling of spatially correlated chromosomal effects. W. Yang* and R. J. Tempelman, *Michigan State University, East Lansing.*

Hierarchical mixed effects models have been effectively used to predict genomic merit of livestock using high density SNP marker panels. Two currently popular approaches, BayesA and BayesB, are based on specifying all SNP-associated effects to be independent of each other. BayesB has been particularly effective as it extends BayesA in allowing a large proportion of SNP markers to be associated with null effects. We propose extensions of these 2 models to attempt to specify these effects as spatially correlated due to the chromosomally proximal effects of causal variants. These 2 methods, respectively labeled ante-BayesA and ante-BayesB, are based on a first order unstructured antedependence specification between SNP effects. Based on a simulation study with 10 replicated data sets, each differing by 6 different LD levels ranging from $r^2 = 0.16$ to 0.30, the antedependence methods had significantly ($P < 0.001$) higher accuracies than their corresponding classical counterparts at higher LD levels ($r^2 > 0.27$) with differences exceeding 3%. A cross-validation comparison was also conducted on the heterogeneous stock mice data resource (http://mus.well.ox.ac.uk/mouse/HS/) using 6 week weights as the phenotype. The data set included 2,296 individuals and 950 randomly selected SNPs to ensure an adjacent average pair-wise LD $r^2 = 0.3$, as representative of current livestock data. The antedependence methods increased cross-validation prediction correlations by up to 3.6% compared with their classical counterparts ($P < 0.001$). We used a final set of simulation studies to demonstrate that it is possible to infer upon key parameters (e.g., proportion of SNPs with null effects, average genetic variance at each SNP) that define the genetic architecture of our antedependence methods. In general, ante-BayesA and ante-BayesB required less than 10% greater computational time compared with their classical counterparts such that they should become increasingly attractive for whole genome selection, particularly as the density of SNP chips increases.

Key words: Bayesian inference, genomic selection, antedependence

34 Incorporating molecular breeding values with variable call rates into genetic evaluations. S. D. Kachman*[1], G. L. Bennett[2], K. J. Hanford[1], L. A. Kuehn[2], E. J. Pollak[2], W. M. Snelling[2], M. L. Spangler[1], and R. M. Thallman[2], *[1]University of Nebraska, Lincoln, [2]U.S. Meat Animal Research Center, Clay Center, NE.*

A partial genotype (PG) for an animal can result from panels with low call rates used to calculate a molecular breeding value (MBV). A MBV can still be calculated using PG by replacing the missing marker covariates with their mean value. This approach is expected to change the distribution of the MBV by reducing the variance and percentage of genetic variation explained by the MBV. Under independence, the variance of a MBV is $2\Sigma b_i 2p_i(1-p_i)$ where b_i and p_i are the effect and the allelic frequency of marker i, respectively. For animal a the proportion, P_a, of the complete genotype (CG) MBV variance accounted for by PG is then the ratio of the variances calculated by summing over the partial and the complete set of markers. Similarly, the genetic covariance between a trait and PG MBV is also proportional to Pa. The proportion of CG covariance between animals a and b with PG was assumed to be proportional to P_aP_b. The PG model for the MBV of animal a, scales the CG genetic effect by P_a and adds a missing genotype effect with variance $P_a(1-P_a)$ times the CG genetic variance. A weaning weight MBV was constructed from 159 Single Nucleotide Polymorphisms using genotype and weaning weight data from 3,327 Cycle VII calves from the US Meat Animal Research Center. Genotype (n = 2,503) and weaning weight (n = 148,897) data from purebred calves of 7 breeds were used to evaluate the MBV. The genotype data had an average call rate of 85.2% (11.3–100%). Two trait analyses were run for each breed separately, both with and without accounting for PG in the model. Overall, MBV heritabilities and its genetic correlation with weaning weight were larger when the effects of PG were incorporated into the analysis (Table 1).

Table 1. Estimated genetic parameters

		Heritability			
	Heritability	Molecular Breeding Value		Genetic Correlation	
Breed	Weaning Weight	Without	With	Without	With
Angus	0.23±0.02	0.87±0.16	0.75±0.12	0.00±0.10	0.15±0.11
Red Angus	0.24±0.03	0.67±0.16	0.89±0.14	0.10±0.10	0.14±0.11
Charolais	0.12±0.03	0.33±0.16	0.47±0.18	0.28±0.15	0.38±0.16
Gelbvieh	0.22±0.02	0.64±0.18	0.62±0.16	0.25±0.13	0.26±0.14
Hereford	0.14±0.04	0.83±0.15	0.96±0.14	0.20±0.20	0.25±0.21
Limousin	0.27±0.02	0.60±0.19		0.24±0.12	
Simmental	0.75±0.03	0.61±0.16	0.73±0.16	−0.05±0.08	−0.03±0.09

Key words: genomic evaluation, mixed models, beef cattle

35 Impacts of inclusion of foreign data in genomic evaluation of dairy cattle. K. M. Olson*[1], P. M. VanRaden[2], and D. J. Null[2], *[1]National Association of Animal Breeders, Columbia, MO, [2]Animal Improvement Programs Laboratory, ARS, USDA, Beltsville, MD.*

The accuracy of genomic predictions tends to increase with larger numbers of animals in the training data set. Because of this, many countries have combined data to increase the size of their training populations. The objective of this study was to investigate different meth-

ods of combining the data using domestic data, a combined domestic and foreign training population, and a domestic and foreign multi-trait method. Foreign bulls with US daughters were considered domestic in this study. The combined foreign and domestic training data set was comprised of bulls and cows that were proven (had daughter or own information) as of August, 2007 and totaled 9,874 Holsteins and 1,473 Brown Swiss. The domestic training animals included cows and bulls and totaled 8,674 Holsteins and 741 Brown Swiss. The foreign training data set had 1,200 Holsteins and 732 Brown Swiss. Over 90% of the foreign data from Holsteins were from Canada, which has a very high genetic correlation to the United States. Most the Brown Swiss data were from Germany and Switzerland, but animals from 6 other countries were included in the data. The validation data sets consisted of US bulls that were unproven as of August, 2007 and proven with daughters in at least 10 herds as of December, 2010. There were 3,094 and 115 Holstein and Brown Swiss validation bulls, respectively. Genetic correlations for the multi-trait method were computed as the weighted average of countries genetic correlation with the United States based from Interbull. Results show a general increase of about 2% from inclusion of foreign data over domestic data only in the Holstein population and an increase of 5% in the Brown Swiss. Multi-trait methodology was beneficial for Brown Swiss and most traits gained reliability and some traits gained as much as 6%. Multi-trait was not advantageous in Holsteins, probably due to the high genetic correlation between the 2 countries. It is recommended that countries with high genetic correlations be treated as a single population. Diverse populations may benefit from the implementation of multi-trait methodology.

Key words: country, dairy cattle, genomic evaluation

36 Optimization of principal component extraction for direct genomic value prediction in a multibreed population. N. P. P. Macciotta*[1], M. A. Pintus[1], R. Steri[1], G. Gaspa[1], D. Vicario[2], E. Santus[3], J. T. H. Van Kaam[4], and P. Ajmone Marsan[5], *[1]Università di Sassari, Sassari, Italy, [2]ANAPRI, Udine, Italy, [3]ANARB, Bussolengo, Italy, [4]ANAFI, Cremona, Italy, [5]Università Cattolica del Sacro Cuore, Piancenza, Italy.*

A joint use of data coming from different breeds is a strategy for mitigating the huge unbalance between number of markers and number of phenotypes in genomic selection (GS) programmes. A further reduction of data asymmetry can be obtained by using Principal component analysis to derive new synthetic variables to be used as predictors in the calculation of direct genomic values (DGV). In the present work the PC approach is used for predicting DGV for dairy traits in bulls of 3 breeds farmed in Italy: 863 Holstein (H), 749 Brown Swiss (BS), 479 Simmental (S), respectively. Animals were genotyped with the 54K Illumina beadchip. SNPs retained after edits were 39,225. PC were extracted from the joint data set of the 3 breeds or separately by each breed. Extraction was carried out by chromosome. Different amounts of PC were retained on the basis of the explained variance: 0.50, 0.70, 0.80 and 0.90. Effect of PC on polygenic EBV was estimated in the reference population with a BLUP model. Traits considered were milk yield, fat and protein percentages. Reference animals were considered those born before 2000. Accuracies were calculated as correlation between DGV and polygenic EBV. The increase of number of retained PC (from 1,255 to 8,452, corresponding to 0.5 and 0.9 of explained variance, respectively) resulted in an increase of DGV accuracy. Higher DGV accuracies were obtained for milk yield in the Simmental bulls (0.45–0.55 depending on the number of PC used) even though this trait showed the highest variability. On average, the increase was more relevant for protein percentage and in the BS bulls. The use of a multibreed approach did not result in an increase of DGV accuracy compared with single breed estimation. Actually values tend to remain similar in the 2 approaches or, as in the case of Brown Swiss for milk yield, to decrease markedly. These results may be linked to the reduced size of the sample but may be also related to the different genetic structure and selection history of the 3 breeds.

Key words: genomic selection, multibreed, principal component

37 Adjustment of deregressed values from cow evaluations to have the similar mean and variance as bull deregressed values. G. R. Wiggans*, P. M. VanRaden, and T. A. Cooper, *Animal Improvement Programs Laboratory, ARS, USDA, Beltsville, MD.*

Traditional evaluations of cows with genotypes have been adjusted since April 2010 to be compatible with evaluations of bulls to improve their accuracy in estimation SNP effects. This adjustment made them not comparable with traditional evaluations of cows. Recent work has improved the adjustment by using a bull only direct genomic value to group cow according to the amount of adjustment required. This adjustment cannot be applied to all cows because the grouping requires a genotype and adjustments based on genotyped cows probably would over adjust other cows. To create an adjustment for all cows, Mendelian sampling (MS), the difference between PTA and parent average (PA), was calculated for milk, fat, and protein. These were deregressed by dividing by a function of reliability with the reliability from parent average removed. Standard deviations (SD) of these values were grouped by reliability. A linear function of reliability was estimated as a multiplicative adjustment to reduce the SD from cows to that of bulls with similar reliability. Averages of PA by birth year were subtracted from PA to create within year PA deviation groups and mean deregressed MS was calculated for bulls and cows by group. These means for bulls fell and those for cows rose with increasing deviation. The differences were fit by linear regression on PA deviation and used to adjust cow deregressed MS. Adjusted cow evaluations were propagated to the PA of progeny. This adjustment reduced the PTA of cows with high PA and increased those of cows with low PA, but did not change the estimates of genetic trend because the adjustment was within birth year. It also reduced the within birth year variance of cow evaluations. This adjustment does not replace the adjustment of evaluations of genotyped cows because the use of bull only direct genomic values more precisely tailors the adjustment to the individual cow. However, it reduces the amount of the genotype based adjustment so should improve the comparability of evaluations of cows with and without genotypes.

Key words: cow evaluation, genomics, Mendelian sampling

38 Effectiveness of genomic selection on milk flow traits in dairy cattle. K. A. Gray*[1], J. P. Cassady[1], A. Rossoni[2], and C. Maltecca[1], *[1]North Carolina State University, Raleigh, [2]Italian Brown Breeders Association, Bussolengo, VR, Italy.*

The objective of this study was to estimate the effect of genomic selection on accuracy of prediction for traits associated with milkability. Milk flow measures for total milking time (TMT), time of plateau (TP), descending time (DT), average milk flow (AVGF) and maximum milk flow (MMF) were collected on 37,213 Italian Brown cows. Estimated breeding values were obtained through standard BLUP techniques. Heritabilies were estimated to be 0.11, 0.31, 0.06, 0.28, 0.41 for TMT, TP, DT, AVGF and MMF, respectively. For 696 sires included in the phenotypic analysis, genomic information for 35,044

informative markers were obtained. Genotyped sires had on average 37 ± 3.9 daughters, and a reliability of ~0.60 averaged across all flow traits. Genotyped sires were partitioned based on their TMT EBV reliabilities into a discovery set (TMT EBV reliability >0.70, n = 381) and a prediction set (TMT EBV reliability <0.70, n = 315). Pseudo-phenotypes for these sires were obtained by EBV de-regression and subsequently employed in obtaining genomic breeding values through a multiple trait GBLUP model. The GEBV reliabilities in the prediction set were compared with de-regressed parental averages (PA) and breeding values obtained using traditional BLUP methods (EBV) on the same individuals. The GEBV reliabilities in the prediction set were 0.64 (0.27 PA), 0.62 (0.28 PA), 0.69 (0.20 PA), 0.71 (0.28 PA), and 0.67 (0.29 PA) for TMT, TP, DT, AVGF and MMF, respectively. Average gain in reliability from genomic information was 0.37, 0.34, 0.49, 0.43 and 0.38. The EBV reliabilities in the prediction set were 0.46, 0.50, 0.29, 0.49, and 0.51 for TMT, TP, DT, AVGF, and MMF, respectively. Loss in accuracy when compared with the genomic model was 0.18, 0.12, 0.40, 0.22 and 0.16 for TMT, TP, DT, AVGF, and MMF, respectively. For all traits, use of a genomic model resulted in increased accuracy of prediction for sires with little or no progeny information. Gain in accuracy increased as heritability decreased. Inclusion of genomic information increased accuracy of prediction for milk flow measures.

Key words: genomic selection, accuracy of prediction, milk flow

39 Visualization of associations between single nucleotide polymorphisms and economically important dairy traits using biplot analysis. A. I. Vazquez[1], K. A. Weigel*[2], G. J. M. Rosa[2], D. Gianola[2], and D. B. Allison[1], *[1]University of Alabama, Birmingham, [2]University of Wisconsin, Madison.*

In food animal species, the breeding objective consists of several interrelated traits, and implementation of genomic selection requires estimation of single nucleotide polymorphism (SNP) effects on these traits. When the number of markers is large and multiple traits are considered, extracting meaningful information from the results is challenging. Biplot analysis is an important tool for this purpose in plant breeding, but its features have not yet been explored in animal breeding. A biplot is a scatter plot that approximates and graphically displays a 2-way table, such that relationships between rows, relationships between columns, and interactions between rows and columns can be visualized simultaneously. Biplots can uncover patterns in estimated SNP effects (rows) on phenotypic traits (columns) and shed light on the causes of genetic correlations between traits. In this study, phenotypes were predicted transmitting abilities for milk, fat, protein, daughter pregnancy rate, somatic cell score, productive life, and lifetime net merit for 3,305 Holstein sires, and genotypes were 32,518 SNP markers. The 32,518 × 7 matrix of estimated SNP effects was decomposed into principal components (PC), of which the first and second explained 42 and 29% of the total variation, respectively. A biplot of the first and second PC showed that SNP effects for milk, fat, and protein tended to lie on a common axis, whereas SNP effects for daughter pregnancy rate, somatic cell score, and productive life tended to lie on a second axis that was nearly perpendicular to the first. Estimated SNP effects for lifetime net merit represented a compromise between the 2; however, sets of individual SNPs had correlations between performance and fitness that were negative, neutral, or positive. The SNPs with largest estimated effects for lifetime net merit differed from those with largest estimated effects for the 6 biological traits. Our study suggests that biplots may facilitate interpretation of genomic data and assist animal breeders in incorporating information about individual SNPs into selection decisions.

Key words: genomic selection, dairy cattle, biplot analysis

40 Using single nucleotide polymorphism to detect selection signature in Hereford beef cattle. Y. Huang*[1], C. Maltecca[1], M. D. MacNeil[2], and J. P. Cassady[1], *[1]Department of Animal Science, North Carolina State University, Raleigh, [2]USDA-ARS, Fort Keogh Livestock and Range Research Laboratory, Miles City, MT.*

The objective of this study was to investigate selection signature in 2 sources of purebred Hereford beef cattle. Data were available from 240 Line 1 Herefords (L1) born between 1953 to 2008, and 311 Industry Herefords (IH) born between 1970 and 2008. Line 1 Herefords were sampled from a closed line mainly selected for post weaning gain. Industry Herefords were a sample of registered US purebred Herefords. A genome-wide scan using 52,156 SNPs revealed different characteristics in L1 and IH. Average minor allele frequency of SNPs was 0.19 ± 0.168 in L1 and 0.23 ± 0.161 in IH. Number of homozygous markers was of 11,382 in L1 and 5,745 in IH. The fixation index was 0.260 and 0.031 for L1 and IH, respectively. To detect differences in selection between the 2 populations, pooled heterozygosity (Hp) was calculated for sliding windows of 6 SNPs across the genome. Low Hp values are indicative of a high degree of fixation and putative selective sweeps. High Hp values can be the result of ongoing selection sweeps, balancing selection, or selection for multiple traits. Average Hp was 0.26 ± 0.10 for L1 and 0.29 ± 0.08 for IH. 225 low Hp windows (Hp <0.05) were identified in L1 while only 25 in IH. Fifty-four known QTLs were previously found to be associated with traits including birth weight and weaning weight, co-localized with low Hp windows that were common in L1 and IH on BTA 1, 3, 6, 13, 14, 15, 16, 18, and 25. Fifty-six known QTLs associated with growth traits such as average daily gain and yearling weight co-localized with low Hp windows that were only found in L1 in BTA 2, 5, 14, 17, 21, and 26. Number of high Hp windows (Hp >0.46) was of 155 in L1 and 78 in IH. This might reflect that L1 being selected for only one trait, while IH was selected on several traits with multiple concurring sweeps. Differences in number of high Hp windows might also indicate regional balancing selection. Based on these results it was concluded that there had been a loss of heterozygosity in Line 1 Herefords. The low Hp windows indicated putative selective sweeps in L1. Further investigations are needed to explain the high Hp windows across the genome.

Key words: Hereford, selection signature, SNP

Extension Education Symposium: Reinventing Extension as a Resource—What Does the Future Hold?

41 National Institute of Food and Agriculture (NIFA) grants and extension: Expectations for integrated projects. M. A. Mirando* and K. M. Whittet, *National Institute of Food and Agriculture, U.S. Department of Agriculture, Washington, DC.*

The Food, Conservation, and Energy Act of 2008 (Public Law 110–246, i.e., the 2008 Farm Bill) established NIFA within the USDA and the Agriculture and Food Research Initiative (AFRI) within NIFA. AFRI is the USDA's largest competitive grants program and is authorized at a funding level of $700 million; however, Congressional appropriation to AFRI in fiscal year 2010, its second year of existence, was approximately $262 million. The Farm Bill requires NIFA to expend at least 30% of the funds appropriated to AFRI in support of projects that integrate at least 2 of the 3 functions of the agricultural knowledge system (i.e., research, education, and extension). In fiscal year 2010, approximately 44% of AFRI funds were expended on integrated projects. Programs supporting integrated projects are located primarily within the 5 AFRI Challenge Area requests for applications. Strong integrated project proposals are stakeholder driven, issue focused, and outcome based. Applications for integrated projects must include the elements of a logic model detailing the activities, outputs, and outcomes of the proposed project. Integrated proposals should contain objectives for each function of the project and no more than 2-thirds of the budget may support a single function. For proposals integrating research and extension, applied research integrates best into an extension program. Integrated extension and research applications can propose extension programming as the first objective(s) and social science research to evaluate and report on the effectiveness of the extension programming (e.g., did the extension program result in behavioral change of the target audience). Peer review panels for all AFRI programs soliciting integrated projects are required to have substantial representation by individuals with expertise in extension. In programs that solicit both research and integrated project proposals, the 2 types of applications are evaluated separately because of the distinct nature of the 2 types of proposals

Key words: competitive grants, extension, integrated projects

42 Integrating extension and research projects. D. J. Patterson*, *University of Missouri, Columbia.*

Projects that integrate extension and research are required to be outcome oriented, stakeholder driven, and problem focused. These expectations create opportunities to generate new knowledge and apply existing knowledge quickly. This approach and the synergy that results from it parallel the fundamental basis upon which extension and the Land Grant System were founded: The use and application of what we know to create knowledge. Integrated projects are and will continue to be essential in the transfer of new agricultural technologies that involve complex biological systems and their associated economic impact related to industry adoption. Furthermore, as research leads to the development of even more sophisticated and complex technologies that fewer people understand or perhaps trust, the need for highly trained professionals that are capable of serving a dual role in research and extension will become even greater. Our approach was to focus on an integrated plan to augment our current understanding of reproductive biology and manipulation of the estrous cycle in the beef heifer, concomitant with the transfer of existing methods that precisely control the time of ovulation relative to fixed-time AI in postpartum beef cows. The specific aims of the project were based on the economic need to improve the competitive position of the US beef industry through an increase in adoption of reproductive procedures that facilitate improvements in reproductive management and adoption of AI. We focused our efforts on integrating the fundamental aspects of control of the estrous cycle in beef cattle with wide-scale application of the technology in the field, both of which are required to enhance competitiveness of the US livestock industry. Justification for this approach centered on the concern that continuation of low adoption rates of these technologies in the US will ultimately erode the competitive position of the US cattle industry. The specific aims of the project facilitated implementation of integrated animal production systems that will contribute to sustainability of beef cattle production and are key to future application of biotechnologies in the beef cattle sector.

Key words: extension, integrated projects, research

43 The role of eXtension in delivering research results to producers and allied industry partners through a national platform. D. M. Amaral-Phillips* and N. L. McGill, *University of Kentucky.*

Today, more than ever, researchers, university instructors, and extension educators need to truly embrace national collaboration to deliver cutting-edge, research-based information and educational programs to our clientele. This collaboration can result in the development and implementation of solutions to problems facing animal agriculture across the United States. eXtension offers the national platform necessary to develop and deliver such integrated programs to these end-users including, but not limited to, producers, allied industry partners, extension and instructional educators, and consumers. Resource materials and educational programs can be delivered via interactive forms such as eXtension's Ask the Expert tool, webinars, live chats, and blogs, or through more classical information delivery systems such as learning lessons, videos, written articles, research summaries, decision aids in the form of spreadsheets, and frequently asked questions. All of these resources are designed to deliver the very best research-based, peer-reviewed information, which is available 24/7 from any internet-ready device. At the current time, resources through eXtension (and supporting communities of practice) are available on animal manure management, beef cattle, dairy cattle, goats, horses, swine, organic farming, and small meat processors, with additional livestock commodities to be added in the future. To learn more about the materials available to the public through eXtension, visit www.extension.org. Each of the commodity groups looks forward to collaborating with research, industry, and educational partners through integrated grants (information can be found at http://about.extension.org) or integrated projects.

Key words: extension, integrated grants, resource materials

44 How can extension use media to connect to and maintain connections and conversations with farmers, ranchers, and producers? J. Blue* and N. Arthur, *Truffle Media Networks, Indianapolis, IN.*

Americans are increasing their use of the internet for news and information. Forty-four percent of Americans say they got news through

one or more internet or mobile digital sources (PEW, 2011). This trend will continue in the foreseeable future. American's use of Facebook and Twitter is also increasing (PEW, 2011), paralleling the digital news consumption. In agriculture, there are numerous groups and individuals using Facebook, Twitter, and LinkedIn. These data provide support for communications plans and actions Extension can develop to connect with their constituents. Extension needs actionable information and resources to address: finding who are producers in the audience, implementing approaches to managing producer / extension connections, locating places on the internet to develop and maintain connections with farmers and ranchers, learning when to stop using one tool and start using another, and discovering what value there is to agriculture and Extension in caring about new, social, and participatory media. In agriculture, more than 80% of large producers are connected with broadband, providing the ability to receive lots of information and make faster decisions. Roughly half the principal farm operators are over 45 years old. Conversely, just under half the principle operators are under 45 years old and their numbers are growing. Digital information means people can read, listen, watch, or participate when they want, where they want, and how they want. For audio and visual media, the number one reason for listening or watching a new media series is flexibility in time. However, new tools are constantly being created to help connect like-minded people to common interests or causes. Three years ago Foursquare, Quora, and Groupon did not exist. Three years ago Twitter and Facebook, combined, had less than 50 million registered users. Saying what will happen with media and communication tools in the next 3 would be very speculative. However, there are approaches for Extension, and others in agriculture, to discover, grow, and maintain connections with farmers and ranchers.

Key words: communication, digital media, new social participatory media

45 Opportunities and challenges associated with the use of technology in extension programming. J. M. Bewley*, *University of Kentucky, Lexington.*

For extension to remain a viable resource for producers in the future, extension educators will need to determine how to best incorporate new technologies into extension programming. Resources such as webinars, social media, online video sharing, blogs, listservs, phone applications, and online document search engines provide new ways to reach extension clientele. In a 2008 survey of Kentucky dairy producers, respondents were asked to identify their preferred delivery method. The most effective delivery methods were printed farm magazines (81.0%), agricultural newspapers (77.4%), printed newsletters from county agricultural agents (75.7%), printed newsletters from university extension (65.0%), and local or regional meetings (55.8%). The least effective delivery methods were university Web sites (11.9%), indirect access through allied industry consultants (11.5%), webinars (2.7%), podcasts (0.4%), and blogs (0.4%). In transitioning to electronic communication methods, it is important to remember that building personal relationships with producers has been an integral part of what has made the Cooperative Extension Service so successful over the past century. People are much more likely to open an email message or attend a webinar if they know the person who is delivering it. Precision Livestock Farming technologies used for physiological and behavioral monitoring of animals also provide an opportunity for extension professionals to demonstrate concepts and conduct applied research projects. For example, Kentucky researchers have used lying behavior monitors as a tool in cow comfort demonstrations and multi-herd research projects. Visual analytic dashboards and spreadsheets can be used to help producers make more informed and economically sound decisions. Lastly, extension professionals can play a critical role in helping producers improve their technical capabilities through training programs for Internet resources, spreadsheet decision making tools, farm-specific software, and Precision Livestock Farming technologies.

Key words: extension, internet, technology

Food Safety Symposium: Safe Food Production: Zoonotic Disease-Control, Responsibility, and Liability

46 Safe food production: Zoonotic disease-control, responsibility, and liability. C. Custer*, *Independent Consultant.*

In the past few decades, the responsibility for food safety has slowly moved from consumers (APHA v. Butz 1974 - "Just cook it") to processors ("Mega Reg") to producers. The "Good News" is that producers are not alone and there are precedents. Dairy products have a long history of quality and safety with proven programs. Animal and plant diseases also have strict controls and those principles can be applied to zoonoses. The Extension Service has also helped farmers and ranchers use science to improve the health and production of crops. In the past 2 decades the Agricultural Research Service and industry associations have given greater focus to "Preharvest" safety. The "Bad News" is that science and technology doesn't always trickle down to the farms, feedlots, and grow out houses. The increase in foodborne outbreaks implicating fruits and vegetables is one example. When STEC are implicated in a produce outbreak, one has to ask, "Were the ruminants up stream, up wind, or in the next field"? Another example is the recent outbreak implicating eggs. Two decades ago, Penn State took the lead when *Salmonella* Enteritidis hit Pennsylvania hatcheries. Extension Service scientists developed control programs that solved the problem. Others adopted those programs but somehow Iowa did not. If there are publicly available control programs and they are not implemented does liability ensue? When does a voluntary program become mandatory to cover one's liability? Where is the line between consumer innocence and responsibility?

47 Fundamentals of foodborne illness litigation – Are you at risk? P. Waller*, *Epidemiologist, Marler Clark Law Firm.*

Each year the Centers for Disease Control and Prevention estimates there are 48 million illnesses, 128,000 hospitalizations, and 3,000 deaths attributable to foodborne illness. Only a small percentage of injured persons pursue legal action as a result of their illness, but it is important for all food-industry players to understand the basis of a legal claim arising out of foodborne illness and injury. The rule of strict liability is the basis behind foodborne illness litigation. Food-industry entities such as growers, processors, and retail establishments can be held liable if the food they produce and serve is unsafe and causes injury. The speaker will discuss the fundamentals of foodborne illness liability such as how liability is determined, the liability process, and why ignorance is a bad defense.

Forages and Pastures: Improving Silage Conservation, Utilization and Performance of Grazing Ruminant

48 Effect of microbial inoculants on the quality and stability of bermudagrass haylage. K. G. Arriola*[1], O. C. M. Queiroz[1], J. J. Romero[1], J. Kivipelto[1], E. N. Muniz[1,2], J. C. Hamie[1], M. A. Zarate[1], L. G. Paranhos[1], and A. T. Adesogan[1], *[1]Department of Animal Sciences, Institute of Food and Agricultural Sciences, University of Florida, Gainesville, [2]Embrapa Tabuleiros Costeiros, Aracaju, SE Brazil.*

The objective was to compare the efficacy of 4 bacterial inoculants at improving the fermentation, and aerobic stability of bermudagrass haylage. Bermudagrass (4-wk regrowth) was harvested, chopped (approximately 2 cm) and treated with 1) deionized water (CON); 2) Buchneri 500 (B500) containing 1×10^5 of *Pediococcus pentosaceus* and 4×10^5 *Lactobacillus buchneri* 40788, 3) Biotal Plus II (BPII) containing $1.2 \times 10^5$of *P. pentosaceus* and *Propionibacteria freudenreichii*; 4) Silage Inoculant II (SI) containing 1×10^5 of *L. plantarum* and *P. pentosaceus* and 5) SiloK (SK), containing 1×10^5 of *L. plantarum*, *Enterococcus faecium*, and *P. pentosaceus*, respectively. Four replicate round bales (441 ± 26 kg) per treatment were wrapped with 7 layers of plastic and stored for 112 d. Four additional bales per treatment were prepared and analyzed for pH after 3, 7 and 30 d of ensiling. The experiment had a completely randomized design and data were analyzed with Proc Mixed of SAS. The pH of Control and inoculated d 3 silages was similar ($P > 0.05$) but B500 had lower pH than SK by d 3, and B500 and BPII had lower pH ($P < 0.001$; 5.79 ± 0.07 vs. 6.16 ± 0.07; 5.02 ± 0.23 vs. 5.69 ± 0.23, respectively) than other treatments by d 7 and 30. Treatments B500, BPII, and SI had lower pH than the Control ($P = 0.003$; 4.76 ± 0.16 vs. 5.2 ± 0.16) after 112 d but SK had similar pH to other treatments. No difference ($P > 0.05$) was found among treatments in NDF digestibility, DM losses, DM, lactic and acetic acid concentrations, and yeast and coliform counts. Other VFA were not detected. Treatments B500, BPII, SI, and SK improved ($P < 0.001$) aerobic stability by 195%, 161%, 162%, and 75%, respectively compared with the Control (273 ± 36 vs. 110 ± 36 h). Treatment B500 and SI had lower mold counts than other treatments ($P = 0.02$; 2.19 ± 1.01 vs. 3.68 ± 1.01 cfu/g), while SK had lower clostridia counts than the Control ($P = 0.02$; 1.15 ± 0.43 vs. 2.42 ± 0.43 cfu/g). All treatments improved the fermentation and aerobic stability of bermudagrass haylage to varying extents.

Key words: bermudagrass, haylage, inoculants

49 The impact of aerobic deterioration of corn silage on feed intake by goats. K. Gerlach*, F. Roß, W. Büscher, and K.-H. Südekum, *University of Bonn, Bonn, Germany.*

This study evaluated the impact of aerobic deterioration of corn silage on feed intake. Corn was harvested at 2 stages of maturity in October 2009 and chopped. Eight whole-crop corn silages were produced differing in dry matter (DM) content (34% and 40%), chopping length (10 mm and 21 mm) and packing density in the silo (high, 275 kg DM/m^3; low, 256 kg TM/m^3). Each factor combination, i.e., treatment, was ensiled in 6 110-L plastic tons for at least 3 mo. At the day of silo opening (d 0) and then at 2-d intervals (d 2, 4, 6, and 8) the following measurements were conducted: temperature, sensory evaluation, chemical composition and microbiological testing. For use in preference trials, samples of silages were taken and stored anaerobically in evacuated and vacuum-sealed polyethylene bags. Eight preference trials with goats (n = 6) were conducted, each one lasting 21 days. Each possible pair of the five silages (days 0, 2, 4, 6, and 8) and one standard alfalfa hay (n = 15 pairs), were offered for 3 hours in the morning. Data were analyzed by analysis of variance and multidimensional scaling (MDS), which was used to develop a spatial arrangement representing the differences expressed as selective forage intake by the animals. For most treatments, the animals showed a strong preference for silages from days 0, 2 and 4 and avoided silages exposed to air for 6 and 8 days ($P < 0.05$). Analysis of variance was conducted after averaging silage intake across all pairs by each animal. During 3 h, average intake for silages from day 0 ranged from 580 to 723 g DM per goat, while the average intake of day 8 silage was between 136 and 464 g DM. Using the Waller-Duncan k-ratio t-test, the minimum significant difference (ranging from 82 g to 128 g DM, $P < 0.05$) was calculated for each treatment. Average DM intake (DMI) by goats (y) was linearly related to silage temperature at the different days of aerobic storage (x, expressed as the difference to ambient temperature): $y = 662.61 - 11.669$ x; $R^2 = 0.6808$; $P < 0.0001$. This study demonstrated the negative impact of aerobically deteriorated silage on preference and DMI by goats.

Key words: aerobic deterioration, corn silage, preference trial

50 Caloric content of brown midrib sorghum silage harvested at two maturities, fed with concentrate at two levels of intake using in vivo, in vitro and prediction equation methods as related to rumen fermentation and fractional passage. J. Lim, M. A. Froetschel*, and L. O. Ely, *The University of Georgia, Athens.*

Four rumen fistulated Holstein yearling steers, were fed brown midrib (BMR) forage sorghum (*Sorghum bicolor* (L.) Moench) harvested at 2 maturities (earlier maturity (EM), flowering stage or later maturity (LM), milk to soft dough stage), in total mixed rations (TMR), 60% BMR sorghum silage (% DM) and were fed at 2 levels of intake (~1.5x maintenance or free access for 5 h/d), to compare methods of estimating digestible energy (DE) as related to rumen fermentation and fractional passage of particulate. A 4 × 4 Latin square design with a 2 × 2 factorial arrangement of treatments was used. The concentrate consisted mainly of corn and soybean meal with chromic oxide as a digestibility marker. Periods were 14 d, 7 d to adapt and 7d for data collection. Daily DMI was measured, feed and fecal samples were collected at incremental 12 h intervals from d 8 to 13. On d 14, rumen contents of steers were evacuated 5, 11, 17 and 23 h after feeding, weighed, sampled for nutrient analysis and returned. Ruminal fluid was collected for ammonia and volatile fatty acid analysis (VFA). The EM silage had less grain development and more NDF (60.7 VS 56.7 ± 0.74), ADF (33.3 VS 31.8 ± 0.41) but lower ADL (4.11 VS 5.12 ± 0.25) and ash (7.16 VS 6.18 ± 0.45) than the LM silage. Apparent DE, and DM digestibility (DMD) were not influenced by BMR maturity or intake. Fractional disappearance rate (FDR) of ruminal DM, NDF, NDS, OM and ash were not influenced by BMR maturity but increased in steers fed at higher intake ($P \leq 0.01$). Apparent DE, DMD and FDR of ruminal DM, NDF, NDS, OM and ash were not influenced by BMR maturity ($P \geq 0.05$). The DE predicted using NRC method correlated with in vitro DE ($y = 0.684x+.838$; $r^2 = 0.82$, $P \leq 0.01$) but not apparent DE. Rumen NH3 was higher at lower intakes and VFA were higher at greater intakes ($P \leq 0.01$). In vitro DE appears to be as accurate as the NRC prediction method to assess caloric content of a 60% BMR (DM%) TMR. DE content of total mixed rations with 60%

BMR sorghum (% DM) as a basal forage was minimally influenced forage maturity.

Key words: forage quality, digestible energy, in vitro

51 Intake and digestibility in steers fed sugarcane ensiled with different levels of calcium oxide. F. H. M. Chizzotti*[1], O. G. Pereira[2], S. C. Valadares Filho[2], M. L. Chizzotti[1], and R. T. S. Rodrigues[3], *[1]Universidade Federal de Lavras, Lavras, MG, Brazil, [2]Universidade Federal de Viçosa, Viçosa, MG, Brazil, [3]Universidade Federal do Vale do São Francisco, Petrolina, PE, Brazil.*

A trial was conducted to evaluate the effects of calcium oxide levels (CO) as additive for sugarcane silage on intake and nutrient digestibility. Thirty-five crossbred steers (Holstein x Nellore), averaging 350 ± 18.3 kg BW, distributed in 7 randomized blocks were used. Diets consisted of 50% roughage and 50% concentrate, formulated to be isonitrogenous (12% CP, DM basis). The 5 treatments consisted of sugarcane ensiled with 4 CO levels (0, 0.5, 1.0, and 1.5%, as fed basis) and a standard diet with corn silage. The experiment lasted 99 d. DMI was measured daily and individually. Indigestible ADF was used as an internal marker to estimate apparent nutrient digestibility and fecal output. A mixed model with random effect of blocks was used. There was a quadratic positive effect ($P < 0.05$) of levels of CO on OM, NDF, non-fiber carbohydrates (NFC) and TDN intakes. The highest TDN intake (6.17 kg) was observed at 0.5% of CO in sugarcane silage. The TDN intake of corn silage diet was similar to TDN intake of diet with 0.5% of CO. There were positive linear effects ($P < 0.05$) of CO levels on apparent total digestibility of DM, OM, CP, NDF and % of TDN of the diets. There was no difference ($P > 0.05$) of DM, OM, and NDF digestibilities of sugarcane silage with CO and corn silage. The addition of calcium oxide (up to 1.5%) in silage improves sugarcane silage quality, increasing apparent digestibility of DM, OM, CP and NDF. However, the TDN intake decreased for CO levels above 0.5% which may decrease animal performance. Sponsored by CNPq/INCT-CA and Fapemig, Brazil.

Key words: additive, feedlot, roughage supplementation

52 Effects of co-grazing dairy heifers with goats on animal performance, pasture composition, and dry matter yield. T. S. Dennis*, M. K. Neary, L. J. Unruh-Snyder, J. E. Tower, and T. D. Nennich, *Purdue University, West Lafayette, IN.*

Various pasture management systems, such as co-grazing, may offer alternative methods for rearing dairy heifers. The objective of this study was to determine the effects of co-grazing dairy heifers with goats on animal performance, pasture composition, and forage DM yield. Twenty-four Holstein heifers (BW = 168.0 ± 1.7 kg) and 6 Boer x Kiko goats (BW = 33.7 ± 0.9 kg) were allocated to 6 paddocks and used to evaluate 2 grazing strategies (heifers grazed alone (HO) or heifers co-grazed with goats (HG)). Additionally, 6 goats were randomly assigned to 2 paddocks and grazed alone to compare parasitism between grazing strategies. Heifers were weighed biweekly and measured monthly for body condition score, hip and withers heights, and heart girth. Blood samples were collected monthly from heifers to measure plasma urea nitrogen (PUN) and glucose. Fecal egg counts (FEC), FAMACHA scores, and PUN were measured monthly in goats. Forage heights before and after grazing were measured to calculate pasture DMI. Pasture samples were collected monthly by manually harvesting forage and photographs were taken to visually estimate composition. Data were analyzed by paddock as repeated records using PROC MIXED of SAS. Total and pasture DMI were greater for HO than HG heifers ($P < 0.01$); however, ADG and feed efficiency were similar between grazing strategies. Final hip and withers heights were greater for HO heifers ($P < 0.01$). Heifer PUN concentrations tended to be greater for HG heifers at 8 wks ($P < 0.10$), and blood glucose concentrations tended to be less for HG heifers over the entire study ($P < 0.10$). Overall FEC, FAMACHA scores, and PUN concentrations were also similar between grazing strategies for goats. Grass and total DM yield tended ($P < 0.10$) to be greater in HO pastures compared with HG pastures after 2 rotations. Using visual estimation, HO pastures had 3.5 times greater weed presence than HG pastures ($P < 0.05$) at the conclusion of the study. In summary, co-grazing did not affect weight gains or feed efficiency of heifers, indicating that dairy heifers can be successfully co-grazed with other livestock species.

Key words: dairy heifer, goat, grazing

53 Forage mineral concentrations and mineral status of beef cattle grazing cool season pastures in northwestern Florida, emphasizing magnesium. J. N. Carter[2], L. R. McDowell*[1], R. O. Myer[2], M. K. Maddox[2], and M. Brennan[2], *[1]University of Florida, Gainesville, [2]University of Florida, Marianna.*

This study evaluated mineral status (particularly Mg) of grazing beef cows (42 Angus, Brangus and Romosinuano crosses in early lactation) on annual ryegrass (*Lolium multiflorum* 'Rio') or oat pastures (*Avena sativa* 'Horizon 474'). The fertilizer used on the oat and ryegrass pastures was 355 kg of 3–7-28 at time of planting per ha. Forage, blood and urine were collected every 2 weeks, while liver biopsies were taken on d 68. From urine was determined creatinine-corrected urine (CCU), Mg and K and fractional clearance ratio (FCR) for Mg. Mineral data for blood, urine and forage samples were analyzed as a completely randomized design with repeated measures over time. Forage mineral concentrations of P, K, Na, Fe, Mn and Mo were normally greater than critical levels for beef cattle, while Mg (<0.20%), Ca (<0.30%), Cu (<10ppm), Co (<0.10ppm), Zn (<30ppm) and Se (<0.10ppm) were at deficient levels. In general ryegrass had greater concentrations of Ca, Mg, P, K, Cu, Mn and Zn than oats. As examples Ca, P and Cu were higher ($P < 0.05$) for 3 collection dates in ryegrass than oats. All plasma mineral levels were greater than critical levels, but plasma Mg was borderline to slightly deficient, (<2.0 mL%). Cows grazing oats had the lowest plasma Mg. There were no difference in liver Cu, Fe, Mn and Se between forage treatment types ($P > 0.05$). The FCR for oats was less than the critical recommended level of 10%, which indicates Mg deficiency, until d 41. However, ryegrass treatment had greater FCR values for all collection days except d 1. Except for d 55, CCU Mg for oats treatment was less than 1.0 mmol/L throughout the trial, the level at which cattle generally respond to Mg supplementation. The ryegrass treatment had higher values than for all oat treatment values; except at d 1. In conclusion higher mineral concentrations are found in ryegrass versus oats. Special attention should be given to Mg supplementation because forages are deficient and contain excess K.

Key words: oats, ryegrass, mineral status

54 In vitro rumen fluid digestion activity of grazing cows as related to productivity and days postpartum. E. G. Tesfaye, M. A. Froetschel*, L. O. Ely, N. S. Hill, and M. J. Mathis, *The University of Georgia, Athens.*

In vitro rumen fluid digestion activity and indigestible fecal NDF were measured in 10 multiparous Angus cows averaging 8 ± 3 years of age, with ≥5 calves from a pure-bred herd (104 cows). Five cows with the lowest and 5 cows with the highest life-time weaning weight ratio (WWR) records (lowest = 6% below herd average; highest = 9.4% above herd average) were selected using breed association data. The cows, were managed with the herd, grazing permanent pasture of primarily Tall Fescue or Bermuda grass depending on seasonality. Rumen fluid was collected by stomach tube from each cow at 3 dates (March 14th, June 25th, and September 23rd, 2008) averaging 64, 167 and 257 d postpartum and used for in vitro incubations. Data was analyzed according to cow productivity and date of sampling in a 2 × 3 factorial designed experiment. Two stage incubations were conducted for 24 and 48 h, in quadruplicate, using a modified Tilley and Terry procedure. A composite sample of mixed pasture grass, collected the previous year (68.7% NDF and 12.1% CP) was used as substrate. In vitro DM and NDF digestion (IVDMD and IVNDFD) were determined as differences in DM and NDF of particulate. Volatile fatty acid (VFA) and soluble protein (SP) production (μ moles/24 or 48 h) were determined from differences in VFA and SP during the time of the incubations (24 and 48 h). Rumen fluid from cows, selected for productivity as based on WWR did not impact IVDMD, IVNDFD and IVSP production ($P \geq 0.05$). The acetate to propionate ratio (A/P) was 6.9% lower in rumen fluid from more productive cows. In vitro propionate and butyrate production (μ moles/24 h) were 9.8 and 16.7% greater and A/P was 9.8 % lower with rumen fluid from more productive cows ($P \leq 0.05$). IVDMD was 9.6% greater with rumen fluid sampled 167 and 257 d post- partum ($P \leq 0.01$). Potentially digestible NDF tended to be lower (29% vs. 33%) in feces from higher productivity cows ($P \leq 0.13$). In vitro rumen fluid digestion activity and fecal parameters were influenced by cow productivity and sampling time postpartum.

Key words: in vitro, cow performance, digestion

55 Forage characteristics and animal performance of beef heifers grazing ′Mulato II′ brachiariagrass in North-Central Florida. J. M. B. Vendramini*[1], G. C. Lamb[2], L. E. Sollenberger[3], J. L. Foster[4], and M. Maddox[2], *[1]UF/IFAS Range Cattle Research and Education Center, Ona, [2]UF/IFAS North Florida Research and Education Center, Marianna, [3]Agronomy Department, Gainesville, FL, [4]Texas Agrilife Research and Education Center, Beeville.*

Mulato II (*Brachiaria* sp.) is a warm-season grass adapted to tropical regions and it has superior nutritive value when compared with other warm-season grasses. The objective of this study was to compare forage production, nutritive value, and animal performance of beef heifers grazing Mulato II, pearl millet (*Pennisetum glaucum* 'Tifleaf 3'), or sorghum-sudangrass (*Sorghum bicolor* 'Hay Day') pastures. The study was conducted in Marianna, Florida (30.7° N) from June to August 2008 and June to September 2009 in a completely randomized design with 3 replicates. Pastures (0.6 ha) were sampled to determine herbage mass (HM), crude protein, and in vitro organic matter digestion (IVODM) every 14 d. Pastures were continuously stocked using a variable stocking rate with 2 testers per pasture [heifers; 426 ± 40 kg initial body weight (BW)]. Additional animals were added to maintain similar stubble height, 30 cm. The data was analyzed using PROC MIXED, by year, with treatment as fixed effect and replicates as random effect. The data was analyzed by year due to the different experimental periods within year. Single degree of freedom contrasts were used to detect difference among treatments. In 2008, there was no difference ($P > 0.10$) in HM (1600 ± 300 kg/ha), IVDOM (62 ± 1 %), CP (18 ± 0.5 %), herbage allowance (HA, 0.9 ± 0.1 kg DM/kg BW), and ADG (0.5 ± 0.05 kg/d) among treatments. Gain per ha was greater ($P = 0.08$, SE = 20) for sorghum-sudangrass (240 kg) than pearl millet (168 kg) and Mulato II (130 kg). In 2009, despite the use of ′put and take′ animals, Mulato II had greater HM ($P < 0.01$, SE = 0.3; 3000 vs. 1500 kg/ha), HA ($P = 0.02$, SE = 0.1; 2.0 vs. 0.8 kg DM/kg BW), IVDOM ($P = 0.06$, SE = 0.1; 65 vs. 59%), and ADG ($P = 0.02$, SE = 0.08; 0.7 vs. 0.4 kg/d) than pearl millet and sorghum-sudangrass. There was no difference in CP concentration ($P > 0.10$; 20 ± 0.4 %) and gain per ha ($P > 0.10$; 302 ± 28 kg) among treatments. Mulato II may be a feasible option as a warm-season annual grass in North Florida for beef cattle.

Key words: Mulato II, pearl millet, sorghum

56 Bermudagrass–legume forage systems for summer stockers. B. M. Nichols[1], C. A. Moffet[1], J. T. Biermacher[1], T. J. Butler[1], R. R. Reuter[1], J. K. Rogers[1], J. A. Guretzky[2], and J. R. Blanton Jr.*[1], *[1]The Samuel Roberts Noble Foundation, Ardmore, OK, [2]University of Nebraska, Lincoln.*

Stocker cattle grazing warm season perennial grasses is an important agricultural enterprise in the Southern Great Plains. Increases in the price of nitrogen fertilizer (N) lead to questions of whether or not alternate grazing systems including the use of legumes differ from the conventional practice of N fertilization. The objective of this study was to determine the effects of interseeding legumes in bermudagrass on performance of stocker cattle compared with N fertilization. Research was initiated in the fall of 2007 at The Noble Foundation Pasture Demonstration Farm on Midland bermudagrass stands established in 1965 near Ardmore, OK and continued for a 3-yr period. Treatments were applied to pastures (1.29 ± 0.11-ha) in a CRD with 3 replications that included 1) N- fertilized bermudagrass (112 kg/ha; control); 2) 18 kg pure live seed (PLS)/ha "Bulldog 505" alfalfa interseeded into bermudagrass (BG+A); and 3) 14.4 kg PLS/ha "AU early cover" hairy vetch, 9 kg PLS/ha "Dixie" crimson clover, and 6 kg PLS/ha "Apache" arrowleaf clover interseeded into bermudagrass (BG+L). The paddocks were stocked with 4 steers in 2008 (3.21 ± 0.30 steers/ha; initial BW = 221 ± 15.9 kg) and 3 steers in 2009 and 2010 (2.35 ± 0.22 steers/ha) with initial BW of 254 ± 5.1 and 321 ± 11.6 kg, respectively. Paddocks were initially stocked to provide 1.15 kg forage per kg animal BW. Grazing days per hectare, ADG, and BW gain per hectare were analyzed by ANOVA with year and paddock considered random. Means were compared using the PDIFF function of SAS. Grazing days did not differ ($P = 0.14$) between control, BG+L, and BG+A (244, 184, and 221 ± 20.4 d/ha, respectively). Average daily gain was not significantly different ($P = 0.92$) between control, BG+L, and BG+A (0.77, 0.78, and 0.74 ± 0.06 kg/d, respectively); and BW gain per hectare was also not different among forage systems ($P = 0.15$; 199, 151, and 148 ± 19.7 kg/ha, respectively). Overall, interseeding bermudagrass pastures with legumes has the potential to decrease the need for producers to employ costly N inputs while maintaining similar animal performance.

Key words: stocker cattle, grazing systems, legumes

57 Stocker production systems utilizing warm-season perennial grass pasture: Cattle performance and nitrogen use efficiency. B. W. Wallis*, P. A. Lancaster, E. D. Sharman, D. B. Arnall, J. G. Warren, T. E. Ochsner, S. R. Lancaster, and G. W. Horn, *Oklahoma Agricultural Experiment Station, Stillwater.*

In grazing systems only 5–10% of ingested nitrogen (N) is retained in BW gain of growing beef cattle. The objective of this study was to evaluate the effects of levels of N fertilizer and source of N for growing beef cattle on N use efficiency of stocker cattle grazing systems using warm-season perennial grass pastures. Mixed-breed heifers (n = 235; 274 ± 33 kg) grazed Plains Old World bluestem pastures (3 pastures/system) in a completely randomized design (Proc GLM of SAS) comparing 4 summer grazing systems: (1) non-fertilized, low stocked (336 kg of BW/ha) pastures (CONT); (2) N fertilized (90 kg N/ha), high stocked (672 kg of BW/ha) pastures (NFERT); (3) N and phosphorus (P) fertilized (39 kg P/ha), high stocked pastures (NPFERT); and (4) non-fertilized, high stocked pastures plus supplementation of dried distillers grains with solubles (DDGS; 0.75% BW•hd^{-1}•d^{-1}). Heifers grazed for 135 d from May 18 to Sept. 28, 2010. Heifers grazing non-DDGS supplemented pastures were fed a protein supplement (0.45 kg•hd^{-1}•d^{-1}) beginning on d 66 to meet the DIP requirement of heifers grazing late-summer forage. Gain per hectare (kg/ha) was greatest for treatment 4 and least for treatment 1 (Table 1). N recovery (%) was greatest for treatment 1 due to low N inputs. However, replacing N fertilizer with DDGS supplementation improved N recovery 2.00 and 1.95-fold compared with treatments 2 and 3, respectively. These data indicate that DDGS can be effectively used to replace N fertilizer in stocker cattle grazing systems to increase stocking rates, increase BW gain/ha, and increase N use efficiency of the production system.

Table 1. Cattle performance and nitrogen use efficiency of stocker grazing systems

Item	CONT	NFERT	NPFERT	DDGS	SEM
Gain, kg/heifer	128[a]	114[b]	117[b]	136[a]	3.54
Gain, kg/ha	162[a]	284[b]	291[b]	344[c]	7.17
N inputs, kg/ha	8.0[a]	99.6[b]	99.8[b]	38.2[c]	0.26
N retention[1], kg/ha	3.4[a]	6.2[b]	6.3[b]	7.1[c]	0.12
N recovery, %	42.6[a]	6.2[b]	6.3[b]	18.6[c]	0.75

[1]Calculated as N in BW gain of heifers using NRC (1996) equations. [a,b,c]Within a row, means without a common superscript letter differ ($P < 0.01$).

Key words: dried distillers grains, N use efficiency, stocker cattle

58 Effect of protein supplementation on intake and digestion of three bermudagrass hays of divergent quality by beef cattle. C. P. Payne*, T. M. Warnock III, J. E. Sawyer, and T. A. Wickersham, *Texas A&M University, College Station.*

Quality of bermudagrass (*Cynodon dactylon*) varies in response to management and environmental factors. Supplementation decisions are complicated by this variability. Therefore, our objective was to determine the effect of 4 protein supplementation levels (0, 82, 119 and 155 mg N/kg BW) on the utilization of 3 bermudagrass hays (5.6, 6.3, and 8.1% CP). Thirteen ruminally fistulated Angus × Hereford steers (BW = 330 ± 19 kg) were used in a 13 × 4 incomplete Latin square with 13 treatments and 4 periods. Treatments were arranged as a 3 × 4 factorial plus a control bermudagrass hay (10.8% CP). Hay was provided ad libitum and protein supplements were offered as range cubes once daily. Periods were 15-d long with intake determinations made on d 10 through d 13 to correspond with fecal grab samples collected from d 11 through d 14. Acid detergent insoluble ash was used as an internal marker of fecal output. Eleven contrasts were used to separate treatment means. Hay OM intake in unsupplemented steers increased quadratic ($P = 0.05$) from 75 to 77, 96 and 94 g/kg BW$^{0.75}$ as hay CP content increased from 5.6 to 6.3, 8.1 and 10.8% CP hays, respectively. There was a linear increase ($P < 0.01$) in total digestible OM intake in response to hay nutritive value from 35 to 45, 51, and 60 g/kg BW$^{0.75}$ for 5.6, 6.3, 8.1, and 10.8% CP hays, respectively. A significant ($P = 0.04$) supplemental × hay CP content interaction was observed for forage OM intake and total OM intake. Forage OM intake of the 6.3% CP hay tended to increase linearly with supplemental protein ($P = 0.08$). Total OM intake increased linearly ($P < 0.01$) when CP was supplemented to the 6.3% CP hay from 77 to 88, 92, and 98 g/kg BW$^{0.75}$ for 0, 82, 119, and 155 mg N/kg BW, respectively. No supplement × hay CP interaction was apparent ($P > 0.10$) for total digestible OM intake; however, supplemental protein tended to increase total digestible OM intake (linear, $P = 0.07$) We conclude that forage quality was the primary driver in determining total digestible OM intake, and the effect of protein supplementation was dependent on forage digestibility and protein content.

Key words: bermudagrass, supplementation, cattle

59 Effect of level and frequency of protein supplementation on utilization of South Texas grass hay. G. R. Monson[1], J. E. Sawyer[1], R. O. Dittmar III[1], M. L. Drewery[1], C. P. Payne[1], K. C. McCuistion[2], and T. A. Wickersham*[1], *[1]Texas A&M University, College Station, [2]Texas A&M University-Kingsville, Kingsville.*

Reducing frequency of supplementation may effectively reduce costs of delivery; however, little research has evaluated the level of supplemental protein required with infrequent supplementation. Our objective was to quantify forage utilization when graded levels of protein were delivered infrequently. Five ruminally cannulated Angus × Hereford steers (BW = 410 ± 43 kg) were used in a 5 × 4 incomplete Latin square. Steers were provided ad libitum access to grass hay (2.3 % CP, 81.8% NDF). Supplemental protein, provided as a range cube (40.7% CP), was fed at 0645h to provide a specified level of N (0, 160, 320, or 480 mg of N/kg BW) daily (/d) or every third day (/3d), resulting in the following treatment combinations: 0/d, 160/d, 160/3d, 320/3d, and 480/3d. Experimental periods were 18 d long. Forage intake was determined from d 10 through 15 to correspond with fecal grab samples collected from d 11 to d 16. Acid detergent insoluble ash was used as an internal marker to estimate fecal output. On d 16 to d 18 of each period ruminal fermentation profiles were evaluated. Hay OM intake was 4.41, 6.18, 5.46, 6.10, and 6.27 kg/d for 0/d, 160/d, 160/3d, 320/3d, and 480/3d. Intake increased linearly ($P < 0.01$) with increasing protein per 3 d, but the 160/d rate did not differ from 160/3d, 320/3d, and 480/3d ($P > 0.05$) provision. Total OM intake responded in a similar fashion, but was lower for 160/3d than 160/d ($P < 0.05$; 7.08 and 5.83 kg/d, respectively). Total digestible OM intake increased quadratically ($P = 0.06$) with increasing protein provision per 3 d (2.02, 2.82, 3.59, and 3.34 kg/d for 0/d, 160/3d, 320/3d, and 480/3d, respectively). When protein was provided at 160/d, total digestible OM intake was 3.30 kg/d, which did not differ from any treatment receiving supplement. There were no significant effects ($P > 0.05$) on digestibility. Reduced levels of protein supplemented infrequently may be an effective means of capturing additional cost savings.

Key words: frequency, protein, cattle

Graduate Student Competition: ADSA Dairy Foods Oral Competition

60 Effect of salt replacers and flavor enhancers to reduce sodium in Cheddar cheese on aging and sensory properties. J. E. Grummer* and T. C. Schoenfuss, *University of Minnesota, Department of Food Science and Nutrition, St. Paul.*

The objective of this study was to produce 60% reduced sodium Cheddar cheese by using salt replacers and flavor enhancers and investigate the effects on aging and sensory properties. Replacement salts were added at levels to create the same water activity as control. Treatments were KCl only, KCl and one of 4 different flavor enhancers or masking agents (hydrolyzed vegetable protein/yeast extract, a bitter blocker, disodium inosinate (IMP) and disodium guanylate (GMP)), and modified KCl only. In duplicate, salt and salt replacer treatments were applied to create 2 different salt-to-moisture ratios (S/M). Target sodium content was 600 mg/100 g cheese for control and 240 mg/100 g cheese for all reduced-sodium cheeses. In reduced sodium cheeses, KCl was applied at 2.45 times the rate of NaCl (wt./wt.) for the high S/M and 2.16 times for the low S/M. Descriptive sensory analysis was conducted by a trained panel over 4 mo of aging in a replicated Latin square design and analyzed by SAS (SAS Institute, Inc., Cary, NC) software. Gross composition and mineral content (sodium, potassium, magnesium, calcium) were determined, and monthly tests conducted during 4 mo of aging (moisture, pH, water activity, water soluble nitrogen, texture profile analysis, and lactic acid bacteria (LAB) counts). Data was analyzed by XLSTAT (Addinsoft; New York, NY) software using 2-way ANOVA with repeated measures. Umami was higher in cheeses with IMP and GMP. Sulfur and sour dairy notes were higher in reduced-sodium cheeses. Sensory differences were observed between the 2 salt-to-moisture ratios, but the number of significant differences declined during aging. Despite similar moisture levels and water activity between reduced sodium and control cheese, differences in pH, LAB and texture were observed indicating that KCl may not have the same effect on reactions as salt. However, sensory analysis showed that salty, bitter and metallic flavors were not significantly different in reduced-sodium cheeses compared with control.

Key words: Cheddar cheese, sodium reduction, salt replacers

61 The influence of NaCl reduction on the properties of cheddar cheese where moisture contents were kept constant. K. V. Grant*[1], S. Govindasamy-Lucey[2], J. J. Jaeggi[2], M. E. Johnson[2], and J. A. Lucey[1], *[1]University of Wisconsin, Madison, [2]Wisconsin Center for Dairy Research, Madison.*

In producing an acceptable reduced NaCl cheese, it is important to have a good understanding of the effects of reducing NaCl on various cheese properties. We previously studied the properties of Cheddar cheese made with reduced and low NaCl levels without altering the cheese make procedure; which resulted in differences in moisture contents. The objective of this study was to investigate the impact of NaCl reduction on cheese properties independent of moisture content. Duplicate trials were conducted resulting in Cheddar cheese with 3 NaCl levels: normal (~1.7%), reduced (~1.2%), and low (~0.7%). Moisture contents (at 3 wk) and pH (at 4 d) were: 36.7% and 5.01, 37.3% and 5.02, and 38.0% and 5.00, in normal, reduced, and low NaCl cheeses, respectively. Different manufacturing procedures (ripening time, curd size, and salting wait times) were used to correct for the moisture contents. Cheeses were analyzed at 4 d, 3 wk, 5 wk, 3 and 6 mo.

Key words: NaCl reduction, Cheddar

62 Concentration of casein micelles: Changes in renneting functionality in the presence of sodium caseinate. P. Krishnankutty Nair*[1,2] and M. Corredig[1], *[1]Department of Food Science, University of Guelph, Guelph, Ont., Canada, [2]Department of Dairy Development, Government of Kerala, India.*

The changes in processing functionality of concentrated milk are caused by several factors, among the most important, the ionic equilibrium and the increase in the interactions between the casein micelles because of their increased volume fraction. This work reports the use of osmotic stressing as a noninvasive method to study concentrated milk, to preserve the ionic balance while reaching very high levels of protein concentration. Objective of the research was to observe the changes in the renneting functionality of casein micelles in the presence of sodium caseinate added either before or after concentration. Protein levels of about 10% were obtained by osmotic concentration for 18h at 4°C, using poly ethylene glycol in permeate. Untreated skim milk with sodium caseinate at 0.2% was concentrated using osmotic stressing. Alternatively, sodium caseinate was added at a similar ratio after concentration. The formation of the rennet-induced gel was followed using rheology and diffusive wave spectroscopy. The amount of soluble casein was quantified using ion exchange chromatography. All experiments were done in triplicate. After 45 min of gelation, the G' were 505 ± 56, 382 ± 41 and 5 ± 5 Pa for control, sodium caseinate added before and after respectively. Similarly, turbidity parameter was 7.26 ± 0.24, 6.21 ± 0.29 and 4.9 ± 0.14 mm^{-1} and self diffusion coefficient was 1.34×10^{-14}, 7.89×10^{-14} and 2.76×10^{-13} m^2s^{-1} observed for control, sodium caseinate added before and after respectively. Analysis of the supernatants confirmed a 10% increase in the area of caseins in samples where the sodium caseinate was added after concentration. Interestingly, the soluble casein added before concentration seemed to re-gain renneting functionality, perhaps because of a higher incorporation in the casein micelles during concentration. This research brings new insights on the rearrangements that may occur to casein micelles during concentration, with important consequences for a better understanding of membrane filtration processes and for the use of casein micelles as functional delivery systems.

Key words: casein micelles, sodium caseinate, renneting

63 Impact of transglutaminase on the functionality of micellar casein concentrate in process cheese product applications. P. Salunke* and L. E. Metzger, *Midwest Dairy Foods Research Centre, South Dakota State University, Brookings.*

Microfiltration (MF) is used for producing micellar casein concentrate (MCC) from skim milk. MCC is an ingredient that has been evaluated in process cheese product (PCP) manufacture. However, MCC provides inferior functionality relative to rennet casein. A potential method to modify the functional properties of milk proteins is to crosslink them utilizing tranglutaminase (TGase, EC 2.3.2.13). The objective of the study was to evaluate the impact of TGase on the functionality of MCC when used in PCP applications. In this study the impact of TGase (Ajinomoto Food Ingredients LLC, Chicago, IL, 100U activity/g) treatment of skim milk before MF as well as TGase treatment after MF was evaluated. Three treatments were utilized and included: TGase treatment (7U/g of protein) before MF (T1); TGase

treatment (7U/g of protein) after MF (T2); and a control. After addition of TGase each of the samples was incubated for 20 min at 50°C, then heated to 70°C and held for 10 min. MF was performed at 20°C using a laboratory scale tangential flow MF system (NCSRT Inc., Apex, NC). A volume concentration factor of 6.2 with diafiltration of 100% of the original skim milk volume was utilized. The experiment was replicated 3 times using 3 different lots of skim milk. After MF each treatment was freeze-dried and subsequently utilized as an ingredient in PCP manufacture. The PCP was formulated to have moisture, fat, salt and protein of 44.0, 25.0, 1.8, and 18.25%, respectively. The ingredients in each formulation were mixed in a Kitchen Aid and PCP was produced using a Rapid Visco Analyzer (RVA). The PCP was analyzed for pH, RVA-Viscosity, Texture profile analysis (TPA) and Dynamic stress rheology. The RVA-Viscosity and TPA-Hardness of PCP made from the TGase treatments was significantly ($P < 0.05$) higher than the control. Additionally the G′, G″, G* and transition temperature of PCP produced from T2 were significantly ($P < 0.05$) higher than T1 and the control. This study demonstrated that TGase treatment modifies the functional properties of MCC when used as an ingredient in PCP.

Key words: transglutaminase, micellar casein concentrate, process cheese product

64 Production of a high concentration liquid micellar casein concentrate (18% protein) with a long refrigerated shelf-life. I. Amelia* and D. M. Barbano, *Cornell University, Ithaca, NY.*

Our objective was to develop a multistage process to produce a high concentration liquid micellar casein concentrate (18% protein-MCC18) with a long refrigerated shelf-life. MCC is a novel milk protein ingredient produced by fractionating skim milk using the filtration technology. To have a long refrigerated shelf-life, the processing of MCC18 was designed to maximize the removal of low molecular weight compounds, e.g., lactose, nonprotein nitrogen (NPN) which can be easily metabolized by microbes for nutrient sources, while minimizing the microbial count in the final product. The production of MCC18 was done over a period of 5 d. The experiment was replicated 3 times with a different batch of raw milk. The raw milk was pasteurized, and skim milk was produced. Skim milk was ultrafiltered to remove more than a half of the lactose and NPN. The UF milk retentate was diluted with RO water and then microfiltered in 4 stages (including 3 stages of diafiltration) to remove approximately 95% of the serum protein and further remove lactose and NPN. The retentate from the last stage of MF was ultrafiltered to concentrate the protein to 18% and batch pasteurized. The final MCC18 contained 18.04% true protein, 0.31% NPN and 0.13% lactose. MCC18 was collected immediately after processing in sterile plastic vials and stored at 4°C. MCC18 at the day of processing contained 100 cfu/mL, 84 cfu/mL, and 190 cfu/mL of total aerobic bacteria and 360 cfu/mL, 62 cfu/mL, and 440 cfu/mL of total spores for replicate 1, 2, and 3, respectively, using the 3M Petrifilm Aerobic Count method. MCC18 was analyzed for the total aerobic bacteria count each week for the 16-week shelf-life at 4°C. The bacterial count didn't change significantly with time (week), however the effect of replicate was significant, as analyzed using the PROC GLM of SAS. The production of MCC could be used to balance excess skim milk supply by concentrating the valuable casein portion, and storing it at refrigeration temperature. This strategy avoids the cost of hauling excess skim milk to a drying plant and the high energy cost of evaporation and drying.

Key words: micellar casein, microfiltration, shelf-life

65 Serum protein removal from skim milk with a 3-stage, 3X ceramic Isoflux membrane process at 50°C. M. Adams* and D. M. Barbano, *Cornell University, Ithaca, NY.*

Our objective was to quantify the capacity of 0.14 μm ceramic Isoflux microfiltration (MF) membranes to remove serum proteins (SP) from skim milk. A 3-stage, 3X, feed-and-bleed MF study with diafiltration in the latter 2 stages was conducted at 50°C using Isoflux membranes to determine cumulative SP removal percentages after each processing stage. The experiment was replicated 3 times starting with different batches of raw milk. The Proc GLM procedure of SAS was used for statistical analysis. In contrast to 3X MF theoretical cumulative SP removal percentages of 68%, 90%, and 97% after 1, 2, and 3 stages, respectively, the 3X Isoflux MF process removed only 39.5%, 58.4%, and 70.2% of SP after 1, 2, and 3 stages, respectively. Previous research has been published that provides the skim milk SP removal capacities of 3-stage, 3X 0.1 μm ceramic Membralox uniform transmembrane pressure (UTP), 0.1 μm ceramic Membralox graded permeability (GP), and 0.3 μm polymeric polyvinylidene fluoride spiral-wound (PVDF SW) MF systems at 50°C. No difference in cumulative SP removal percentage after 3 stages was detected ($P > 0.05$) between the Isoflux and previously published PVDF SW (70.3%) values, but SP removal was lower ($P < 0.05$) than published GP (96.5%) and UTP (98.3%) values. To remove 95% of SP from 1000 kg of skim milk in 12 h it would take 7, 3, 3, and 7 stages with 6.86, 1.91, 2.82, and 14.24 m^2 of membrane surface area for the Isoflux, GP, UTP, and PVDF SW systems, respectively. The MF systems requiring more stages would produce additional permeate at lower protein concentrations. The ceramic MF systems requiring more surface area would incur higher capital costs. Possible reasons why SP removal with the Isoflux membranes was lower than theoretical include: a range of membrane pore sizes existed (i.e., some pores were too small to pass SP), the selective layer modification and reverse flow conditions at the membrane outlet combined to reduce the effective membrane surface area, and the geometric shape of the Isoflux flow channels promoted fouling of the membrane and rejection of SP by the foulant.

Key words: microfiltration, serum protein, ceramic membrane

66 The manufacture of linoleic acid-modified chitosan/β-lactoglobulin nanoparticles as a delivery system of quercetin. H.-K. Ha*, M.-R. Lee, and W.-J. Lee, *Division of Applied Life Sciences (Institute of Agriculture and Life Science), Gyeongsang National University, Jinju, Korea.*

The nutritional delivery and absorption of poorly bioavailable materials, such as quercetin, can be improved by entrapping such nutrients inside of nanoparticles. The hypothesis of this study was that attractive forces between chitosan and β-lactoglobulin (β-lg) may play a critical role in the formation and physicochemical properties of linoleic acid-modified chitosan (CS-LA)/β-lg nanoparticles containing nutrients with low bioavailability, such as quercetin. The objective of this research was to investigate how manufacturing variables, such as degree of substitution (DS) of CS-LA and incubation temperature, affect the formation and physicochemical properties of CS-LA/β-lg nanoparticles. CS-LAs with different DS (2.7, 4.6, and 8.4%) determined by ^{1}H NMR were synthesized via carbodiimide-mediated coupling reaction. CS-LA/β-lg mixtures at pH 4.4 were incubated at 5, 10, 15, and 20°C for 30 min. The morphological and chemical properties of CS-LA/β-lg nanoparticles were determined by atomic force microscopy and electrophoretic light scattering spectrophotometer. Encapsulation efficiency of quercetin was determined by high perfor-

mance liquid chromatography. In atomic force microscopy images, spherically-shaped particles with a diameter from 170 to 350 nm were observed indicating that nanoparticles were successfully formed. Zeta-potential value of nanoparticles was ~+18 mV. As DS was increased from 2.7 to 8.4%, which may enhance hydrophobic attractions between chitosan and β-lg, the size of CS-LA/β-lg nanoparticles was significantly ($P < 0.05$) increased from 275 to 351 nm and encapsulation efficiency of quercetin was significantly ($P < 0.05$) increased from 52 to 56%, respectively. As incubation temperature was increased from 5 to 20°C, a significant ($P < 0.05$) increase in the size of CS-LA/β-lg nanoparticles from 183 to 319 nm was observed while encapsulation efficiency of quercetin was significantly ($P < 0.05$) decreased from 56 to 53%. In conclusion, DS and incubation temperature were the major key-parameters determining the size of nanoparticles and encapsulation efficiency of quercetin.

Key words: β-lactoglobulin, chitosan, nanoparticles

67 Alternative bleaching methods for 80% whey protein concentrate. E. J. Kang* and M. A. Drake, *North Carolina State University, Raleigh.*

Whey protein concentrate (WPC) is an important ingredient in the food industry due to its nutritional and functional properties, including a bland flavor and color. To remove residual annatto colorant, fluid whey is bleached during processing to WPC. Recent studies have shown that the 2 approved bleaching agents in the United States, hydrogen peroxide (HP) and benzoyl peroxide, remove color but negatively impact flavor. The objective of this study was to evaluate alternative methods for bleaching WPC80: UV radiation (UV), acid-activated bentonite (BT) and Maxibright (MB). Cheddar cheese colored with annatto (15mL/454kg milk; 3% norbixin content) was manufactured following standard procedures and liquid whey was collected. Following pasteurization and fat separation, liquid whey was subjected to one of 5 treatments: control (CT) (no bleaching; 50°C, 60 min), HP (250 mg/kg; 50°C, 60 min), UV (1 mL/min exposure; 50°C), BT (0.5% w/w; 50°C, 60 min), or MB (2 dairy bleaching units/mL with 0.5mM HP; 35°C, 30 min). The treated whey was then ultrafiltered, diafiltered at 50°C, and spray-dried to make WPC80. The entire experiment was replicated 3 times. Color (norbixin extraction), descriptive sensory and instrumental volatile analysis were conducted on WPC80. Norbixin recovery rates were 73, 61, 21, and 10% for HP, UV, BT and MB treatments, respectively. Bleaching reduced sweet aromatic flavor in WPC80 compared with CT WPC80 regardless of bleaching agent ($P < 0.05$). The HP WPC80 had higher cardboard and fatty flavors compared with CT WPC80 while the UV and MB WPC80 displayed distinctive mushroom/burnt or potato flavor, respectively. Consistent with sensory results, guiacol (smoky/burnt) and methional (potato) were detected, respectively, in the UV and MB WPC80. Volatile lipid oxidation products were higher in HP, UV and MB WPC80 compared with BT and CT WPC80, respectively ($P < 0.05$). Based on bleaching efficacy and flavor profiles of WPC80, BT and MB may be potential alternatives to HP for bleaching whey.

Key words: WPC80, bleaching, flavor

68 Impact of bleaching whey on the sensory and functional properties of 80% whey protein concentrate. S. M. Jervis*[1], R. E. Campbell[1], K. Wojciechowski[2], D. M. Barbano[2], and M. A. Drake[1], *[1]North Carolina State University, Raleigh, [2]Cornell University, Ithaca, NY.*

Whey is a highly functional food that has found wide-spread use in a variety of food and beverage applications. Whey proteins used in such applications are largely from annatto colored Cheddar cheese, where the resulting color is undesirable and must be bleached. The objective of this study was to compare 2 commercially approved bleaching agents, benzoyl peroxide (BP) and hydrogen peroxide (HP), and their effects on the flavor and functionality of whey protein concentrate 80 % (WPC80). Colored and uncolored liquid whey were bleached with BP or HP, ultrafiltered, diafiltered and spray-dried. WPC80 from unbleached colored and uncolored Cheddar whey were manufactured as controls. All treatments were manufactured in triplicate. WPC80 were evaluated by sensory, instrumental analyses, functionality, color, and proximate analysis. HP bleached WPC80 were higher in lipid oxidation compounds than other bleached or unbleached WPC80, specifically hexanal, heptanal, octanal, nonanal, decanal, dimethyl disulfide, and 1-octen-3-one ($P < 0.05$). HP treatments were higher in fatty and cardboard flavors compared with the unbleached and BP bleached samples ($P < 0.05$). WPC80 bleached with BP had lower norbixin concentrations compared with WPC80 bleached with HP ($P < 0.05$). Hunter CIE Lab color values (L* a* b*) of WPC powders were distinct on all 3 color scale parameters and HP bleached WPC80 had the highest L* values. Iron concentration was lower in the HP-bleached WPC80 ($P < 0.05$), all other mineral and proximate values were not different among treatments ($P > 0.05$). HP treatments had more soluble protein after 10 min of heating at 90oC at pH 4.6 and pH 7 than the unbleached and BP treatments. Overall, HP bleaching caused more lipid oxidation products than BP bleaching but enhanced the solubility of the WPC80.

Key words: whey protein, bleaching, flavor

69 The complete genome sequence of *Bifidobacterium animalis* ssp. *animalis* ATCC 25527^T and analysis of growth in milk. J. R. Loquasto*[1], R. Barrangou[2,1], E. G. Dudley[1], and R. F. Roberts[1], *[1]The Pennsylvania State University, University Park, [2]Danisco USA Inc., Madison, WI.*

Bifidobacteria are putative probiotic organisms commonly added to fermented dairy products. The number of complete bifidobacterial genomes is increasing and analysis of these genomes has provided important insight into the physiology of these organisms. The objective of this work was to sequence the genome of *B. animalis* ssp. *animalis* ATCC 25527^T with the aim of providing insight into the genetic diversity responsible for phenotypic differences reported between *B. animalis* ssp. *animalis* (Baa) and *B. animalis* ssp. *lactis* (Bal). The genome of ATCC 25527^T was shotgun sequenced using 454 technology. After contig assembly, alignment and several rounds of gap closing, the complete 1,932,963 bp genome was determined and verified by comparison to a *Kpn*I optical map. The genome was annotated using Rapid Annotation using Subsystems Technology (RAST) and at NCBI. Comparative analysis of the Baa ATCC 25527^T and Bal DSMZ 10140^T genomes revealed high degrees of both synteny and homology. Comparison of the Baa and Bal genomes for differential content revealed 108 and 121 genes that were unique to and absent in, the BAA genome, respectively. Unique genes were identified as having less than 10% amino acid identity between protein sequences of both genomes, as detected by RAST. Among the differential gene content are a set of unique CRISPR-associated genes and a novel CRISPR locus containing 31 spacers in the genome of Baa. Although previous research has suggested one of the defining phenotypic differences between Baa and Bal is the ability of Bal strains to grow in milk and milk-

based medium, no obvious differences in gene content responsible for this phenotype were identified between the 2 genomes. Furthermore, growth and acid production in milk and milk-based medium did not differ significantly in experiments examining Bal (DSMZ 10140^T and Bl04) and Baa (ATCC 25527^T). These data suggest that this widely accepted defining phenotypic trait may not distinguish the subspecies.

Key words: bifidobacteria, probiotics, genome sequencing

70 Ruminal fermentation characteristics and lactational performance of Holstein dairy cows fed whole safflower seeds. C. M. Dschaak*[1], C. T. Noviandi[1], J.-S. Eun[1], V. Fellner[2], A. J. Young[1], D. R. ZoBell[1], and C. E. Israelsen[3], *[1]Department of Animal, Dairy, and Veterinary Sciences, Utah State University, Logan, [2]Department of Animal Science, North Carolina State University, Raleigh, [3]Cooperative Extension, Utah State University, Logan.*

A lactation trial was conducted to determine the effects of supplementing whole safflower seeds (SS) on ruminal fermentation and lactational performance. Nine multiparous Holstein cows (DIM = 110 ± 20) were used in a replicated 3 × 3 Latin square design. Each period lasted 21 d with 14 d of adaptation and 7 d of data collection. Within square, cows were randomly assigned to a sequence of 3 dietary treatments as follows: cottonseed TMR (CST), conventional SS (variety S-208) TMR (CSST), and Nutrasaff SS (Safflower Technologies International, Sidney, MT) TMR (NSST). Diets contained approximately 63% forage (36% alfalfa hay, 4% grass hay, and 23% corn silage) and 37% concentrate supplemented with 2% cottonseed to the CST and 3% conventional or Nutrasaff SS to the CSST or the NSST, respectively. Intake of DM averaged 21.8 kg/d and did not differ ($P > 0.10$) across diets. Digestibility of DM was similar ($P > 0.10$) between diets, whereas feeding the CSST decreased ($P < 0.05$) fiber digestibility compared with the CST and the NSST. Milk yield was greater ($P = 0.03$) with the NSST (31.4 kg/d) when compared with the CST (30.2 kg/d). Milk protein increased with the NSST compared with the CST ($P = 0.05$). Diets had no effect ($P > 0.10$) on total or molar proportions of ruminal VFA and ammonia-N. Ruminal C16:0 and C18:0 concentrations increased with the CST ($P < 0.02$). Feeding the CST also increased milk C16:0 concentration, whereas C18:0, C18:1 cis-9, C18:1 trans-9, and C18:1 cis-11 increased with the NSST ($P < 0.03$). Supplementing whole SS in dairy diets at 3% of dietary DM can be an effective strategy of fat supplementation to lactating dairy cows without negative impacts on lactational performance.

Key words: safflower seeds, ruminal fermentation, lactational performance

71 The effects of NPH insulin and insulin glargine on milk yield and composition by lactating dairy cows. L. A. Winkelman* and T. R. Overton, *Cornell University, Ithaca, NY.*

Our study investigated the effects of neutral protamine hagedorn insulin (H) and insulin glargine (L) on milk composition in 30 cows (88 ± 25 DIM). Cows were blocked into 2 groups, balanced for DIM and production, and randomly assigned to 1 of 3 treatments (Control (C), H, and L). Subcutaneous injections of 0.2 IU/kg BW for H and L were given 2x/d every 12 h for 10 d. Blood samples were taken 2x/d, immediately before the morning injection and 6 h postinjection. Mammary tissue was biopsied on d 11. Cows were milked 2x/d and milk composition was determined on d 2, 4, 6, 8, and 10. Treatment means herein are presented in the following order: C, H, and L. Milk yield ($P = 0.46$) and DMI ($P = 0.58$) did not differ by treatment. Treatment with H and L increased milk protein content (3.00, 3.20, and 3.29 (±0.05)%; $P = 0.001$) and milk protein yield was increased by L (1.46, 1.49, and 1.54 (±0.03) kg/d; $P = 0.08$). Fat content (3.17, 3.32, 3.50 (±0.11)%; contrast C vs. L: $P = 0.04$) and yield (1.50, 1.55, 1.65 (±0.05) kg/d; contrast C vs. L: $P = 0.05$) were increased by L. Milk lactose content was reduced (4.84, 4.76, 4.70 (±0.02)%; $P = 0.001$) by treatment. Lactose yield was reduced by L ($P = 0.02$) but not H ($P = 0.13$) and averaged 2.34, 2.26, and 2.21 (±0.04) kg/d. Casein content ($P = 0.02$) and yield ($P = 0.09$) were increased by treatment with H and L, but casein as a percent of true protein did not differ ($P = 0.70$). Plasma glucose was reduced by treatment with H and L (56.8, 52.0, and 48.1 (±0.99) mg/dl; $P < 0.001$). Plasma urea nitrogen was reduced by L ($P = 0.004$) but not H ($P = 0.57$). Plasma NEFA was higher for cows treated with H (166, 197, and 181 (±9) μEq/L; $P = 0.013$). Western blot of mammary protein lysates indicated that the ratio of phosphorylated Akt:total Akt differed by treatment and was greatest for H (1.16, 1.72, 0.96 (±0.62) arbitrary units; $P = 0.05$) but the ratio of phosphorylated rpS6:total rpS6 did not differ by treatment ($P = 0.60$). Overall, H and L improved milk component production, but more research needs to be conducted to further elucidate the mechanism underpinning the effects of insulin on milk composition.

Key words: insulin, milk protein

72 The effects of degradable nitrogen level and degradation rate on nitrogen balance and urea kinetics in Holstein steers. V. B. Holder*[1], J. Tricarico[2], D. H. Kim[1], N. B. Kristensen[3], and D. L. Harmon[1], *[1]University of Kentucky, Lexington, [2]Alltech, Brookings, SD, [3]Aarhus University, Tjele, Denmark.*

The objective of this study was to compare nitrogen metabolism and urea kinetics between diets containing either rapidly degrading or slow degrading non protein nitrogen (NPN) at varying levels of degradable intake protein (DIP). Treatments were slow release urea (Optigen II, OPT) fed at 101 and 114% and feed grade urea (Urea) fed at 89 and 100% of calculated DIP requirements. Eight Holstein steers (209 ± 15 kg) implanted with Synovex Plus were used in a replicated 4 × 4 Latin square. Periods were 27 d, with 19 d adaptation followed by 7 d of urine and fecal collection and 1 d of blood sampling. Continuous (78h) intravenous infusion of $^{15}N^{15}N$-urea allowed estimation of urea kinetics. Dry matter intake was not different between treatments (7.2 kg/d). Increasing DIP had a tendency to increase dry matter digestibility (DMD) for both Urea and OPT. Urea had higher DMD than OPT. Increasing DIP increased urinary N output, and increased N-retention with OPT but not Urea. Increasing DIP increased urea–N entry rate (UER) and urinary urea-N excretion (UUE) for both OPT and Urea. Gastrointestinal entry of urea-N, urea-N lost to feces and urea-N apparently used for anabolism were not different between treatments. Plasma urea concentration was greater in higher DIP diets and higher for Urea than OPT at 100% DIP. Therefore increasing DIP level will increase N-excretion related to higher urea production and excretion in urine but may also increase diet digestibility. Most changes in N metabolism were driven by N intake; however, providing a slow release DIP source may allow for greater N retention when DIP is not limiting.

Table 1. Experiment results

	Treatment					Contrasts		
Item	114% DIP OPT	101% DIP OPT	100% DIP Urea	89 % DIP Urea	SEM	114% vs. 101%, OPT	100% vs. 89 %, Urea	100% Urea vs. 101% OPT
DMD, %	59.8	58.2	60.7	58.8	1.6	0.09	0.06	0.01
Urine N, g/d	62.2	53.6	54.3	41.7	7.4	<0.001	<0.001	0.75
N Retention, g/d	39.6	31.3	34.8	34.1	4.0	0.001	0.73	0.10
UER	70.1	57.8	56.7	45.4	8.1	0.002	0.004	0.75
UUE	36.3	26.5	26.6	15.5	2.5	<0.001	<0.001	0.96
Plasma Urea, mM[1]	2.8	2.3	2.5	1.8	0.1	<0.001	<0.001	0.02

[1]Data were transformed for statistical analysis. SE of original data reported.

Key words: urea recycling, nitrogen metabolism, cattle

73 Effects of monensin on metabolic parameters, feeding behavior, and productivity of transition dairy cows. C. R. Mullins*[1], L. K. Mamedova[1], M. J. Brouk[1], C. E. Moore[2], H. B. Green[2], K. L. Perfield[2], J. F. Smith[1], J. P. Harner[1], and B. J. Bradford[1], *[1]Kansas State University, Manhattan, [2]Elanco Animal Health, Greenfield, IN.*

The effects of monensin on transition cow metabolism may be dependent on modulation of feeding behavior, ruminal pH, and/or expression of metabolic genes. Multiparous Holstein cows (n = 16 per treatment) were alternately assigned, based on calving date, to control or monensin (400 mg/d) treatments 21 d before expected calving date, and cows remained on treatments through 21 d postpartum. Feeding behavior and water intake data were collected daily. Liver biopsies were obtained, after assessing BCS and BW, on d −21, −7, 1, 7, and 21 relative to calving (RTC), for analysis of triglyceride (TG) content and mRNA abundance of phosphoenolpyruvate carboxykinase 1(PCK1) and carnitine palmitoyltransferase 1a (CPT1a). Blood samples were collected on d −21, −7, −4, 1, 4, 7, 14, and 21 RTC for plasma NEFA, β-hydroxybutyrate (BHBA), glucose, insulin, and haptoglobin analyses. Ruminal pH was collected every 5 min on d 1 to 7 RTC by a wireless indwelling probe. On d 7 RTC, a caffeine clearance test was performed to assess liver function. Data were analyzed using mixed models with repeated measures over time. Monensin decreased mean plasma BHBA (734 vs. 616 ± 40 μM; $P < 0.05$) and peak concentrations (1076 vs. 777 ± 70 μM on d 4 RTC; $P < 0.01$). Monensin also decreased time between meals prepartum (143 vs. 126 ± 5.0 min; $P < 0.03$) and postpartum (88.8 vs. 81.4 ± 2.9 min; $P < 0.08$), which was likely related to a smaller ruminal pH variance in the first day after cows changed to a lactation ration (SD = 0.31 vs. 0.26 ± 0.015 units; $P < 0.02$). Monensin increased liver mRNA abundance of CPT1a (0.10 vs. 0.15 ± 0.002 arbitrary units; $P < 0.04$), which corresponded with a slower rate of liver TG accumulation from d −7 to +7 RTC (412 vs. 128 ± 83 mg TG/g protein per 2 wk, $P = 0.03$). There were no significant effects of monensin supplementation on milk production, liver PCK1, plasma NEFA, glucose, insulin, or haptoglobin. No effects on disease incidence were detected, but sample size was small for detecting such effects. Overall, results confirm that the effects of monensin on transition cows extend beyond altered propionate flux.

Key words: monensin, transition cow, feeding behavior

74 The effect of ketoprofen following left displaced abomasum surgery on lying behaviour and ketosis. N. C. Newby*[1], S. J. LeBlanc[1], K. E. Leslie[1], D. L. Pearl[1], M. A. G. von Keyserlingk[2], and T. F. Duffield[1], *[1]University of Guelph, Guelph, Ontario, Canada, [2]University of British Columbia, Vancouver, British Columbia, Canada.*

Surgical correction of left displaced abomasum (LDA) is common in lactating dairy cattle, but it is not common practice to administer analgesia following LDA surgery although surgery is normally associated with pain. The objectives of this research were to examine the effect of administering a label dose of the non-steroidal anti-inflammatory drug ketoprofen on lying behavior and ketosis (blood β-hydroxybutyrate (BHB)), as well as on farmer's perception of recovery following LDA surgery. A total of 148 Holstein cows were enrolled in a field study following LDA surgery (standing right flank (RF) or paramedian (P) approaches). Using a double-blind randomized method, each animal was assigned to receive either 3 mg ketoprofen/kg body weight or saline by intramuscular injection, immediately following surgery and 24 h post-operatively. A subset of cows (n = 37) were fitted with a 3-axis accelerometer on the hind leg to access lying activity. Farmers were asked to provide information on the cow's appetite in the days following surgery. Lying time data were analyzed using multivariable linear models with a random effect for cow and binary outcomes were analyzed using a mixed logistic model. Cows subjected to P surgery lay down less (β = −3.8 h; 95% C.I.: −2.3, −5.4 h; $P < 0.01$) in the first 3 d, and had higher heart rate (β = 9.4 beats/min; 95% C.I.: 6.9 – 12 beats/min; $P < 0.05$) 2–4 d after surgery, compared with animals that underwent RF surgery. In all cows, regardless of surgical procedure or ketoprofen treatment, BHB significantly decreased from surgery to d 2–4 (β = −1.9; 95% C.I.: −2.1, −1.7; $P < 0.001$) and d 8–10 (β = −2.0; 95% C.I.: −0.2.2, −1.8; $P < 0.001$). Based on observations by producers (who were blinded to treatment status), animals that received ketoprofen were more likely to begin eating when provided fresh feed on the first 3 d following surgery compared with those that received saline (OR = 4.2; 95% C.I.: 1.4, 12.5; $P = 0.01$). These results suggest that that P surgery of LDA may result in more pain than the RF approach. Further investigation of assessment and management of post-surgical pain is warranted.

Key words: displaced abomasum surgery, post-surgical pain, dairy cattle behaviour

75 Ruminal fermentation and nutrient digestion by dairy cows fed different concentrations of forage and dried distillers grains with solubles. S. D. Ranathunga*, K. F. Kalscheur, A. R. Hippen, and D. J. Schingoethe, *South Dakota State University, Brookings, South Dakota, USA.*

The study objective was to investigate the effects of concentrations of forages and dried distillers grains with solubles (DG) on ruminal fermentation and nutrient digestion in lactating dairy cows. Four Holstein cows with ruminal fistula were assigned to a 4 × 4 Latin square 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 DG at 0 or 18% of diet DM. Ground corn and soybean feeds were partially replaced by DG from 0% DG diets to formulate 18% DG diets. Average DMI was not affected by diets (23.8 kg/d). Rumen evacuation at 4h post-feeding showed that rumen digesta DM were greater for cows fed HF regardless of the addition of DG. There was a tendency for digesta NDF (7.00 vs. 7.49 kg) to be less for cows fed LF compared with HF, whereas digesta starch (0.53 vs. 0.33 kg) were greater for cows fed LF compared with HF. Lower ruminal pH

(6.10 vs. 6.34) was observed in cows fed LF whereas there was no DG effect on ruminal pH. Cows fed LF had greater total VFA concentration compared with cows fed HF (122 vs. 116 mM). Acetate concentrations were lesser for LF (57.5 vs 62.6 mol/100 mol) and 18% DG (61.3 vs 58.7 mol/100 mol) diets whereas propionate concentration were greater for LF (26.0 vs 20.1 mol/100 mol) and 18% DG (21.9 vs 24.2 mol/100 mol) diets. Greater acetate:propionate ratio was observed in HF and 0% DG diets. Total tract digestibility for DM, NDF, CP, and starch was not affected by diets. Results suggest that forage and DG concentration in diets affect ruminal degradability of nutrients.

Table 1.

	LF	LF	HF	HF		
Item	0DG	18DG	0DG	18DG	SEM	P-value a
Digesta DM, kg	11.2	13.2	13.9	12.9	1.84	F
Digesta NDF, kg	6.52	7.48	7.56	7.42	1.02	FT, F×D
Digesta starch, kg	0.62	0.44	0.32	0.35	0.05	F
Rumen pH	6.17	6.02	6.32	6.36	0.09	F
Total VFA, mM	119	124	117	114	3.59	F
VFA, mol/100 mol						
Acetate	58.9	56.0	63.8	61.3	0.72	F, D
Propionate	24.2	27.7	19.5	20.6	0.88	F, D, F×D
A:P ratio	2.53	2.05	3.32	3.00	0.12	F, D

[a]F or D= Forage or DG effect; F×D=Forage and DG interaction ($P < 0.05$); FT= Forage effect (tendency) ($P < 0.10$).

Key words: distillers grains, forage, rumen

76 On-farm validation of two rapid methods to estimate IgG in bovine colostrum. K. M. Morrill*[1], E. Conrad[1], A. Lago[2], J. D. Quigley[2], and H. D. Tyler[1], *[1]Iowa State University, Ames, [2]APC Inc., Ankeny, IA.*

Our objective was to validate a rapid, cow-side method to estimate IgG in bovine maternal colostrum (MC) based on caprylic acid (CA) fraction of MC followed by refractometry of the IgG-rich supernatant. Samples of MC (n = 827) were collected from 67 farms in 12 states. Samples were fresh (not stored; n = 196), previously frozen (n = 490) or refrigerated (n = 152). One ml of MC was added a tube containing 75 µL CA and 1 mL 0.06 M acetic acid and refractive index (nD) of the IgG-rich supernatant was determined. We also measured nD of whole (non-fractionated) MC and IgG of whole MC by radial immunodiffusion. Correlation of nD of CA supernatant to IgG (r = 0.53) was low, whereas the correlation between nD of whole MC and IgG was greater (r = 0.73). Correlations of nD of CA supernatant and IgG (r = 0.93) and nD of whole MC and IgG (r = 0.89) of MC samples that and were not stored before analysis (n = 146) were much greater, suggesting that storage of MC impaired our ability to measure nD or IgG. Correlations of whole nD of MC and IgG were similar for Holsteins (r = 0.77) and Jerseys (r = 0.80). Regression equations were used to estimate the IgG concentration of samples based on the nD of CA supernatant or whole MC. The equation created from nD of CA supernatant resulted in 34.3% of samples accurately estimated within 10 mg/ml, 23.7% of samples estimated within 10–20 mg/ml, 14.5% of samples estimated within 20–30 mg/ml and 27.5% of samples estimated to greater than 30 mg/ml of actual IgG concentration. Equation created from the nD of whole MC resulted in 43.8% of samples estimated within 10 mg/ml, 28.0% of samples within 10–20 mg/ml, 14.4% of samples within 20–30 mg/ml and 13.8% of samples greater than 30 mg/ml compared with actual IgG concentration. These results suggest that the nD of whole MC provides a more accurate estimation of colostral IgG concentration than the nD of CA supernatant and both tests are most accurate on fresh colostrum samples.

Key words: colostrum, refractometer, IgG

77 Physiological and transcriptional adaptations in adipose tissue of dairy cows in response to prepartal plane of dietary energy. P. Ji*, J. S. Osorio, J. K. Drackley, and J. J. Loor, *University of Illinois, Urbana.*

Our objective was to determine the effect of prepartal energy overfeeding during the close-up period on physiological and transcriptional responses of adipose tissue (AT) of dairy cows during the transition period. Multiparous Holstein cows (n = 14) were randomly assigned to either a controlled-energy diet (CON; NE_L = 1.30 Mcal/kg DM) for the entire dry period or CON during the far-off period (d −50 to −21 relative to expected parturition) followed by a moderate-energy diet (Overfed; NE_L = 1.49 Mcal/kg DM) during the close-up period (d −21 to calving). Both groups were fed the same lactation diet postpartum (NE_L = 1.67 Mcal/kg DM). Blood samples were collected before morning feeding twice weekly. Subcutaneous AT was biopsied from tail-head regions at d −10, 7, and 21 for total RNA extraction. Quantitative RT-PCR was utilized to analyze mRNA expression of 50 genes. Overfeeding energy increased DMI ($P = 0.05$) and serum insulin concentration ($P < 0.01$) during the close-up period, but tended to increase serum BHBA concentration postpartum ($P = 0.06$). Overfed cows experienced more marked increases in serum NEFA and BHBA postpartum ($P < 0.05$). Milk yield did not differ ($P = 0.89$) between diets. Compared with CON, close-up overfeeding led to greater expression of genes ($P < 0.05$) associated with fatty acid (FA) biosynthesis (ACLY, ACACA, and FASN), FA import, FA activation and desaturation (LPL, ACSS2, ACSL1, and SCD), NADPH production (G6PD and IDH1), triglyceride synthesis (GPAM and DGAT2), transcriptional regulation of lipogenesis (PPARG, CEBPA, and THRSP) and basal lipolysis (PNPLA2 and ABHD5) at d −10. Abundance of mRNA for these genes decreased between d −10 and d 7. The expression of IRS1, AKT2, GLUT4, and INSIG1 was downregulated in both groups at d 7 compared with d −10 ($P < 0.05$). Overall, overfeeding energy during the close-up period may increase both lipid accumulation and basal lipolysis in AT through transcriptional regulation. Decreased circulating insulin and lower expression of IRS1, AKT2, and GLUT4 in the early postpartum period may contribute to the downregulation of lipogenic genes.

Key words: adipose tissue, energy overfeeding, transition period

78 Expression of novel, putative stem cell markers in prepubertal and lactating bovine mammary glands. R. K. Choudhary*[1], C. M. Evock-Clover[2], and A. V. Capuco[2,1], *[1]Department of Animal Sciences, University of Maryland, College Park, [2]Bovine Functional Genomics Lab, USDA-ARS, Beltsville, MD.*

Mammary stem cells (MaSC) are essential for growth and maintenance of the mammary epithelium. Two main phases of mammary growth include ductal elongation before puberty and lobulo-alveolar growth during pregnancy. Some studies utilized morphological characteristics and retention of bromodeoxyuridine (BrdU) label to identify MaSC. However, these approaches may not be feasible or require considerable expertise. An alternative approach to identify resident MaSC is based on detection of appropriate protein markers by immunohisto-

chemistry. The focus of this study was to evaluate staining patterns (in prepubertal and lactating mammary tissue) of 3 novel, candidate markers for bovine MaSC. These proteins were identified as candidate MaSC markers because their transcripts were highly expressed in laser microdissected-MaSC, which were identified by BrdU label retention and basal location within the mammary epithelium. The 3 novel candidate markers for MaSC were: nuclear receptor subfamily 5 group A member 2 (NR5A2), nucleoporin 153 (NUP153) and fibronectin type III domain containing 3B (FNDC3B). We also evaluated presumptive MaSC markers [aldehyde dehydrogenase 1 (ALDH1) and Musashi 1 (Msi1)] and differentiation factors [Notch 3 receptor (Notch3) and cytokeratins (CK) 14 and19] that have been used in other species. We found that NR5A2 and NUP153-positive nuclei were more abundant in prepubertal than lactating mammary glands and their distributions were consistent with expectations for a MaSC marker. FNDC3B was localized mainly in the nucleus prepubertally and in the cytoplasm during lactation. Preliminary results showed colocalization of the novel markers with label retaining MaSC. Abundant expression of ALDH1 precludes its use as a marker for bovine MaSC, whereas Msi1 staining was distributed in a fashion consistent with MaSC localization. Additionally we noted that onset of lumen formation in terminal ducts of prepubertal glands were coincident with Notch3 expression in luminal cells. This study demonstrates that nuclear expression of NR5A2, NUP153 and FNDC3B are potential markers for bovine MaSC.

Key words: mammary stem cell, novel biomarker

79 Effect of dietary protein level and rumen-protected methionine supplementation on performance of lactating dairy cows. C. Lee*[1], A. N. Hristov[1], T. Cassidy[1], H. Heyler[1], H. Lapierre[2], G. A. Varga[1], and C. Parys[3], *[1]Pennsylvania State University, University Park, [2]Agriculture and Agri–Food Canada, Sherbrooke, QC, Canada, [3]Evonik Degussa GmbH, Hanau, Germany.*

The objective of this experiment was to investigate the effect of rumen–protected Met (RPMet) supplementation of a low-CP diet on dairy cow performance. The experiment was conducted for 12 wks with 36 Holstein cows (95 ± 6.2 DIM). Following a 2-wk covariate period, cows were assigned to one of the following treatments: 15.6% CP diet [HighCP; metabolizable protein (MP) balance: +26 g/d], 14.0% CP diet (LowCP; MP balance: –313 g/d) supplemented with 100 g/cow/d of rumen-protected Lys (AminoShure-L, 24 g/d estimated digestible Lys supply), and 14.0% CP diet supplemented with rumen-protected Lys plus 24 g/cow/d RPMet (Mepron, 15 g/d estimated digestible Met supply; LowCPMet). DMI and milk yield were not affected by treatment (24.8 ± 0.40 kg/d and 38.4 ± 0.80 kg/d, respectively). Compared with HighCP, LowCP decreased milk protein content ($P = 0.02$); with LowCPMet the effect was not significant ($P = 0.07$). Milk protein yield was not different ($P = 0.22$) among diets. Milk urea–N concentration was decreased (by 15%; $P = 0.05$) by LowCP and LowCP-Met compared with HighCP. Plasma Lys and Met concentrations were not affected by treatment. His and Val concentrations were 48 and 22% lower ($P = 0.001$ and 0.016) and Thr, Arg, Phe, and Gln tended to be lower ($P = 0.08$ to 0.05) for the LowCP diets compared with HighCP. The LowCP diets decreased ($P = 0.01$) blood urea–N concentrations and NDF and ADF apparent digestibilities compared with HighCP. Urinary excretion of purine derivatives was lower (by 13%; $P = 0.03$) for LowCP compared with HighCP. Compared with HighCP, the LowCP diets resulted in lower ($P < 0.001$) urinary total (by 31%) and urea-N (by 51%) excretions. Ammonia emission from LowCP manure was 37% lower ($P < 0.001$) compared with HighCP manure. In conclusion, the LowCP diets, supplemented with rumen–protected amino acids maintained milk production similar to the HighCP diet, except that protein concentration was significantly decreased without RPMet supplementation. Nitrogen losses and ammonia emissions from manure were decreased with the LowCP diets.

Key words: dietary protein, rumen-protected methionine, dairy cow

80 Summer assessment and validation of metabolic profile reference values for transition Holstein dairy cattle. K. J. Lager*[1,2], E. R. Jordan[1], and D. R. Topliff[2], *[1]Texas AgriLife Extension Service, Texas A&M System, College Station, [2]West Texas A&M University, Canyon.*

Dairy cattle genetics and management continue to evolve over time, but it is not known whether the available diagnostic tools have kept pace with the ever changing industry. The objective of this project was to assess the validity of current metabolic profile reference values in relation to current dairy cattle genetics and management strategies. Blood samples (n = 1787) were collected between late August and mid-September, 2010 from cows within the transition period via coccygeal vessel venipuncture into nonheparinized vacuum blood tubes at morning feeding on 8 commercial dairies ranging in approximate size from 1800 to over 5000 head of lactating cows. One day per dairy was utilized to collect blood samples for cows within the transition period. Samples were placed on ice immediately following collection until processing. Following centrifugation, samples were stored frozen (−20°C) in duplicate before laboratory analysis for calcium, phosphorus, magnesium, albumin, urea, glucose, cholesterol, sodium, potassium, chloride, and nonesterified fatty acids. Data points were excluded for cows experiencing dystocia, retained placenta, displaced abomasum, twin births, and stillbirths, as well as for cows being dry <40 d or >80 d. Mean lactation number and days dry were 3.0 ± 1.2 and 57.8 ± 7.5, respectively. Serum phosphorus values (mg/dl) for wk −3, −2, −1, 1, 2, and 3 relative to calving were 5.23 ± 0.83, 5.43 ± 0.74, 5.48 ± 0.95, 5.39 ± 1.2, 4.90 ± 0.88, 5.31 ± 0.80, respectively; while calcium values (mg/dl) were at 8.94 ± 0.43, 8.87 ± 0.54, 8.87 ± 0.54, 8.26 ± 0.86, 8.76 ± 0.74, 9.08 ± 0.53, respectively. Nonesterified fatty acids were numerically greatest in wk 1 (0.67 mEq/l ± 0.36), while sodium and chloride were reacted similarly (143.65 mEq/l ± 2.4 and 108.89 mEq/l ± 2.6, respectively) at wk −1 relative to calving. Serum cholesterol concentrations were numerically lowest in wk 1 (74.54 mg/dl ± 17.8), displaying a non-static trend similar to that of other metabolic profile analytes for the duration of the transition period.

Key words: dairy cow, metabolic profile, transition cow

81 Effect of follicular wave and progesterone (P4) concentration during follicle growth on fertility of dairy cows. R. S. Bisinotto*[1], H. Ayres[1], M. R. Carvalho[1], E. S. Ribeiro[1], R. L. A. Cerri[2], L. F. Greco[1], F. S. Lima[1], M. G. Favoreto[1], A. P. Monteiro[1], M. C. Perdomo[1], W. W. Thatcher[1], and J. E. P. Santos[1], *[1]University of Florida, Gainesville, [2]University of British Columbia, Vancouver, BC, Canada.*

Effects of wave of the ovulatory follicle and P4 concentration during follicle growth on corpora lutea (CL) function and conceptus development were evaluated in dairy cows. Nonlactating Holstein cows had their estrous cycles synchronized with GnRH and a controlled internal drug release (CIDR) device containing P4, followed 7 d later by CIDR removal and 2 injections of $PGF_{2\alpha}$ 24 h apart. All cows received GnRH 1 d after the 2nd $PGF_{2\alpha}$ which, for cows induced to ovulate a first wave follicle (FW, n = 13) or a FW follicle supplemented with P4 (FWP4, n = 8), was the 1st GnRH of the timed artificial insemination (AI)

protocol (d-9 GnRH, d-2 and d-1 $PGF_{2\alpha}$, d0 GnRH and AI, d1 AI). Cows induced to ovulate a second wave follicle (SW, n = 12) received the timed AI protocol beginning 6 d after the previous GnRH. Cows in FWP4 received 3 CIDR, one at 12, 24 and 48 h after the GnRH (d-9), that were removed at the $PGF_{2\alpha}$ (d-2). Blood was sampled from d-9 to 17 for P4 and estradiol (E2) analyses. Cows were slaughtered on d17 and uteri flushed. Interferon-tau (INF-τ) on uterine flush was quantified. Concepti IFN-τ mRNA expression was accessed by RT-PCR. Orthogonal comparisons were performed to determine the effects of P4 (FW vs. FWP4+SW) and follicle wave (SW vs. FWP4). Ovulation of a FW follicle reduced pregnancy and this effect was mediated by low P4 concentration during their development. Luteal function during early gestation, concepti elongation and their ability to produce IFN-τ were not compromised by ovulation of follicles developing under low concentrations of progesterone.

Table 1.

	Treatment			*P*-value	
	FW	FWP4	SW	Wave	P4
P4, ng/mL					
d-9 to −2	1.4±0.2	3.8±0.3	5.4±0.3	<0.01	<0.01
d4 to 16	6.3±0.2	5.0±0.3	5.0±0.3	0.84	<0.01
Ovulatory follicle (d0), mm	17.9±0.6	15.3±0.7	14.7±0.6	0.47	<0.01
E2 peak before AI (d-1), %	58.3	12.5	0.0	0.77	0.01
E2 at peak, pg/mL	8.0±0.6	7.0±0.7	5.9±0.6	0.25	0.05
CL on d7, mm^3	5.2±0.5	3.6±0.6	4.2±0.5	0.39	0.03
Pregnant, %	50.0	87.5	72.7	0.45	0.10
Conceptus length, cm	17.5±2.8	13.7±2.6	11.2±2.6	0.52	0.15
INF-τ on uterine flush, ng/mL	300±92	211±86	60±92	0.06	0.22
INF-τ mRNA, dCt ratio	1.5±0.2	1.6±0.2	1.2±0.2	0.13	0.78

Key words: dairy cow, follicle, progesterone

Graduate Student Competition: ADSA Southern Section

82 Production response to corn silage produced from normal, brown midrib, or waxy corn hybrids. J. S. Barlow*, J. K. Bernard, and N. A. Mullis, *The University of Georgia, Tifton.*

The starch in Waxy corn hybrids is 100% amylopectin which has been suggested to be more digestible than that of normal corn hybrids, but the production response to feeding silage produced from these hybrids has been inconsistent. In contrast, brown midrib (BMR) corn varieties have lower lignin concentrations and have been shown to support higher DMI and milk yield. The objective of this study was to evaluate the nutrient intake and milk production response of lactating dairy cows to diets based on corn silage produced from 3 different types of corn hybrids. Thirty-six multiparous and primiparous Holstein cows (77 DIM and 37.1 kg/d milk) were used in an 11 wk completely randomized design trial during the fall of 2009. Experimental diets contained 36.4% of the dietary DM from corn silage from either a normal (Agratech 1021), BMR (Mycogen F2F797), or Waxy (Master's Choice 590) hybrid. All cows were fed the diet containing normal corn silage during the first 2 wk of the trial before being assigned to one of 3 treatments for the following 9 wk. Data collected during the first 2 wk were used as a covariate in the statistical analysis. No difference ($P = 0.81$) was observed in DMI among treatments which averaged 22.6 kg/d. Milk yield was highest ($P = 0.03$) for cows fed BMR (37.6 kg/d) compared with Waxy (35.2 kg/d) but similar to control (36.2 kg/d). Milk fat percentage tended to be lower ($P = 0.10$) for cows fed control (3.28%) compared with BMR (3.60%) or Waxy (3.55%) corn silage. Milk protein percentage ($P = 0.07$) tended to be lower for cows fed normal (2.79%) compared with Waxy (2.89%) but similar to BMR (2.85%). No differences were observed in yield of milk components. Energy-corrected-milk (ECM) yield, dairy efficiency (ECM/DMI), and BW change did not differ among treatments. Results of this trial are consistent with previous reports in which cows fed diets based on corn silage produced from BMR hybrids have higher milk yield compared with other hybrids. Corn silage produced from the waxy hybrid supported similar yield of ECM because of higher milk components, but milk yield was not improved compared with the normal.

Key words: waxy corn silage, BMR corn silage, milk yield

83 Ruminal escape and intestinal digestibility of experimental ruminal protected lysine supplements. Z. Wu*[1], J. K. Bernard[1], R. B. Eggleston[2], and T. C. Jenkins[3], *[1]University of Georgia, Tifton, [2]University of Georgia, Athens, [3]Clemson University, Clemson, SC.*

Recent research has focused on the development of LYS supplements that resist ruminal degradation but are digestible in the small intestine using various fat coatings. Hydrogenated fats are poorly digested in the small intestine, so inclusion of polyunsaturated fatty acids (PFA) such as oleic acid may improve digestibility in the small intestine. The objective of this study was to determine the effect of the addition of 2 or 4% PFA to a hydrogenated fat coating applied to an experimental supplement with 55 or 58% supplemental LYS on ruminal escape and intestinal absorption of LYS. Two lactating Holstein cows (103 DIM and 45.1 kg/d milk) previously fitted with ruminal and duodenal cannula were individually housed and fed a corn silage based ration. In situ and mobile bag techniques were utilized as outlined in NRC (2001) to evaluate the 4 test products. Twenty 10 × 20 cm nylon bags of each product (5 g each) were incubated for 16 h in each cow. After ruminal incubation, products were repackaged (0.8g) into 5 × 10 cm nylon bags (20 per test product), soaked in pepsin/HCl solution for 2 h before inserting into the duodenum and subsequently collected in the feces. All samples were analyzed for DM, N, LYS and acid hydrolysis fat concentrations. The percentage of DM and fat escaping the rumen decreased ($P < 0.001$) as PFA increased from 2 to 4% or as the proportion of supplemental lysine increased. An interaction ($P < 0.01$) was observed between PFA and LYS proportion because of a greater reduction of N and LYS escaping ruminal fermentation and flowing to the small intestine for the product with 58% supplemental lysine and 4% PFA in comparison to the other products. No differences were observed in intestinal digestibility of DM, N, LYS, or fat or the amount of lysine digested in the small intestine. Results of this trial indicate that increasing the proportion of PFA in the coating applied to supplemental lysine increases ruminal degradation. The extent of the degradation increases as the proportion of lysine in the product increases.

Key words: rumen protected lysine, ruminal escape, intestinal digestibility

84 Effect of sample processing on in situ protein degradability of distillers grains. M. L. Drewery*[1], J. E. Sawyer[1], N. M. Kenney[1], W. E. Pinchak[2], and T. A. Wickersham[1], *[1]Texas A&M University, College Station, [2]Texas AgriLife Research, Vernon.*

Precise measurements of nutrient availability are important when formulating rations. The high moisture content of wet distillers' grains (DG) creates challenges for nutrient analysis and sample processing. Therefore, our objective was to determine how sample processing affects measures of rate and extent of protein degradation in wet DG samples. Three ruminally cannulated steers were fed a ration (15% CP) containing 38.5% corn, 28% hay, and 28% dried DG. Samples of wet DG were divided and a portion was frozen at −20°C while the remainder was dried at 55°C in a forced-air oven for 96 h. Dried samples were ground to pass a 2-mm screen. Five g of each sample was placed in Dacron bags, pre-incubated in tepid water, placed in a weighted mesh polyester bag, and incubated in the rumen for 4, 6, 12, 24, 48 and 72 h. Samples were rinsed in cold water and dried at 60°C. Nitrogen content was determined. Protein was fractionated into A, B, and C fractions. Degradation rate of the B fraction was calculated as the slope of the natural log of N remaining against time. Rate of passage was set at 3%/h. The A fraction was greater ($P < 0.01$) for frozen (43.3%) than dried samples (24.0%). In contrast, the B fraction was less ($P < 0.01$) for frozen than dried samples 52.1 and 70.0%, respectively. The C fraction differed ($P = 0.01$) between frozen and dried; however, the magnitude of this difference was small 4.5 and 5.9%, respectively. Degradation rate of the B fraction was greater ($P < 0.01$) for frozen than dried samples 1.31 versus 1.86%/h, respectively. Accordingly, estimated degradability was observed to be greater ($P < 0.01$) for frozen than dry samples 59.4 and 51.1%, accordingly. These results suggest drying wet DG impacts the measures of protein degradability.

Key words: distillers grains, degradability, protein

85 Effects of heat stress and increased protein and energy fed in milk replacers on health parameters of neonatal Holstein bull calves. A. J. Krenek*[1], G. A. Holub[1], T. A. Tomaszewski[1], and C. C. Stanley[2], *[1]Texas A&M University, College Station, [2]Land O Lakes Purina Feed, Amarillo, TX.*

The objectives were to evaluate if calves in non-heat stress environment (NHS) were healthier than calves in heat stress environment (HS) or if feeding increased protein and fat in milk replacer (HPMR; 1135 g/d, 28% CP, 20% fat) verses a conventional milk replacer (CMR; 454 g/d, 20% CP, 20% fat) diet affected the health status of calves in the 2 environments. Calves were fed 6 L of HPMR or 4 L of CMR per day. Holstein bull calves (n = 52) < 3 d of age were assigned to a 2 X 2 factorial trial based on initial BW, physical health score, and total serum protein levels. Half of each nutrition group was housed indoors with temperature control non-heat stress (NHS) or outside under a metal roof in heat stress (HS) environment. The study was conducted for 56 d from, June 19 to August 13, 2010. The average Thermal Heat Index (THI) was calculated for each day by averaging the 24 recorded temperatures and RH%. The 56 d average, low, and high range THI for the HS was 79, 67, and 86 respectively, while THI for the NHS was 69, 66, and 74 respectively. Fecal scores (FS) of 1 to 4 (1 = hard, firm, 2 = soft, firm, 3 = no form, and 4 = watery) were recorded d to monitor scouring. Calves with a FS of 4 were considered to have diarrhea requiring treatment. Respiration rates (RR) were recorded at 0600 (AM) and 1800 (PM) d to monitor respiratory challenges while rectal temperatures (RT) were also measured using a digital thermometer daily in AM and PM to monitor febrile events. If RT was greater than 39.2°C for NHS calves and 39.7°C for HS calves, they were treated for fever (FE). The calves in HS had a higher RT AM, RT PM, RR AM, and RR PM ($P = < 0.01$) than calves in NHS (38.87 vs. 38.77 ± 0.02), (39.03 vs. 38.79 ± 0.05), (35.79 vs. 32.77 ± 0.3), and (55.73 vs. 38.58 ± 0.6) respectively. The calves in NHS had a higher FE ($P = < 0.01$) than the HS calves (6.24 vs. 2.33 ± 0.94). The HPMR calves had a higher FS ($P = < 0.01$) than the CMR calves (2.05 vs. 1.73 ± 0.03). This indicates calves in HS were experiencing higher RT AM, RT PM, RR AM, and RR PM. Also, the increased amount of protein and energy fed to the HPMR treatment had higher FS.

Key words: calf, milk replacer, heat stress

86 Effects of resistant starch in milk replacer on health and performance of neonatal Holstein heifer calves. B. L. Fisher*, B. F. Jenny, C. C. Williams, C. F. Hutchison, A. H. Dolejsiova, and R. G. Morell, *LSU AgCenter, Baton Rouge, LA*.

Forty-two female Holstein calves were assigned to one of 3 treatments at d 2 of age to study the effects of adding resistant starch (RS) to the milk replacer on health and performance. Treatments were control (no RS), 4g RS, or 8g RS mixed into the reconstituted replacer. Calves were housed in individual calf hutches and fed milk replacer once daily until d 42 of age. An 18% crude protein calf starter and water were offered ad libitum beginning d 3 throughout the duration of the trial. Calves remained in their hutches until 56 d of age to determine immediate postweaning performance. Body weights were measured at birth and d 14, 28, 42, and 56 of age. Wither height (WH), hip height (HH), and hip width (HW) were measured on d 14, 28, 42 and 56 of age. Feed intake, body temperatures, and fecal scores were recorded once daily through d 56. On d 14, 28, 42, and 56, fecal samples were collected for analysis of pH and volatile fatty acids (VFA), and blood was collected for analysis of plasma urea nitrogen (PUN) and total protein (TP). PUN and TP did not differ ($P > 0.05$) and were within normal ranges suggesting that there were no major metabolic problems. There was no effect ($P > 0.05$) of treatment on body weight, HH, HW, WH, or body temperatures. There was a treatment by week interaction ($P < 0.01$) and a week effect ($P < 0.01$) for grain intake, with all calves increasing intake throughout the duration of the study. There was a treatment by week interaction ($P < 0.01$) and a week effect ($P < 0.01$) for fecal scores, with calves having lower fecal scores at the end of the study compared with the beginning. Fecal pH increased as calves aged ($P < 0.01$). There was a treatment by week interaction ($P < 0.05$) with an effect of both week ($P < 0.01$) and treatment ($P < 0.05$) for propionate concentration in the feces. There was an effect of week ($P < 0.01$) for acetate and butyrate concentrations as well as on total VFA concentration in the feces. Overall, incorporation of RS in the milk replacer of neonatal dairy calves did not show any significant effects on growth or gut health of Holstein dairy calves.

Key words: dairy calves, resistant starch, milk replacer

87 Potential for estrus detection in dairy cattle using reticular temperature monitors. W. A. Smith*, W. J. Silvia, and J. M. Bewley, *University of Kentucky, Lexington.*

An experiment was designed to evaluate the utility of reticular (RT) and vaginal (VT) temperatures in predicting the time of ovulation in dairy cows. Lactating Holstein and crossbred (n = 30) cows were synchronized using an OVSYNCH protocol preceded by G6G. The first injection of prostaglandin Fα (PGF) was administered 40 to 90 d postpartum. OVSYNCH was modified by omitting the last injection of GnRH. The RT and VT were monitored using SmartBoluses (TenXsys Inc., Eagle, ID) inserted at least 5 d before anticipated estrus. Boluses were placed in the reticulum according to the manufacturer. Boluses were fixed to CIDR devices lacking progesterone (Pfizer Animal Health, NY) and inserted into the vagina using the CIDR speculum. Beginning at 48 h after the PGF injection of OVSYNCH, jugular venous blood samples were collected at 2 h intervals for LH and rectal temperatures were measured. After each sampling, cows were observed for estrus behavior. Beginning 72 h after PGF, ultrasonography was performed every 4 h to determine time of ovulation. Intensive sampling was maintained for 60 h or until ovulation was confirmed. Venous blood samples were collected daily for progesterone as an indicator of ovulation. The time intervals from injection of the OVSYNCH PGF, onset of estrus, LH surge, peak rectal temperature, and first detected increase in RT and VT to ovulation were determined. The mean and standard deviation for each interval was calculated. Only 18 cows ovulated within the sampling time frame and were used in this analysis. The average intervals in hours (±SD) from injection of the OVSYNCH PGF, onset of estrus, LH surge, peak rectal temperature, first detected increase in RT and VT to ovulation were 93 ± 11, 31 ± 8, 24 ± 6, 46 ± 11, 47 ± 31, 45 ± 27, respectively. The most precise predictor of interval to ovulation was the LH surge. The variation associated with the interval estimates based on RT and VT was high and precludes their usefulness as reliable predictors of the time of ovulation. Supported by the KY Agr Expt Stn and Genex Cooperative, Inc., Shawano, WI.

Key words: temperature, estrus, ovulation

Lactation Biology Symposium: Circadian Clocks and Photoperiod in Mammary Development and Lactation

88 Circadian timekeeping mechanisms. P. Hardin*, *Texas A&M University, College Station.*

Animals, plants, fungi and even some prokaryotic organisms display daily rhythms in physiology, metabolism and behavior. These rhythms are not passively driven by environmental cycles (e.g., light) but are controlled by endogenous circadian clocks that keep time even in the absence of environmental time cues. Environmental cycles are nevertheless required to entrain these clocks so that they activate rhythmic processes at the appropriate time of day. Circadian clocks are comprised of an input pathway that receives environmental cues and transmits them to the circadian oscillator, a circadian oscillator that keeps circadian time and activates output pathways, and output pathways that control various metabolic, physiological and behavioral processes. Considerable effort has been focused on determining how the circadian oscillator keeps time. Genetic and molecular studies in the fruit fly, *Drosophila melanogaster*, have contributed significantly to our understanding of the circadian oscillator. Identification and isolation of the first clock gene from Drosophila, period, and subsequent analysis of its expression led to the first molecular model of the circadian oscillator - an autoregulatory feedback loop in gene expression. Discovery of additional clock genes in Drosophila not only support the feedback loop model, but add to its mechanistic detail and complexity. Importantly, many components of the Drosophila circadian feedback loop have orthologs and/or functional equivalents in mammals, thus making Drosophila a useful model for circadian oscillators in higher organisms. New methods of identifying clock genes in Drosophila promise to uncover novel oscillator components that may be amenable to pharmacological manipulation. In animals, circadian oscillators reside in a variety of tissues, including the brain and numerous internal organs. Although these oscillators are largely photoreceptive and directly light-entrainable in Drosophila, oscillators in peripheral tissues of mammals are synchronized by systemic cues from the light-entrained central clock in the brain. Consequently, local oscillators and systemic cues control rhythms in mammalian physiology and metabolism.

Key words: circadian clock, molecular mechanisms, peripheral tissues

89 Circadian clocks in mammary gland development and differentiation. W. Porter*, *Texas A&M University, College Station.*

Biological clocks play a key role in how an organism adapts to daily and annual changes in the environment by regulating rhythmic fluctuations in metabolism, hormone and neurotransmitter release, sensory capabilities and a variety of behaviors. In vertebrates, these physiological responses are controlled by the suprachiasmatic nucleus (SCN) of the anterior hypothalamus. In addition, peripheral tissues including the liver, heart, kidney and mammary gland contain functional endogenous clocks. These peripheral clocks, which regulate numerous physiological processes including proliferation and apoptosis, are similar to the central clock and are influenced by the SCN via a combination of neural and hormonal signals. We have recently shown that members of the molecular clock are differentially regulated during mammary gland development and present new data demonstrating their involvement in normal virgin ductal morphogenesis and functional differentiation during lactation. Moreover, these responses are intrinsic to the mammary gland and not dependent upon the central clock. Furthermore, we have also found that the molecular clock cross-talks with other transcription factor pathways to regulate lactation-dependent gene expression. Together, these results suggest that the peripheral mammary clock is required for normal mammary gland development and function.

Key words: mammary gland, circadian rhythms

90 Circadian clocks as mediators of the homeorhetic response to lactation. T. Casey* and K. Plaut, *Purdue University, West Lafayette, IN.*

The transition from pregnancy to lactation is the most stressful period of a cow's life. During this transition, homeorhetic adaptations are coordinated across almost every organ and are marked by tremendous changes in hormones and metabolism to accommodate for the increased energetic demands of lactation. Recent data from our lab showed that changes in circadian clocks occur in multiple tissues during the transition period in rats and suggest that the circadian system regulates the coordinated changes in the dam's physiology needed to support lactation. Circadian rhythms coordinate the timing of physiological processes and synchronize these processes with the animal's environment. Circadian rhythms are generated by molecular circadian clocks located in the master clock of the hypothalamus and peripherally in every organ of the body. The master clock receives environmental and physiological cues and in turn synchronizes internal physiology by coordinating endocrine rhythms and metabolism through peripheral clocks. The effect of the circadian clock on lactation may be inferred by the photoperiod effect on milk production, which is accompanied by coordinated changes in the dam's endocrine system and metabolic capacity in response to changes in day length. We have shown that bovine mammary epithelial cells possess a functional clock that can be synchronized by external stimuli, and the expression of ARNTL, a positive limb of the core clock, is responsive to prolactin in bovine mammary explants. Others showed that 7% of genes expressed in breasts of lactating women had circadian patterns of expression, and we report that the diurnal variation of composition of cow's milk is associated with changes in expression of mammary core clock genes. Together these studies suggest that the circadian system coordinates the metabolic and hormonal changes needed to initiate and sustain lactation, and that the dam's capacity to produce milk and cope with metabolic stresses in early lactation is related to her ability to set circadian rhythms during the transition period.

Key words: homeorhesis, lactation, circadian

91 Effects of photoperiod on mammary gland development and lactation. G. E. Dahl*, S. Tao, and I. M. Thompson, *University of Florida, Gainesville.*

Photoperiod, or the daily sequence of light and dark, has dramatic effects on many physiological systems across animal species. Light patterns alter melatonin secretion profiles and subsequently the release profiles and circulating concentrations of several hormones that influence a variety of physiological responses. Although the impact of photoperiod on reproductive processes is perhaps the most common example, it is often the seasonal aspects of ovulation and anestrus that

are considered. However, in cattle, the final phase of reproduction, i.e., lactation, is significantly influenced by photoperiod. In contrast to short days (SD; 8h light:16 h dark), exposure to long days (LD) of 16 to 18 h of light and 6–8 h of darkness increase milk yield 2–3 kg/d, regardless of the stage of lactation. There is evidence that this LD effect is due to increased circulating insulin-like growth factor-I independent of any effect on growth hormone concentrations. Cows that are housed under SD during the dry period have increased mammary growth and produce 3–4 kg/d more milk in the subsequent lactation compared with cows on LD when dry. While on SD, circulating prolactin (PRL) diminishes but expression of PRL-receptor increases in mammary, liver and immune cells. Moreover, PRL signaling pathways within those tissues are affected by photoperiod. Further, replacement of PRL to cows on SD partially reverses the effects of SD on production in the next lactation. Thus, effects on dry cows are mediated through a PRL dependent pathway. Before maturity, LD improve mammary parenchymal accumulation and lean body growth which lead to greater yields in the first lactation. The accumulated evidence supports the concept that photoperiod manipulation can be harnessed to improve the efficiency of production across the life cycle of the dairy cow.

Key words: prolactin, insulin-like growth factor I, milk yield

92 Supplemental dietary phytase alters gut microbiota of weanling pigs. L. Wang and X. G. Lei*, *Cornell University, Ithaca, NY.*

Past phytase research has been largely focused on nutritional values of the enzyme, and has not explored its impact on gut microbiota of animals. The objective of this study was to determine effects of supplemental *Escherichia coli* AppA2 and *Aspergillus niger* PhyA phytases on composition changes of the 4 major intestinal bacteria in weanling pigs. A total of 30 crossbreds (3-week old, Yorkshire-Landrace-Hampshire) were allotted to 3 groups (n = 10) and fed a corn-soybean-mean basal diet (BD, supplemented with 0.35% inorganic phosphorus), the BD plus 3,500 units of AppA2/kg (Optiphos, JBS United, Sheridan, IN), or the BD plus 3,500 units of PhyA/kg (Natuphos, BASF, Florham Park, NJ) for 6 weeks. At the end, 8 pigs of each treatment group were killed to collect ileum and colon adherent samples for terminal restriction fragments length polymorphism analysis of 16s rRNA genes. After the total genomic DNA was extracted, the 16s rRNA genes were isolated using PCR with universal primer sets. Compared with the BD, both phytases increased ($P < 0.05$) *Bifidobacteria*, *Clostridium*, *E. coli*/*Salmonella*, and lactobacilli in ileum. There was no consistent effect of either phytase on any of the detectable bacteria in colon except for that pigs fed AppA2 had slightly higher ($P < 0.05$) *Bifidobacteria* content than those fed PhyA. In conclusion, both AppA2 and PhyA phytases showed a stronger impact on microbiota in ileum than in colon. Our finding reveals a novel function of phytase beyond nutrition.

Key words: microbiota, phytase, swine, T-RFLP

93 Effects of phytase on standardized total tract digestibility of P in copra expellers, palm kernel expellers, and palm kernel meal fed to growing pigs. B. L. Almaguer*[1], R. C. Sulabo[2], and H. H. Stein[2], *[1]Universidad Autónoma de Querétaro, Mexico, [2]University of Illinois, Urbana.*

A total of 66 barrows (initial BW: 27 ± 3 kg) were used to determine the effects of phytase on standardized total tract digestibility (STTD) of P in copra expellers (CE), Asian palm kernel expellers from Indonesia (PKE-IN), African palm kernel expellers from Costa Rica (PKE-CR), African palm kernel meal from Costa Rica (PKM), and in soybean meal (SBM). Pigs were housed individually in metabolism cages and allotted to a randomized complete block design with 11 diets and 6 replicate pigs per diet. Five diets were formulated by mixing cornstarch and sucrose with CE, PKE-IN, PKE-CR, PKM, or SBM. Five additional diets identical to the initial 5 diets with the exception that they contained 500 units of phytase (OptiPhos 2000, Enzyvia, Sheridan, IN) were formulated. A P-free diet was used to measure basal endogenous P losses (EPL). Feces were collected for 5 d based on the marker to marker approach after a 5-d adaptation period. Analyzed total P in CE, PKE-IN, PKE-CR, PKM, and SBM was 0.52, 0.51, 0.53, 0.54, and 0.67%, respectively. Phytate P was calculated to be 0.22, 0.35, 0.38, 0.32, and 0.44% in CE, PKE-IN, PKE-CR, PKM, and SBM, respectively. Addition of phytase increased ($P < 0.05$; SEM = 5.0) the ATTD of P from 60.6 to 80.8, 39.1 to 56.5, 38.2 to 59.9, 48.9 to 64.1, and 48.7 to 73.5% in CE, PKE-IN, PKE-CR, PKM, and SBM, respectively. The basal EPL was estimated to be 216 ± 70 mg/kg DMI. The STTD of P increased ($P < 0.05$; SEM = 5.7) from 70.6 to 90.3, 49.4 to 66.4, 48.7 to 69.9. 57.9 to 73.5, and 57.3 to 81.1% in CE, PKE-IN, PKE-CR, PKM, and SBM, respectively, with added phytase. In summary, added phytase increased P digestibility of all the test ingredients, and CE had greater STTD of P than PKE, PKM, and SBM when fed to growing pigs.

Key words: alternative feedstuffs, phosphorus, pigs

94 Supplementing a xylanase alone or a combination of xylanase and β-glucanase on growth performance, health, and nutrient digestibility of nursery pigs. Y. Han* and A. Ludger, *Nutreco R & D, Boxmeer, the Netherlands.*

It remains questionable if non-starch polysaccharide degrading enzymes should be used in pig diets. Two experiments were conducted to investigate the impact of adding a xylanase alone or a combination of xylanase and β-glucanase (XG) on nursery pigs fed a wheat-based diet. In Exp 1, 200 weaned piglets (28 d old, 7.1kg BW) were allocated to 10 blocks of 4 pens (5/pen). The 4 dietary treatments included a control diet and control with Xylanase (4000 U/kg), XG1 (xylanase 1500 U/kg, β-glucanase 200 U/kg) or XG2 (xylanase 2500 U/kg, β-glucanase 200 U/kg). All diets were pelleted and fed for 5 wks in a 2-phase program (d7–21, d22–42). In Exp 2, 32 piglets (28 d old, 8.5kg BW) were housed individually in metabolic cages. The same diets as in Exp 1 were used with 3% SiO_2 included as the marker for digestibility. A similar feeding program was followed. Fecal samples were collected in each phase and the ileal content was collected at the end of the study. In Exp 1, pigs fed the XG2 diet showed significant improvement on the cumulative feed efficiency in comparison to the control and the Xylanase diet. Compared with the control group, adding XG2 improved feed efficiency by 3.8% ($P < 0.035$). The Xylanase and XG2 treatment also reduced diarrhea incidence compared with the control ($P < 0.049$). In Exp 2, the treatment did not impact ileal digestibility. However, fecal digestibility differed significantly. Both XG1 and XG2 treatment improved ash digestibility ($P < 0.042$). Organic matter ($P < 0.004$) and NDF digestibility ($P < 0.001$) were improved by all 3 enzymes. While Xylanase and XG1 improved ADF digestibility ($P < 0.002$), energy digestibility was significantly enhanced by Xylanase and XG2. Besides, XG2 addition tended to increase protein digestibility ($P = 0.08$). In conclusion, Xylanase alone increased nutrient digestibility but failed to improve growth performance. A combination of xylanase and β-glucanase XG2 improved nutrient digestibility, feed efficiency and health of the animal.

Key words: piglets, xylanase, β-glucanase

95 Effect of different dietary calcium concentrations on the digestive and metabolic response of growing pigs to microbial phytase. X. Rousseau*[1,2], M. P. Letourneau-Montminy[3], M. Magnin[2], A. Narcy[1], and C. Pomar[3], *[1]INRA UR[83] Poultry Research, Nouzilly, France, [2]BNA Animal Nutrition, Chateau-Gontier, France, [3]Agriculture and Agrifood, Lennoxville, QC, Canada.*

An experiment was conducted to assess the effect of dietary calcium (Ca) concentration on the response of growing pigs to microbial phytase in terms of phosphorus (P) and Ca utilization at the digestive and metabolic levels. Sixty 3 pigs, for each period, were fed a 2-phase feeding experiment (25–50 and 50–80 kg BW) according to a 3 × 3 factorial arrangement in which dietary Ca (5.8, 7.2, 8.4 g/kg for phase 1 and 4.1, 5.8, 7.4 g/kg for phase 2) and microbial phytase (0, 350 and 700 FTU/kg for both phases) were provided at constant P concentrations (4.8 g/kg and 3.9 for phases 1 and 2, respectively). Pigs

were individually fed while raised in one large group. At the beginning and at the end of each period pigs were weighed and 4 pigs per treatments scanned with Dual energy x-ray absorptiometry (DXA) to estimate total body and lumbar spine region (L2-L4) bone mineral content (BMC) and density (BMD). After slaughter, femur was removed and scanned with DXA. No differences were observed among treatments for ADG and ADFI during the first feeding period, whereas during the second period ADG was depressed by dietary Ca concentration (P = 0.003) while ADG and ADFI were both increased by phytase (respectively, P = 0.036, P = 0.026). Total body and L2-L4 BMD (respectively, $P < 0.001$, P = 0.002) and BMC ($P < 0.001$, $P < 0.05$) were linearly increased by microbial phytase. Similarly, femur BMD and BMC were linearly increased by microbial phytase for first (respectively, P = 0.021; $P < 0.001$) and second (respectively, $P < 0.001$; $P < 0.001$) feeding periods. Regardless of the feeding phase, dietary Ca concentration had no effect on bone mineralization. This last criterion was improved by microbial phytase independently of Ca.

Key words: calcium, phytase, pigs

96 Effects of supplemented NSP-degrading enzymes on nutrient digestibility of diets containing wheat and wheat millrun fed to grower pigs. D. Shrestha*[1], J. Broz[2], and R. T. Zijlstra[1], [1]*University of Alberta, Edmonton, AB, Canada,* [2]*DSM Nutritional Products, Animal Nutrition and Health R&D, Basel, Switzerland.*

A critical issue of current swine production is high feed cost that might be ameliorated by co-products including wheat millrun. However, feedstuffs such as millrun have physicochemical limitations such as a high non starch polysaccharide (NSP) content. The NSP hinder nutrient digestibility but are also a potential energy source if hydrolyzed by bacteria or NSP-degrading enzymes. The objective was to determine the effect of NSP-degrading enzymes on diets containing wheat or wheat and wheat millrun on nutrient digestibility. Effects of diet (96% wheat or 56% wheat plus 40% wheat millrun) and xylanase (0 or 16,000 units xylanase and 15,600 units β-glucanase/kg of feed) were investigated in a 2 × 2 factorial arrangement with a N-free control diet for a total of 5 diets. Five pigs were fed 5 diets in a 5 × 5 Latin square. Arabinoxylans constituted 50 and 57% of the total NSP in wheat and millrun, respectively. The wheat used in this study contained 3.80 Mcal DE/kg of DM, 16% CP, and 11% NSP, whereas the millrun contained 2.90 Mcal DE/kg of DM, 17% CP, and 25% NSP. Supplementation of NSP-degrading enzymes to the wheat diet did not alter the apparent ileal digestibility (AID) of energy, AID of CP, or the apparent total tract digestibility (ATTD) of energy. Supplementation of NSP-degrading enzymes to the wheat millrun diet increased ($P <$ 0.05) the AID of energy and CP by 5% and increased ($P < 0.05$) the ATTD of energy by 5%. The improved energy digestibility of the millrun diet was supported by an increase ($P < 0.05$) of the AID and ATTD of NSP by 36 and 47%, respectively. Supplementation of NSP-degrading enzymes increased ($P < 0.05$) the content of ileal digested energy and DE of millrun by 0.34 and 0.41 Mcal/kg of DM. In conclusion, exogenous NSP-degrading enzymes match with the NSP contained in wheat millrun and can improve energy and protein digestibility of diets containing wheat millrun for grower pigs.

Key words: pig, wheat millrun, xylanase

97 Capillary electrophoresis coupled with inductively coupled plasma mass spectrometry (CE-ICP-MS) enables identification and quantification of copper and manganese glycinate complexes in enriched feed samples and the study of their bioavailability. C. Ionescu*[1], V. Vacchina[2], R. Lobinski[3], and D. Bravo[1], [1]*Pancosma, Geneva, Switzerland,* [2]*UT*[2]*A, Pau, France,* [3]*CNRS, Pau, France.*

Copper and Manganese glycinate complexes (BT Cu and BT Mn) are introduced in feeds, but up to date, there was no analytical method enabling their identification and quantification in such matrixes. The first objective was to check if capillary electrophoresis coupled with inductively coupled plasma mass spectrometry (CE-ICP-MS) could be used to do so.

Key words: traceability, glycinate complexes, feed

98 Effects of feeding tribasic copper chloride or copper sulfate on growth and efficiency of nursery pigs. E. A. Koutsos*[1], G. L. Allee[2], and T. J. Prince[3], [1]*Micronutrients, Indianapolis, IN,* [2]*PorkTech LLC, Columbia, MO,* [3]*Prince Nutrition Service LLC, Auburn, AL.*

Tribasic copper chloride (TBCC) is a covalently bonded copper source that has been shown to have significantly higher bioavailability in monogastrics and ruminants than copper sulfate ($CuSO_4$). The objective of this trial was to determine the effects of adding graded levels of copper (Cu) from TBCC on performance of nursery pigs and compare TBCC to 200 ppm Cu from $CuSO_4$. 1188 pigs weaned at 20 +/− 2 d of age were allotted by weight and sex into 48 pens (8 reps of 6 treatments, 24–25 pigs/pen). Treatments were added Cu levels from TBCC at 15, 61.25, 107.5, 153.75, or 200 ppm and 200 ppm Cu from $CuSO_4$. Pigs were fed complex diets for phase 1 (0–7 d) and phase 2 (7–21 d) and a corn-soy diet for phase 3 (21–42 d). Added Zn levels (from ZnO) were 3000 ppm in phase 1 and 2500 ppm in phase 2 and all diets contained an AGP. Increasing dietary Cu from TBCC linearly increased BW at d 7 ($P < 0.04$), d 21 ($P < 0.01$) and d 42 ($P < 0.01$). Addition of Cu from TBCC increased ADG for 0–7 d ($P < 0.02$), 0–21 d ($P < 0.01$) and 0–42 d ($P <$ 01). G:F improved linearly ($P <$ 01) with increasing Cu from TBCC for 0–42 d. Feeding 200 ppm Cu from TBCC increased BW ($P < 0.06$), ADG ($P < 0.02$), and improved G:F ($P < 0.12$) for phase 1 compared with 200 ppm Cu from $CuSO_4$. Break-point analysis showed the optimum level of Cu from TBCC to be 150 ppm for ADG at d 0–21, 143 ppm for ADG at 0–42 d, and 133 ppm for the 0–42 d G:F. Cu from TBCC is effective for improving ADG and G:F of nursery pigs.

Table 1.

Cu Source	TBCC					$CuSO_4$	Significance (P <)	
Cu level, ppm	15	61.25	107.5	153.75	200	200	Linear	Cu source
Init. Wt., kg	5.28	5.27	5.27	5.28	5.28	5.27		
D21 Wt., kg	11.44	11.51	11.80	11.87	12.02	11.94	0.01	0.70
Final Wt., kg	22.46	23.06	23.75	24.05	24.44	23.97	0.01	0.29
D0-7								
ADG, kg/d	0.13	0.13	0.14	0.14	0.16	0.13	0.02	0.02
G/F	0.81	0.76	0.80	0.84	0.77	0.68	0.22	0.12
D0-21								
ADG, kg/d	0.29	0.29	0.31	0.31	0.32	0.32	0.02	0.01
G/F	0.75	0.75	0.75	0.76	0.76	0.77	0.20	0.54
D0-42								
ADG, kg/d	0.41	0.42	0.44	0.45	0.45	0.44	0.02	0.01
G/F	0.66	0.67	0.67	0.68	0.68	0.68	0.01	0.88

Key words: copper, nursery pig, tribasic copper chloride

99 Intestinal, liver, kidney, serum and biliary Cu concentrations in piglets fed Cu proteinate or $CuSO_4$. B. Aldridge*[1], R. F. Power[2], K. A. Dawson[2], and S. Radcliffe[1], *[1]Purdue University, Department of Animal Science, West Lafayette, IN, [2]Center for Animal Nutrigenomics and Applied Animal Nutrition, Alltech, Nicholasville, KY.*

Eighty crossbred barrows were weaned at 20 ± 1 d of age and used in 2 blocks (5 reps/block) of a 2 × 3 factorial experiment to investigate the effects of Cu source ($CuSO_4$ and Bioplex Cu, Alltech Inc.) and concentration (4, 25, and 125 ppm Cu) on growth performance, serum ceruloplasmin activity and Cu concentration in proximal jejunum (PJ), liver, kidney, serum and gall bladder contents (GBC). A negative control diet containing no supplemental Cu was also fed. Pigs were blocked by BW and randomly assigned to diets offered in 2 daily feedings at 9% of metabolic BW for 14 d. The PROC MIXED procedure in SAS was used to determine the main and interactive effects of Cu source and concentration. In addition, PROC GLM linear and quadratic contrasts were determined for increasing Cu concentrations. Pig served as the experimental unit. Overall ADG and G:F did not differ between Cu sources ($P > 0.05$).However, ADG and G:F approached a positive linear trend ($P = 0.12$ and $P = 0.11$, respectively) as dietary Cu was increased from 0 to 125 ppm Cu. During wk2, ADG and G:F (227.8, 227.9, 267.1 and 260.7 g/d, $P = 0.07$; and 0.59, 0.56, 0.68 and 0.65, $P = 0.06$, respectively) tended to increase in a quadratic fashion for pigs fed 0, 4, 25, or 125 ppm from Bioplex Cu. Serum ceruloplasmin activity was not altered ($P > 0.05$) by Cu source or concentration fed. An interaction ($P < 0.02$) between Cu source and concentration was observed for serum Cu concentrations. When dietary Cu was fed at 125 ppm, serum [Cu] was 12% higher for Bioplex Cu fed pigs compared with $CuSO_4$ fed pigs was observed in the serum, compared with $CuSO_4$, though when fed. However, at 25 ppm, serum [Cu] was 10% lower for Bioplex Cu fed pigs. There were no ($P > 0.10$) interactive effects of Cu source and concentration, nor were there any effects of Cu source observed for Cu concentrations in PJ, liver, kidney and gall bladder. However, increasing dietary Cu linearly increased ($P < 0.001$) Cu concentration in the PJ, liver, kidney, serum and gall bladder contents. These data suggest that Cu from $CuSO_4$ and Bioplex Cu accumulate in a positive linear fashion in the PJ, liver, kidney and GBC, but can differ in the serum.

Key words: copper, pig, absorption

100 Effect of dietary calcium on gastric ulceration in yearling horses. C. W. Waters*[1], D. H. Sigler[1], N. D. Cohen[2], and P. G. Gibbs[1], *[1]Texas A&M University Department of Animal Science, College Station, [2]Texas A&M University College of Veterinary Medicine, College Station.*

Equine gastric ulcer syndrome (EGUS) is a complex and common disorder observed in horses used in many different events, from part-time show horses to performance and race horses. Previous studies have indicated alfalfa hay to be beneficial in reducing severity of EGUS. Due to possible buffering effect of significantly higher concentration of calcium in alfalfa hay compared with Bermuda grass hay, understanding the role of calcium in gastric ulceration is needed. The objective of this study was to evaluate the effect of high Ca diet on severity of EGUS in young horses. Nineteen yearling Quarter Horses were used in a randomized cross over study, and were fed either a high Ca (1.85%) diet or a normal (1.03% Ca) pelleted diet for 28-d periods, separated by a 21-d washout period. At the beginning and end of both periods, horses were evaluated endoscopically and EGUS scores were assigned by a veterinary practitioner using a 1–4 scoring system. Initial EGUS score averaged 1.4 at the beginning of the trial and were not different between treatment groups. Horses tended to increase (more severe) in EGUS score while confined in dry lots and individually fed either control or high Ca diet for 28-d. Diet had no effect on EGUS ($P = 0.334$), or on change in EGUS score ($P = 0.42$). The sequence in which diets were fed tended to effect EGUS score ($P = 0.095$) with a mean ulcer score of 2.3 for horses fed the treatment diet followed by control vs. 1.9 for horses fed control followed by treatment. Horses that received the control diet initially had a longer period to adjust to the lower Ca diet before being put on the high Ca diet. Reported causes of EGUS are multiple and are interrelated to stress and diet. In this study, there appeared to be little effect of added Ca on severity of EGUS. Other nutrient differences between alfalfa and coastal Bermuda grass hay warrant further investigation.

Key words: equine gastric ulcer syndrome, EGUS

101 Ovarian follicular development, luteal function, and fertility in lactating Holstein cows treated with 14dCIDR_PGF or 2xPGF_Ovsynch56 for first insemination timed AI (TAI). R. C. Escalante*, S. E. Poock, D. J. Mathew, W. R. Martin, E. M. Newsom, J. L. Denbigh, E. C. Adkins, and M. C. Lucy, *University of Missouri-Columbia, Columbia.*

Progesterone-containing devices (CIDR) inserted for 14 d can be used to presynchronize the estrous cycle in heifers before TAI ("14-day CIDR-PG" program; http://beefrepro.unl.edu). The objective was to test a similar program for lactating dairy cows. Holstein cows (n = 71; 35 to 60 d postpartum) were assigned to 2xPGF_Ovsynch56 (Control program; $PGF_{2\alpha}$, 14 d, $PGF_{2\alpha}$, 12 d, GnRH, 7 d, $PGF_{2\alpha}$, 56 h, GnRH, 16 h, TAI; n = 34) or 14dCIDR_PGF (14dCIDR_PGF program; CIDR in, 14 d, CIDR out; 19 d; $PGF_{2\alpha}$, 56 h, GnRH, 16 h, TAI; n = 37) that began on d 0 and ended on d 36 with TAI. Ultrasound exams and blood sample collections were performed on d 0, 14, 19, 26, 28, 33, and 35 and blood sampling alone was done on d 42 to monitor follicular development, ovulation and the corpus luteum. After the presynchronization step (CIDR or 2xPGF; d 0 to 14), the percentages of cows observed in estrus (47%) and having ovulation within 5 d (73%) were similar for 14dCIDR_PGF and control. The interval to estrus after CIDR removal/PGF injection (d 14), however, was less (50 ± 5 and 75 ± 5 h; $P < 0.001$) and the size of the largest follicle (LF) at CIDR removal/$PGF_{2\alpha}$ injection (d 14) was greater (20.4 ± 0.8 and 16. ± 8.8 mm; $P < 0.01$) for 14dCIDR_PGF compared with control. Plasma progesterone concentrations (P4) increased ($P < 0.001$) after the presynchronization step from 0.9 ± 0.3 (d 19) to 7.0 ± 0.3 (d 33) ng/mL. There was a tendency ($P < 0.10$) for 14dCIDR_PGF cows to have greater P4 than control from d 26 to d 33 (6.6 ± 0.6 and 5.2 ± 0.6 ng/mL for 14dCIDR_PGF and control, respectively). Diameters of the LF at $PGF_{2\alpha}$ (d 33; 15.6 ± 0.7 mm) and before the GnRH injection (d 35; 17.0 ± 0.6 mm) were similar for 14dCIDR_PGF and control. Percentages of cows ovulating (89%) and becoming pregnant after TAI (48%) were similar for 14dCIDR_PGF and control. Conclusions were that the 14dCIDR_PGF program was effective for synchronizing lactating dairy cows for TAI. Greater P4 during the luteal phase before TAI (theoretically advantageous to fertility) in 14dCIDR_PGF may be explained by the ovulation of a persistent follicle after CIDR withdrawal.

Key words: estrous synchronization, dairy, cow

102 Prostaglandin $F_{2\alpha}$ and GnRH administration increase progesterone, luteal number, and proportion of dairy cows with corpora lutea before a timed AI program. J. S. Stevenson*, S. L. Pulley, and H. I. Mellieon Jr., *Kansas State University, Manhattan.*

The objective was to increase the proportion of cows having a functional corpus luteum (CL) and elevated progesterone (P4) at the onset of the Ovsynch protocol. Postpartum Holsteins in 1 herd were stratified by parity at calving (Sep. 2009 to Oct. 2010) and assigned randomly to 2 treatments: 1) PRE (n = 134): 2 25-mg injections of PGF2α (PG) 14 d apart (Presynch); and 2) PG3 (n = 134) one 25-mg injection of PG 3 d before 100 μg GnRH (PreGnRH) with the PG injection administered at the same time as the second PG in the PRE treatment (10 d before Ovsynch). Cows were enrolled in the Ovsynch protocol (injection of GnRH 7 d before [GnRH-1] and 56 h after [GnRH-2] PG with AI 16 to 18 h after GnRH-2) 10 d after the last or only PG injection. Blood samples for P4 analysis (103 cows per treatment) were collected at d −34, −31, −20, −17, −10, −3, 0 (GnRH-2), and d 1. Ovarian structures were measured by ultrasonography on d −17, −10, −3, 0, and 7 to determine ovulation and follicle diameters. Although P4 concentration did not differ between treatments before PreGnRH injection, number of CL per cow and proportion of cows having at least 1 CL were greater for PG3 than PRE cows, and more cows ovulated after PreGnRH than ovulated spontaneously in PRE. At GnRH-1, P4 concentration, number of CL per cow, and proportion of cows with at least 1 CL were greater for PG3 than PRE. Neither follicle diameter nor percentage of cows ovulating after GnRH-1 differed between treatments. At PG injection during the week of AI, P4 concentration tended to be greater for PG3 than PRE and PG3 had more CL per cow than PRE. Pregnancy rates per AI at d 32 for PG3 vs. PRE cows were 58.2 vs. 50.0% for 103 and 106 cows inseminated during nonsummer months ($P = 0.28$) and 7.7 vs. 8.8% for 39 and 34 cows inseminated during summer ($P = 0.28$), respectively. We concluded that the PreG treatment effectively increased ovulation and luteal function 7 d before the onset of Ovsynch resulting in improved follicular synchrony and potentially predisposing improved pregnancy rates per AI in lactating dairy cows.

Table 1.

Item	PG3	PRE	*P*-value
Energy-corrected milk at AI, kg	48.1 ± 1.3	47.2 ± 1.2	
PreGnRH			
CL per cow, no.	0.6 ± 0.08	0.2 ± 0.08	0.002
Cows with CL, %	49.5	35.9	0.007
Ovulation, %	79.6	50.1	0.002
Follicle size, mm	12.6 ± 0.6	14.3 ± 0.5	0.041
GnRH-1			
P4, ng/mL	3.5 ± 0.3	2.5 ± 0.3	0.018
CL per cow, no.	1.5 ± 0.1	0.8 ± 0.1	0.001
Cows with CL, %	94.2	76.7	0.001
Breeding week PG			
P4, ng/mL	5.0 ± 0.4	4.1 ± 0.4	0.130
CL per cow, no.	2.1 ± 0.1	1.6 ± 0.1	0.001

Key words: ovulation, luteal function, presynchronization

103 Evaluation of LH release after the intrauterine administration of gnrh in lactating dairy cattle. S. Bas*, C. G. Pinto, M. L. Day, and G. M. Schuenemann, *The Ohio State University, Columbus.*

The purpose of this study was to determine the preovulatory release of LH and ovulatory response after the intrauterine (i.u.) administration of GnRH (Gonadorelin) in lactating dairy cattle. Lactating cows (n = 23) were presynchronized with 2 injections of PGF2α given 14 d apart (starting at 26 ± 3 DIM) followed by Ovsynch (OV; GnRH-7 d-PGF2α-56 h-GnRH 16 h-timed-AI; TAI) 12 d later. Ovarian structures were recorded and a blood sample collected for each animal at the time of first GnRH of OV. Only those cows presenting a CL ≥15 mm and at least one follicle ≥10 mm in diameter remained in the study. Additionally, blood samples were collected and ovarian structures recorded at the time of PGF2α of OV. At the time of the second GnRH of OV (h 0), cows were blocked by parity and randomly assigned to 1 of 3 groups: 1) control group (CON; n = 7) received 2 mL, i.m., of sterile water, 2) intramuscular group (IM; n = 8) received 100 μg, i.m., of GnRH, and 3) intrauterine group (IU; n = 8) received 100 μg, i.u.,

of GnRH. Blood samples for determination of LH serum concentrations were collected at h 0, 0.5, 1, 1.5, 2, 3 and 4. Furthermore, ultrasonography was performed twice daily (12 h interval) from h 0 to 60 for determination of ovulation. Serum progesterone concentrations at h 0 did not differ ($P > 0.05$) between groups. Concentrations of LH were greater ($P < 0.05$) in the IM than IU and CON groups at h 0, 0.5, 1, 1.5, 2, and 4 h but not at h 3 between the IM and IU group. Cows in IU started increasing LH concentrations at 1 h reaching maximum levels at 2–3 h post GnRH while LH concentrations did not increase during this period in CON cows. The proportion of cows that ovulated by h 60 was greater ($P < 0.05$) for the IM (8/8) and IU (7/8) groups as compared with CON cows (2/7). Administration of GnRH i.u. resulted in lower serum concentrations of LH than in the IM group, but the proportion of cows that ovulated by h 60 did not differ between treatments. In summary, these findings provide evidence that i.u. administration may be an alternative route of delivery for treatment with GnRH to synchronize ovulation in estrous synchronization programs.

Key words: dairy cow, intrauterine GnRH, ovulation

104 Effect of presynchronization strategy prior to ovsynch on fertility at first service in lactating dairy cows. A. Keskin[1], G. Yilmazbas-Mecitoglu*[1], E. Karakaya[1], A. Alkan[2], H. Okut[3], A. Gumen[2], and M. C. Wiltbank[4], *[1]Department of Obstetrics and Gynecology, Faculty of Veterinary Medicine, University of Uludag, Bursa, Turkey, [2]Tarfas Company, Bursa, Turkey, [3]Biometry and Genetics, Faculty of Agriculture, University of Yuzuncu Yil, Van, Turkey, [4]Department of Dairy Science, University of Wisconsin-Madison, Madison.*

The aim of this study was to evaluate the effect of presynchronization with or without detection of estrus on first service Pregnancy per Artificial Insemination (P/AI) and Ovsynch outcome in lactating dairy cows. A total of 511 cows were divided randomly but unevenly into 3 treatment groups at 44–50 d in milk (DIM). Ovsynch was started at the same time in all 3 groups (69–75 DIM). Cows in the Ovsynch group (n = 126) received no presynchronization before Ovsynch and all cows were bred by TAI. Cows in Presynch with estrus detection (PED) and Presynch with only TAI (PTAI) groups received 2 doses of $PGF_{2\alpha}$ 14 d apart starting at 44–50 -DIM- and Ovsynch was initiated 11 d after the last $PGF_{2\alpha}$ treatment. Cows in PED (n = 267) received AI if estrus was detected after either $PGF_{2\alpha}$ injection and cows that were not detected in estrus after $PGF_{2\alpha}$ received Ovsynch and TAI. Cows in PTAI (n = 118) were not inseminated to estrus with all cows receiving TAI after Ovsynch. Ovulatory response to the first GnRH of Ovsynch was different ($P = 0.002$) among treatment groups (83.1% in PTAI, 72.6% in PED, and 62.7% in CON). However, ovulatory response to the second GnRH of Ovsynch did not differ among treatments. A total 132 of 267 PED cows (49.4%) exhibited estrus and were inseminated. The P/AI at the 31 d pregnancy diagnosis was not different between cows with AI after estrus (37.8%; 50/132) or Ovsynch (34.1%; 46/135) in the PED group. The P/AI for the Ovsynch group (46.8%; 59/126) was greater than the PED group ($P < 0.05$) with Ovsynch greater ($P = 0.04$) than PED cows receiving TAI but not than PED cows bred to estrus ($P = 0.16$). The cows in PTAI had greater P/AI (55.9%; 66/118) at the 31 d pregnancy diagnosis than PED ($P < 0.01$; either estrus or TAI) and tended to be greater ($P = 0.08$) than Ovsynch. Thus presynchronization with $PGF_{2\alpha}$ (PTAI) increased ovulatory response to Ovsynch and improved P/AI in dairy cows. Interestingly, breeding of cows to estrus during Presynch reduced fertility to the TAI. These results indicate that maximal fertility is obtained when all cows receive TAI after the Presynch protocol.

Key words: dairy cow, presynchronization, Ovsynch

105 Effects of presynchronization (PRE) and length of proestrus (LP) on pregnancy per AI (P/AI) of grazing dairy cows subjected to the 5d-Cosynch protocol. E. S. Ribeiro*, A. P. A. Monteiro, F. S. Lima, R. S. Bisinotto, H. Ayres, L. F. Greco, M. Favoreto, R. S. Marsola, W. W. Thatcher, and J. E. P. Santos, *University of Florida, Gainesville.*

Objectives were to compare the effects of method of PRE and LP on fertility of grazing dairy cows subjected to the 5d-Cosynch protocol. Lactating cows (n = 1,754) were blocked by breed, parity, and d postpartum, and randomly assigned to 1 of 2 PRE protocols: Presynch, 2 injections of PGF given 14 d apart, on study d −24 and −10, and starting the timed AI protocol (TAI) 10 d later; or Double-Ovsynch (DO), study d −17 GnRH, d −10 PGF, d −7 GnRH, and starting the TAI protocol 7 d later. The TAI protocol consisted of GnRH on d 0, PGF on d 5 and 6, and $GnRH^{+}AI$ either at 58h (COS58) or 72h (COS72) after the d5 PGF. Ovaries were scanned twice before enrollment in the study. Blood was sampled and analyzed for estradiol on the day of AI. The P/AI was determined 30 and 65 d after TAI. Data were analyzed using PROC GLIMMIX. Presynch increased ($P = 0.02$) estrus at AI compared with DO (25.9 vs. 20.8%), but it did not affect estradiol concentration at AI (6.0 vs. 7.1 pg/mL), or P/AI on d 30 (59.1 vs. 56.8%, $P = 0.39$) and 65 (51.2 vs. 51.7%, $P = 0.30$) after insemination. The COS72 increased estrus (28.5 vs. 10.8%, $P < 0.01$) and estradiol concentration at AI (7.2 vs. 5.8 pg/mL, $P = 0.04$) compared with COS58. The LP did not affect P/AI on d 30 (58.7 vs. 56.1%, $P = 0.20$), but COS72 was superior ($P = 0.04$) than COS58 on d 65 (52.8 vs. 48.1%). This difference was caused by a tendency ($P = 0.08$) for interaction between PRE and LP, in which COS58 resulted in smaller P/AI in Presynch than DO cows (43.9 vs. 52.4%), whereas COS72 resulted in greater P/AI in Presynch than DO cows (54.2 vs. 51.4%). Pregnancy loss was greater for Presynch than DO (12.7 vs. 8.3; $P = 0.01$) and for COS58 than COS72 (13.5 vs. 9.4%; $P = 0.03$). Anovular cows had smaller ($P < 0.01$) P/AI than cyclic cows on d 30 (35.4 vs. 61.6%) and 65 (30.4 vs. 54.8%), but no interaction ($P > 0.50$) between cyclic status and either PRE or LP treatments were detected. Presynch and DO resulted in similar fertility, but extending the LP to 72h improved fertility in the 5-d Cosynch protocol, primarily in cows receiving Presynch.

Key words: cow, presynchronization, proestrus

106 Two- and three-wave estrous cycles in dairy cows, investigated with a mechanistic mathematical model. M. Boer*[1,3], S. Röblitz[2], C. Stötzel[2], R. Veerkamp[1], B. Kemp[3], and H. Woelders[1], *[1]Animal Breeding and Genomics Centre, Wageningen UR Livestock Research, Lelystad, the Netherlands, [2]Computational Systems Biology Group, Zuse Institute Berlin, Berlin, Germany, [3]Adaptation Physiology Group, Department of Animal Sciences, Wageningen University, Wageningen, the Netherlands.*

A normal bovine estrous cycle contains 2 or 3 waves of follicle development. However, it is unknown how the number of waves per cycle is regulated. Some studies report a better fertility of 3-wave cycles compared with 2-wave cycles, suggesting that older and larger ovulatory follicles in cycles with 2 waves contain oocytes of less quality than cycles with 3 waves. A better understanding of the endocrine mechanisms regulating follicle development is important to obtain more precise control of the estrous cycle, which can help to improve pregnancy rates. Our aim was to investigate which mechanisms are likely can-

didates for regulation of the number of waves. A mechanistic mathematical model that describes the dynamics of the bovine estrous cycle, using a set of 13 linked differential equations with 57 parameters, was developed. The model includes the processes of follicle and corpus luteum development and the working of key hormones that interact to control these processes. In the bovine, the follicle that is dominant at the moment of corpus luteum regression ovulates. Therefore, it was hypothesized that the number of follicle waves in a cycle is determined by follicle growth rate and time point of corpus luteum regression. Ten parameters related to these mechanisms were tested, of which 6 had an effect on the number of waves. The model output changed from 3 to 2 waves in a cycle when the effect of follicle stimulating hormone or of progesterone on follicle growth was changed, or when the time course of the luteal phase was changed. In the simulations, 2-wave cycles had a shorter cycle length compared with 3-wave cycles. Depending on the parameterization, the model simulated repeated as well as alternated cycles with 2 or 3 waves. Intermediate values of parameters related to follicle growth rate frequently resulted in irregularities, while gradual shifts in the length of the luteal phase often still resulted in a regular cycle. Therefore, these simulation results suggested that a cycle has a ′default′ number of waves based on follicle growth rate, which can be influenced by the time point of corpus luteum regression.

Key words: bovine estrous cycle, follicle waves, mathematical model

Production, Management and the Environment: Dairy Production I

107 A meta-analysis of the impact of stocking rate on the productivity of pasture-based milk production systems. B. McCarthy*[1,2], L. Delaby[3], K. M. Pierce[2], F. Journot[1], and B. Horan[1], *[1]Animal and Grassland Research and Innovation Centre, Teagasc Moorepark, Fermoy, Co. Cork, Ireland, [2]School of Agriculture, Food Science and Veterinary Medicine, University College Dublin, Belfield, Dublin, Ireland, [3]INRA, AgroCampus Ouest, UMR 1080, Production du Lait, Saint-Gilles, France.*

The objective of this paper is to quantify the milk production response per cow and per hectare (ha) for an incremental stocking rate (SR) change, based on a meta-analysis of published research papers. Suitable experiments for inclusion in the database required a comparison of at least 2 SRs under the same experimental conditions in addition to details on experimental length and milk production results per cow and per ha. Each additional increased SR treatment was also described in terms of the relative milk production change per cow and per ha compared with the lower base SR. A database containing 109 experiments of various lengths with 131 comparisons of SR was subdivided into: Type I experiments (common experimental lengths) and Type II experiments (variable experimental lengths). Actual and proportional changes in milk production according to SR change were analyzed using linear mixed model procedures with study included as a random effect in the model. Low residual standard errors indicated a good precision of the predictive equations with the exception of proportional change in milk production per cow. For all milk yield variables analyzed, the results illustrate that while production per cow is reduced, a strong positive relationship exists between SR and milk production per ha. A SR increase of one cow/ha resulted in a decrease in daily milk yield per cow of 7.4% and 8.7% for Type I and II data respectively, while milk yield per ha increased by 20.1% and 19.6%, respectively. Within the Type II data set, a one cow/ha increase in SR also resulted in a 15.1% reduction in lactation length (equivalent to 42 d). The low predictability of proportional change in milk production per cow according to the classical SR definition of cows/ha over a defined period suggests that SR may be more appropriately defined in terms of the change in available feed offered per animal within each treatment.

Key words: dairy cow, stocking rate, meta-analysis

108 Claw length and angle in lactating Jersey cattle, field measurements. D. J. Tomlinson*[1], L. Rodriguez[1], M. L. McGilliard[2], and K. Burgi[3], *[1]Zinpro Performance Minerals, Eden Prairie, MN, [2]Virginia Tech, Blacksburg, [3]Dairyland Hoof Care Institute Inc., Baraboo, WI.*

Low claw angle and/or long toe length may lead to development of claw lesions. Previous research and field observations indicate claws of Holstein cattle typically have an angle of 48 to 50 degrees and length of 75 to 85 mm. However, little information is available for Jersey cattle. The objective of this study was to determine length and angle of the dorsal wall of lateral claws of Jersey cows. Observations were made (n = 1654) on 7 Jersey dairy farms located in Hilmar, California. Measurement of dorsal wall angle and length were made on the lateral claw of the rear feet. Measures were made with a digital angle gauge and caliper in the milking parlor. All measures were made over the course of 3 d. Observations represented 56% first lactation cows, 20% second and 24% older animals. Mean lateral toe length of the rear claw was 71 mm with angle of 43 deg, for cows 121 d DIM and milk yield (MY; 27 kg/d). Toe length was correlated with angle −0.44, MY 0.30, and DIM 0.16. Stepwise regression of toe length, with farm and lactation number held in the model, eliminated non-significant dependent variables from a list of angle, DIM, MY, with their squares and cross-products. The model contained linear and quadratic angle, DIM and DIM*angle for an R2 = 0.49. The Glimmix procedure of SAS 9.2 indicated no interactions of these variables with farm. Our final model contained random effects of farm and residual (variances of 1.6 and 14.2), a lactation effect, and regressions on linear (−1.58) and quadratic (0.0129) foot angle, DIM (0.045) and DIM*angle (−0.00075). LSmeans for toe length were 68.6, 72.4, 74.5 mm for first through third+ lactation with SE of 0.50. Relative to average toe length, toe length at 50 DIM was 6 mm longer at 32 deg angle and 5 mm shorter at 56 degree angle, whereas toe length at 450 DIM was 15 mm longer at 32 deg angle and 4 mm shorter at 56 deg angle. There was a slight quadratic effect of angle and its interaction with DIM but no interaction with lactation number. This study demonstrated that Jersey cattle in these 7 CA dairies have a lower claw angle and shorter dorsal wall length than reported in Holstein cattle.

Key words: claw angle, claw length, lameness

109 A ranking system based on stochastic modeling to identify efficient dairy farms using farm-level inputs. A. S. Atzori*[1], A. Cannas[1], and L. O. Tedeschi[2], *[1]Dipartimento di Scienze Zootecniche, Università di Sassari, Sassari, Italy, [2]Department of Animal Science, Texas A&M University, College Station.*

A ranking system to classify dairy cow farms based on their production efficiency and profit using on-farm measurements was developed. A development database (dDB) containing 135 dairy farm from Sardinia, Italy, was gathered from Oct 09 to Sep 10. Input variables (IV, n = 18) were collected monthly either by the farmers' association (e.g., physiological stages (PS), #of lactating, dry, and culled cows, 305-d equivalent milk yield, age at first calving and culling, #of calves, and d open) or from a milk processing plant (e.g., milk sold (MkS), milk quality and price). Revenue was milk revenue plus $70/calf sold and feeding costs were based on NEl requirement and $0.195/Mcal of the diet. Income over feeding cost (IOFC, $/L) was revenue minus feeding costs. The annual average of IV for each farm was used. The distributions and correlations of IV from the dDB were used to obtain data (n = 5000) via Monte Carlo technique and stored into a database (sDB). The sDB data were used to obtain the standardized eigenvalues using the principal component analysis. Two regressions were obtained: selected principal components (PC) were regressed on the observed IOFC (REG1) and eigenvectors of the selected PC were used to compute PC values for each farm in the dDB (REG2). This computed PC values were then used with REG1 coefficients to predict IOFC, which was the ranking index (RI). Four PC were identified for milk efficiency (PS and MkS), milk quality and payment (milk quality and price), management (longevity, genetic level, SCC), and reproduction; and explained 37.4, 20.2, 15.6, and 4.4% of the sDB variance, respectively. The RI had a β distribution (mean = 0.119, SD = 0.0187) and explained 72% of the IOFC variance in the sDB. Farm allocation based on RI was 20 farms in [<-1SD], 30 in]-1SD, 0], 70 in]0, 1SD[, and 15 in [>1SD]. RI explained 79% of the IOFC variance in the dDB (root of mean square error = 0.012 $/L and 90% random errors). This approach provided a broad ranking system because it accounts for possible variability of the input variables and different weights can be used for each PC depending on the long-term goal of the dairy farm.

Key words: profitability, simulation, Monte Carlo

110 Predictors of primiparous and multiparous transition cow success from an automatic milking system. R. F. Leuer*, J. K. Reneau, J. M. Lukas, and M. I. Endres, *University of Minnesota, St. Paul*.

Analysis of performance early in lactation gives insight to future success. The objective of this retrospective study was to identify best indicators of transition success by parity and week. Lactation records (n = 191) from a Holstein dairy herd in Minnesota with a voluntary milking system were collected to identify factors associated with the success or failure of the primiparous (n = 51) and multiparous (n = 140) transition period. Metrics available were lactation number (LAC), milk production (MP), moving average production (MA), milk production average to week (MW), daily milkings (DM), milking refusals (REF), milking failures (FAI), concentrate feed consumed (CF), unconsumed concentrate feed (UCF), activity (ACT), rumination minutes (RM), and body weight (WT). Daily totals of each metric were used to calculate weekly averages. Total milk produced by 100 d was used to evaluate success of the transition period. To identify key metrics that indicate a successful transition period, best subsets regression was used to identify the combination of predictor variables for the first, second, and third week in the lactation. Fit was assessed with Mallows' Cp. Predictor variables for first week in lactation for primiparous cows ($R^2 = 0.60$), were mean MP and maximum UCF and ACT. Predictors for first week for multiparous cows($R^2 = 0.49$) were mean REF, maximum MP, CF, and UCF, and standard deviation REF and UCF. Predictor variables for second week for primiparous cows ($R^2 = 0.77$) were minimum UCF, mean MA, REF, and ACT, maximum MA, REF, FAI, and ACT, and standard deviation FAI and RM. Predictors for second week for multiparous cows ($R^2 = 0.54$) were LAC, minimum MA, maximum MA, and standard deviation of MA and DM. Finally, predictors for the third week for primiparious cows ($R^2 = 0.85$) were MW, minimum MP and RM, mean of MA and UCF, and maximum MA and RM whereas predictors for multiparous cows ($R^2 = 0.75$) were minimum WT, mean MA and UCF, maximum MA, MP, and UCF, and standard deviation of MP and UCF. Significant predictors changed week to week and between primiparous and multiparous cows.

Key words: precision dairy farming, automatic milking system, transition cow success

111 Effects of sodium bicarbonate or calcium magnesium carbonate on intake, digestibility and milk yield and composition of high producing dairy cows. R. E. Rauch*[1,2], P. H. Robinson[2], D. D. Simms[3], and L. J. Erasmus[1], *[1]University of Pretoria, Pretoria, South Africa, [2]University of California, Davis, [3]MIN-AD, Amarillo, TX.*

The rumen buffer sodium bicarbonate (SB) is a common dairy feed supplement, although recent research of its efficacy in modern low starch diets is limited. In California, new environmental regulations limit salt (including sodium) discharge from dairies. Our aim was to determine effects of SB or calcium magnesium carbonate (CMC; a potential alternative not classed as a salt), on performance of early lactation high producing Holstein cows. The study was a Latin square design with 3 periods of 28 d, 3 treatments (i.e., control (C), SB, CMC) and 3 pens of ~310 cows. The total mixed ration was supplemented with 0.8% dry matter SB or CMC, and contained 51.9% DM and 15.8% CP, 33.4% aNDF and 16.0% starch (all DM basis). Dietary cation anion difference (DCAD) for the C, SB and CMC diet was 195, 276 and 202 mEq (Na^+K-Cl^-S)/kg DM, respectively. Dry matter intake for C, SB and CMC did not differ (28.2, 28.5, 28.6 kg/d, respectively), and feed intake patterns during early (07:00–08:50 h) and late (08:50–11:00 h) morning were similar between treatments (time*treatment interaction: $P = 0.18$). The SB diet tended ($P = 0.053$) to reduce DM digestibility (63.7 vs. 65.6%) and increase ($P = 0.09$) fecal pH (6.65 vs. 6.60) compared with C. CMC cows had a higher ($P < 0.0001$) fecal pH than C cows (6.76 vs. 6.60), but digestibility did not differ. SB cows had lower ($P < 0.01$) milk yield (45.2 vs. 46.2 kg/d) and higher ($P < 0.01$) milk fat % (3.56 vs. 3.43%), but milk fat yield did not differ (1.60 vs. 1.58 kg/d) compared with C. CMC and C cows did not differ in milk yield (45.7 vs. 46.2 kg/d) or composition. Changes in body condition score were similar for C, SB and CMC (−0.08, −0.08, −0.04 units/30 d), and net energy (NEl) output (41.1, 40.9, 41.3 Mcal/d) and diet NEl concentration (1.46, 1.44, 1.44 Mcal/kg DM) for C, SB and CMC did not differ. Results suggest that SB buffered the rumen and/or improved acid base balance by increased DCAD, and that CMC buffered the abomasum and lower gastrointestinal tract. However, for diets and conditions comparable to this study, use of neither supplement is supported.

Key words: buffer, dietary cation anion difference, sodium

112 Withdrawn

113 Quantification of phytate in dairy digesta and feces using alkaline extraction and high performance ion chromatography. P. P. Ray*, C. Shang, J. P. Jarrett, and K. F. Knowlton, *Virginia Polytechnic Institute and State University, Blacksburg.*

The quantification of phytate in feed, digesta, and feces from dairy cows is important in nutrition and environmental research. Development of accurate, sensitive, robust, and inexpensive quantification methods for undigested phytate in ruminant feces and digesta samples is essential to advance knowledge of phytate degradation and phosphorus (P) excretion in ruminants. Established quantification methods give satisfactory results for feedstuffs and nonruminants manures but recovery of phytate is incomplete for ruminant feces and digesta samples because of complex sample matrix and low ratio of phytate to inorganic P. The objective was to develop a robust, accurate, sensitive, and inexpensive method to analyze phytate in wide variety of samples including ruminant feces and digesta. Diets varying in phytate content were fed to dairy heifers, dry cows and lactating cows to generate digesta and feces samples of widely varying composition to challenge extraction and quantification methods. Samples were extracted with 0.5 M HCl and 0.25 M $NaOH^+$0.05 M EDTA, independently. Acid extracts were mixed with a 20% NaCl solution, alkaline extracts were acidified to final acidity of 0.35 M and then both extracts were clarified via elution through C_{18} cartridges. High performance ion chromatography (HPIC) was used to quantify phytate. In feed samples, phytate in alkaline extracts was comparable to that in acid extracts (2965 vs 3085 μg/g DM). In digesta and feces samples, alkaline extraction yielded greater estimates of phytate content than in acid extracts (40.7 vs 33.6 and 202.9 vs 144.4 μg/g DM). Acidification and C_{18}–cartridge elution of alkaline extracts overcame the interference from sample matrix allowing HPIC analysis. Pure phytate added to dry samples before extraction was almost complete recovered (88 to 105%). This indicates higher extraction efficiency, no adverse effect of pretreatment and accurate quantification of phytate. The proposed method is rapid, inexpensive, and robust and allows more accurate phytate quantification in ruminant feces and digesta samples.

Key words: high performance ion chromatography, dairy feces, phytate

114 Use of rumen fluid to inoculate dairy excrement for bio-fuel production by anaerobic digestion. C. L. Ross*, K. C. Das, and M. A. Froetschel, *University of Georgia, Athens.*

A series of in vitro fermentations were conducted to test the viability of rumen fluid inoculations for anaerobic digestion utilizing different sources of rumen fluid, different sources of dairy excrement, and activated charcoal in buffered and un-buffered systems. To test the viability of rumen fluid to inoculate anaerobic digestion, rumen fluid from dairy cattle and fresh excrement were tested using a 3x3 factorial design. Three dilutions (w/v, H2O) of excrement were inoculated with 3 mixtures of viable and nonviable (heated to 80°C) rumen fluid (100% viable, 50:50 viable-nonviable, and 100% nonviable). A phosphate-carbonate buffer was used in buffered systems. Dry matter and gross energy digestion, volatile fatty acids, pH, and methane (CH4) production were measured after 2d and 7d incubations. All measurements were corrected for rumen fluid contributions. Results of the un-buffered system were highly variable but the effects of rumen fluid inoculation were still evident. After 2d fermentations the viable rumen fluid had 34% to 47.4% greater acetate ($P = 0.0001$) tended to produce more CH4 (67%; $P = 0.21$) than fermentations inoculated with nonviable ($P = 0.21$). 7d fermentations inoculated with viable rumen fluid produced 137.6% more CH4 when un-buffered and 182.2% more CH4 when buffered compared with fermentations inoculated with nonviable ($P = 0.07$). Another in vitro experiment using different sources of rumen fluid and activated charcoal vs. buffer to enhance anaerobic digestion was conducted. Rumen fluid inoculants from feedlot, grazing, and dairy cattle were incubated with dried dairy excrement as substrate using a 3x2 factorial design with 3 levels of activated charcoal (0%, 1.5%, and 15%) and 2 levels of buffer in 2d fermentations. Measurements were conducted as described previously. Final pH of all fermentations were above 6.0 and digestion, VFA, and CH4 were unaffected by buffer or activated charcoal indicating dried excrement was not as fermentable and as suited a substrate for modeling anaerobic digestion as fresh excrement. These results provide evidence that inoculation and buffering conditions can stimulate methane production for anaerobic digestion of dairy excrement.

Key words: anaerobic digestion, biofuel production, rumen fluid inoculation

115 Effects of corn processing method and dietary inclusion of wet distillers grain with solubles on carbon-nitrogen balance of finishing cattle. K. E. Hales*[1], N. A. Cole[1], and J. C. MacDonald[2], *[1]USDA-ARS-CPRL, Bushland, TX, [2]Texas Agrilife Research Center, Amarillo.*

The growing ethanol industry in the Southern Great Plains has increased the use of wet distillers grains with solubles (WDGS) in beef cattle finishing diets. Effects of corn processing method and WDGS on carbon (C) and nitrogen (N) balance were evaluated in 4 Jersey steers using respiration calorimetry chambers. A 2 × 2 factorial arrangement of treatments was used in a Latin square design. The factors consisted of corn processing method (steam flaked corn [SFC] or dry-rolled corn [DRC]) and inclusion of corn-based WDGS (0 or 30% on a DM basis). Thus, the 4 treatment combinations consisted of: (1) SFC-based diet with 0% WDGS (SFC-0); (2) SFC-based diet with 30% WDGS (SFC-30); (3) DRC-based diet with 0% WDGS (DRC-0); and (4) DRC-based diet with 30% WDGS (DRC-30). Diets were balanced for DIP and fat. Total C (including gaseous-C) excretion ($P < 0.01$) and methane-C ($P < 0.04$) were greater for cattle consuming DRC than SFC-based diets, and cattle consuming SFC diets retained a greater ($P < 0.01$) quantity of C than those consuming DRC diets. Inclusion of WDGS did not affect ($P > 0.52$) C balance, except that cattle consuming diets containing 30% WDGS excreted more ($P < 0.01$) C in the urine than cattle consuming diets with no WDGS. No differences in N balance were detected ($P > 0.19$) between grain processing methods, although apparent N digestibility was greater ($P = 0.02$) for cattle consuming DRC- than SFC-based diets and N retained tended ($P = 0.10$) to be greater for cattle consuming DRC than SFC-based diets. Due in part to greater N intake, cattle consuming diets containing 30% WDGS excreted more ($P = 0.01$) total N and excreted a greater ($P < 0.01$) quantity of N in the urine. Apparent N digestibility (g/d and % of N intake; $P < 0.03$) and N retained ($P < 0.05$) were also greater in cattle consuming 30 compared with 0% WDGS. From these results we conclude that finishing cattle excrete a greater amount of C when fed DRC compared with SFC-based diets, and that dietary inclusion of 30% WDGS increases urinary N excretion when diets are balanced for equal DIP concentration.

Key words: distillers grain, corn processing, nitrogen

116 Effects of corn processing method and dietary inclusion of wet distillers grain with solubles on energy metabolism and enteric methane emissions of finishing cattle. K. E. Hales*[1], N. A. Cole[1], and J. C. MacDonald[2], *[1]USDA-ARS-CPRL, Bushland, TX, [2]Texas Agrilife Research Center, Amarillo.*

Few studies have used steam-flaked corn (SFC)-based diets to evaluate the effects of wet distillers grains with solubles (WDGS) in finishing cattle diets, and a reliable estimate of the net energy value of WDGS has yet to be determined. Effects of corn processing method and WDGS on energy metabolism and enteric methane (CH_4) production were evaluated in 4 Jersey steers using respiration calorimetry chambers. A 2 × 2 factorial arrangement of treatments was used in a Latin square design. The factors consisted of corn processing method (SFC or dry-rolled corn [DRC]) and inclusion of corn-based WDGS (0 or 30% on a DM basis). Thus, the resulting 4 treatment combinations consisted of: (1) SFC-based diet with 0% WDGS (SFC-0); (2) SFC-based diet with 30% WDGS (SFC-30); (3) DRC-based diet with 0% WDGS (DRC-0); and (4) DRC-based diet with 30% WDGS (DRC-30). The diets were balanced for DIP and fat. Each Latin square period consisted of 14 d diet adaptation and 7 d of fecal, urine, and gas (oxygen consumption, and carbon dioxide and CH_4 production) collections. As a proportion of gross energy (GE) intake, grain processing method did not affect ($P > 0.12$) fecal, digestible, urinary, and metabolizable energy or heat production. In contrast, retained energy tended to be greater ($P = 0.09$) for cattle consuming SFC- than DRC-based diets. Inclusion of WDGS did not affect ($P > 0.17$) fecal, digestible, urinary, metabolizable, and retained energy, or heat production as a proportion of GE intake. Steers consuming SFC diets produced less ($P < 0.04$) CH_4 (L/kg of DMI, % of GE intake) than steers consuming DRC diets. No differences were noted ($P > 0.55$) for CH_4 production between inclusion levels of WDGS. Results suggest that cattle consuming SFC diets produce less CH_4 and retain more energy than cattle fed DRC diets; however, dietary inclusion of WDGS at 30% seems to have little effect on CH_4 production and energy metabolism when diets are balanced for DIP and fat.

Key words: distillers grain, corn processing, methane

117 Effects of spoilage of wet distillers grains plus solubles on feedlot performance. J. L. Harding*, B. N. Nuttleman, K. R. Rolfe, T. J. Klopfenstein, and G. E. Erickson, *University of Nebraska-Lincoln.*

A study was conducted using 60 individually fed crossbred steers (399 ± 30 kg initial BW) in a CRD to evaluate the impact of spoilage of wet distillers grains plus solubles (WDGS) on feedlot performance. The 3 treatments included a dry-rolled corn based diet (control) and 2 diets containing 40% WDGS replacing DRC. The WDGS was purchased from the same ethanol plant on the same day and split equally within semi-load into either an uncovered bunker (spoiled WDGS) or into a silo bag and stored anaerobically (non-spoiled WDGS). Storage occurred 38 d before the initiation of the experiment. To ensure representative quality, samples of both WDGS were collected daily after allowing the WDGS to mix alone in the truck before diet mixing. Samples were composited by week for nutrient analysis. Composition of non-spoiled WDGS was 33.4% DM, 5.6% ash, 14.8% fat, 31.7% NDF, 30.8% CP, and a pH of 4.2. Composition of spoiled WDGS was 35.2% DM, 6.4% ash, 14.1% fat, 33.3% NDF, 30.8% CP, and a pH of 4.8. Nutrient analyses on the non-spoiled and spoiled WDGS samples were used to calculate nutrient loss for the spoiled WDGS. Calculations suggest 12% of DM was lost during storage of spoiled WDGS, with 16% fat and 8% NDF also lost compared with non-spoiled WDGS. No differences were observed in mycotoxins between spoiled and non-spoiled WDGS. Feeding control, non-spoiled WDGS, or spoiled WDGS did not affect DMI ($P = 0.50$). No differences ($P \geq 0.26$) in ADG (1.39 ± 0.30 kg), final BW (571 ± 46 kg), or G:F were observed between non-spoiled and spoiled WDGS treatments with 0.135 and 0.140 observed for G:F, respectively. However, both WDGS treatments were greater ($P \leq 0.04$) in ADG, final BW, and G:F compared with control (1.17 ± 0.24 kg ADG, 550 ± 43 kg final BW, and 0.117 G:F). No differences were observed for LM area ($P = 0.35$), fat ($P = 0.86$), marbling ($P = 0.57$), or yield grade ($P = 0.67$). Even though spoiled WDGS changed in nutrient composition, it did not affect feedlot performance of finishing steers.

Key words: cattle, spoilage, wet distillers grains plus solubles

118 Effect of partially replacing barley grain with wheat bran alone or in combination with condensed liquid whey on performance of backgrounding steers. A. D. Friedt*[1], T. A. McAllister[2], B. Wildeman[3], and J. J. McKinnon[1], *[1]University of Saskatchewan, Saskatoon, SK, Canada, [2]Agriculture and Agri-Food Canada, Lethbridge Research Centre, AB, Canada, [3]Pound-Maker Agventures Ltd., Lanigan, SK, Canada.*

Debranning of wheat can increase starch throughput and thus increase the efficiency of ethanol production. It also generates a unique byproduct, wheat bran (WB) that can potentially be used as cattle feed. Few published results are available on WB as a feed source for cattle, particularly in combination with other byproducts such as condensed liquid whey (CLW). The objective of this trial was to evaluate the use of WB as a replacement for rolled barley (RB) in backgrounding diets, alone or in conjunction with CLW. Angus cross steers (n = 312, 303 ± 65 kg) were randomly assigned to 1 of 24 pens and fed 1 of 6 diets in a 2x3 factorial design. Dietary treatment included 2 levels of CLW (0 and 4.5%) and 3 levels of WB (0, 14 and 28%). Diet 1 consisted of 31.8% RB, 40.6% grass hay, 13.5% barley silage, 7.3% corn/wheat blend DDGS and 6.9% supplement (DM basis). Diet 2 was identical to diet 1 except 4.5% of RB was replaced with CLW. In the remaining diets, at each level of CLW, WB replaced RB at 14 and 28% (DM basis). Performance data over a 90 d period was analyzed as a completely randomized design with a factorial treatment arrangement with pen as the experimental unit. No ($P > 0.10$) WB by CLW interactions were detected. As well, no ($P > 0.10$) influence of CLW was seen on any performance parameter. Dry matter intake (DMI) was increased ($P < 0.01$) at each level of WB. Average daily gain (ADG) was not ($P > 0.05$) affected by treatment, however gain:feed was reduced ($P < 0.01$) at each level of WB inclusion. As a result, NE_m and NE_g of the diets, calculated based on animal performance was lower ($P < 0.01$) in the WB diets. Ultrasound l. dorsi area and subcutaneous fat thickness were not ($P > 0.10$) affected by treatment. The results of this study indicate that WB from front end processing of wheat at ethanol production facilities is a viable source of energy for growing cattle when fed with or without CLW. However, dietary NE_g concentration will be up to 16% lower when WB is fed as a replacement for RB at levels up to 28% of diet DM.

Key words: wheat bran, NE_g, backgrounding

119 Effects of wet distillers grains plus solubles on health and performance of high-risk calves. J. J. Wagner*, C. R. Krehbiel, D. B. Burken, B. K. Wilson, D. L. Step, and C. J. Richards, *Oklahoma State University, Stillwater.*

A randomized complete block design utilizing 180 high-risk crossbred yearling steers (initial BW = 212.3 ± 1.9 kg) was used to study the effects of including wet distillers grains plus solubles (WDGS) in a receiving diet on ADG, DMI, G:F, and morbidity over a 42-d period. Steers were sorted into light and heavy weight blocks and randomly assigned within block to 15 pens, each with 6 animals. Experimental treatments consisted of diets with inclusion of 0%, 15%, or 30% WDGS. Pens were considered the experimental unit and each treatment diet was fed to calves in 10 pens. Cattle were fed 2 times daily with approximately 50% of the daily allowance fed at each feeding. Feed refusals were measured following adverse weather and on weigh days. Steers were individually weighed at the start of the experiment, on d 14, and on d 42. During the experiment, 3 steers on the 0% treatment were diagnosed as chronically morbid with bovine respiratory disease (BRD) and were removed from the experiment. Average daily gain ($P < 0.20$; 0.96, 1.13, and 1.14 kg/d), DMI ($P < 0.27$; 4.75, 5.16, and 5.04 kg/d), G:F ($P < 0.79$; 0.222, 0.213, and 0.212), and animals treated for BRD ($P < 0.20$; 0.19, 0.20, 0.23) did not differ among treatments for 0, 15, or 30% WDGS, respectively. There were 3 chronics and no deaths during this experiment. Feeding WDGS receiving diets to high-risk calves did not impact animal health or performance. We conclude that up to 30% WDGS can be included in receiving diets for high-risk calves.

Key words: WDGS, high-risk calves, yearling steers

120 Effect of feeding crude glycerin on prevalence of *E. coli* O157:H7 in growing cattle. C. Aperce*, J. Heidenreich, C. J. Schneider, and J. S. Drouillard, *Kansas State University, Manhattan, Kansas.*

The objective of this study was to evaluate the effect of crude glycerin inclusion on *E. coli* O157:H7 prevalence in feces of cattle fed growing diets. Three levels of crude glycerin, 0, 4 or 8%, were added to growing diets containing dry-rolled corn, corn silage, alfalfa hay, and corn steep liquor. Each treatment was represented by 16 pens, each containing 7 to 8 heifers. Fecal grab samples were taken once/wk for 6 wk during summer of 2010. One gram of feces was incubated for 6 h at 40°C in gram-negative broth with cefixime (0.05 mg/L), cefsulodin (10 mg/L), and vancomycin (8 mg/L). One milliliter of broth was then added to *E. coli* O157 beads, subjected to immunomagnetic separation (IMS), and plated onto MacConkey agar with sorbitol, cefixime, and tellurite (CT-SMAC). After overnight incubation at 37°C, non-sorbitol fermenting colonies were picked and tested for indole production and O157 antigen agglutination. Positive colonies for both tests were confirmed as *E. coli* O157:H7 using the API 20E kit. Treatment effects and interactions were analyzed using Proc Glimmix of SAS. There was no interaction between sampling day and level of crude glycerin ($P > 0.2$). Percentages of samples that tested positive for *E. coli* O157:H7 were 1.3, 0.8, 4.3, 8.8, 4.3, and 5.8% during wk 1 through 6, respectively (effect of sampling day, $P < 0.01$). Fecal incidence rates of *E. coli* O157:H7 were 5.8, 4.3, and 2.4% for heifers fed 0, 4, and 8% glycerin, respectively (Linear, $P < 0.01$). Prevalence in heifers fed 4% glycerin tended to differ from that of cattle fed 8% glycerin ($P = 0.06$), but was not different from that of cattle fed the diet with 0% glycerin. Glycerin previously has been shown to inhibit the activity of cellulolytic bacteria in the rumen. Consequently, changes in fecal prevalence of *E. coli* O157:H7 observed in this study might be explained by alterations in gastrointestinal flora, with higher levels of glycerin producing a less favorable environment for the proliferation of pathogenic *E. coli*. Glycerin may be useful as a means of decreasing fecal prevalence of *E. coli* O157:H7 in cattle.

Key words: *E. coli* O157:H7, glycerin

121 Effects of distillers grain with soluble and supplemental copper and molybdenum on ammonia emissions and nitrogen retention. L. D. Cross*, S. R. Rust, and W. J. Powers, *Michigan State University.*

When moderate to high levels of DGS are fed, dietary CP is elevated, which may contribute to environmental pollution from increased nitrogen (N) emissions. A study was conducted to evaluate the effects of dried distillers grain with soluble (DDGS) on ammonia (NH_3) emissions. Twelve Holstein steers were housed in environmentally controlled rooms; 4 steers per dietary treatment. Three dietary treatments were fed; 0% DDGS (control), 40% DDGS, and 40% DDGS plus 6 ppm molybdenum (Mo) and 60 ppm copper (Cu) added to the diet. The

diet supplemented with Mo and Cu will be referred to as 40% DDGS plus. The study was divided into phases; phase 1 monitored emissions data for 22 d from the animal and manure (feces and urine mixture) and phase 2 monitored emissions for 4 d while steers were fitted with fecal bags to separate feces from urine. Ammonia emissions across all treatments were reduced from 74.8 mg/g N intake (NI)/d during phase 1 to 11.2 mg/g NI/d during phase 2 ($P < 0.01$). Within phase 1, both 40% DDGS diets had significantly greater NH_3 emissions at 83.0 mg/g NI/d compared with the control diets at 58.5 mg/g NI/d ($P < 0.01$). The 40% DDGS diet also differed in NH_3 emissions from 76.3 mg/g NI/d to 89.7 mg/g NI/d in 40% DDGS plus ($P = 0.05$). Total N balance was calculated from data collected during phase 2. Nitrogen intake increased from 129.8 g/d to 214.1 g/d in both 40% diets ($P < 0.01$). Nitrogen loss from gas (NH_3, NO_2, and NO^-) and feces were similar among treatments; however urine increased from 43.2 g/d to 78.1 g/d in both 40% DDGS diets ($P < 0.01$). The 40% DDGS plus diets had the greatest levels of total expelled N at 155.4 g/d compared with the control diets at 108.1 g/d. Additionally, inclusion of DDGS at 40% increased N retention from 21.7 g/d in the control diets to 69.3 g/d in the 40% DDGS diet ($P = 0.03$). The 40% DDGS plus diets had a mean N retention of 57.0 g/d, which was not significantly different from the control diets.

Key words: distillers grain with soluble, ammonia & nitrogen, molybdenum & copper

122 Effect of adding rumen degradable protein to a dried distillers grain supplement on growth performance and body composition in yearling Angus and Brangus heifers. E. N. Alava*, A. M. Monari, M. J. Hersom, and J. V. Yelich, *University of Florida, Gainesville.*

The objective of the experiment was to evaluate addition of a RDP source to a dried distillers grain (DDG) supplement in Angus (n = 30; 229 ± 4 kg) and Brangus (n = 30; 250 ± 4 kg) yearling heifers. On d 0, heifers were stratified by BW, breed, and sire to 12 pens of 5 heifers per pen and pens were randomly assigned to one of 3 supplementation treatments: DDG only (DDG), DDG plus soybean meal at 7.5% of total supplement (DDG+7.5), and DDG plus soybean meal at 15% of total supplement (DDG+15). Heifers were supplemented at a rate of 0.75% of BW, based on mean pen BW, and adjusted on a 28 d basis. All treatment groups also received ad libitum access to bermudagrass (*Cynodon dactylon*) round bale silage. Supplement was offered 3 d/wk. From d 0 to 140, BW and BCS were collected every 14 d and hip height (HH) every 28 d. On d 0 and 140 ultrasound measurements of the LM area (REA), 13th rib fat thickness (RIBFT), rump fat thickness (RMPFT), and intramuscular fat (IMF) were taken. Data were analyzed using MIXED procedure of SAS. There were no treatment differences ($P > 0.05$) in BW (351 ± 4.1 kg), BCS (5.6 ± 0.05) or HH (121 ± 0.5 cm) at d 140. Hip height was greater ($P \leq 0.05$) for Brangus than Angus at d 0 (115 ± 1.4 vs. 109 ± 1.4 cm) and d 140 (123 ± 1.2 vs. 118 ± 1.2 cm), respectively. There were no treatment differences ($P > 0.05$) for d 140 IMF, REA/100 kg BW, RMPFT, RIBFT, or ADG. However, DDG+15 (61.5 ± 1.6 cm^2) had a larger ($P \leq 0.05$) REA than DDG+7.5 (57.0 ± 1.6 cm^2) and DDG (57.2 ± 1.6 cm^2). Angus heifers had greater d 140 IMF ($P \leq 0.05$; 4.8 ± 0.2 vs. 3.1 ± 0.2 %), smaller REA ($P \leq 0.05$; 54.3 ± 1.3 vs. 62.8 ± 1.3 cm^2), smaller REA/100 kg BW ($P \leq 0.05$; 15.8 ± 0.3 vs. 17.5 ± 0.3 cm^2), and less RMPFT ($P \leq 0.05$; 0.54 ± 0.02 vs. 0.31 ± 0.25 cm) than Brangus, respectively. Final pregnancy rates were similar ($P > 0.05$; DDG = 95.0, DDG+7.5 = 78.9, DDG+15 = 80.0%) across treatments. Addition of RDP to a DDG supplement provided no additional benefit to growing yearling Angus or Brangus heifers.

Key words: *Bos indicus*, dried distillers grain, heifer

123 Feeding distillers grains containing elevated sulfur concentration depresses performance of feedlot steers. S. Uwituze[1], C. L. Van Bibber*[1], K. A. Miller[1], K. K. Karges[2], L. C. Hollis[1], J. J. Higgins[3], and J. S. Drouillard[1], *[1]Department of Animal Sciences and Industry Kansas State University, Manhattan, [2]Poet Nutrition, Sioux Falls, SD, [3]Department of Statistics Kansas State University, Manhattan.*

Crossbred yearling steers (n = 50; 462 ± 26.6 kg BW) were used in a finishing trial to evaluate effects of feeding dried distillers grains with solubles (DDGS) containing elevated sulfur levels on feed consumption, growth performance, and carcass traits. The study was a randomized complete block design with 3 treatments: chronic high S (CHS; 0.60% DM), chronic intermediate S (CIS; 0.50% DM), and sporadic intermediate S (SIS; 0.40 or 0.60% DM). Two DRC-based finishing diets (0.40 and 0.60% S) containing 30% DM of DDGS were mixed each morning. The CIS diet was made by mixing (50:50) 0.40 and 0.60% S diets. The SIS treatment consisted of intermittent feeding of either 0.40 or 0.60% S based on a random feeding schedule. The CIS and SIS treatments delivered same S content over the entire study period. Steers were blocked by weight and randomly assigned within block to treatments and 50 individual concrete surfaced pens equipped with feed bunks and water fountains that allowed free access to feed and clean water. Steers were fed once daily at approximately 0800 h and feed refusals were determined at approximately 0700 h the following day, thus making it possible to determine actual daily DMI. Steers were harvested on d 100 (n = 27) and 135 (n = 23). There were no treatment effects on carcass traits ($P > 0.10$). Treatment effects on growth performance are summarized below. Elevated dietary S depresses feed intake by feedlot cattle.

Table 1. Treatment effects on performance of feedlot steers

	Treatments				
Item	CHS	CIS	SIS	SEM	*P*-value
DMI, kg/d[1]	9.8[a]	10.9[b]	10.4[b]	0.28	0.02
ADG, kg/d	1.19	1.41	1.33	0.072	0.09
G:F	0.119	0.128	0.127	0.006	0.46
HCW, kg	381.2	391.2	390.9	5.33	0.35

[1]within a row, numbers bearing different superscripts are different, $P < 0.05$.

Key words: distillers grains, feedlot, sulfur

124 Effects of crude glycerin in byproducts diets on performance and carcass characteristics of feedlot cattle. E. H. C. B. van Cleef*[2], S. Uwituze[1], C. L. Van Bibber[1], K. A. Miller[1], C. C. Aperce[1], K. L. Blaine[1], J. J. Higgins[1], and J. S. Drouillard[1], *[1]Kansas State University, Manhattan, [2]São Paulo State University, Jaboticabal, São Paulo, Brazil.*

Crossbred heifers (n = 374; 334 ± 37 kg BW) were used to evaluate feedlot performance and carcass traits when fed diets containing 0, 7.5, or 15% crude glycerin. Treatments (5 diets) consisted of a control diet containing 31% dry-rolled corn, 10% corn silage, 35% wet corn gluten feed, 20% soybean hulls, 0.3% salt, and 3.7% supplement, and diets containing 7.5 or 15% glycerin (DM basis) with and without 0.3% salt. Glycerin replaced dry-rolled corn. Heifers were vaccinated against common viral and clostridial diseases, de-wormed, implanted,

and stratified by initial BW. Within strata, heifers were assigned randomly to 25 feedlot pens (5/treatment). Over a period of 21 d, heifers were transitioned from diets containing 50% concentrate to their respective 90% concentrate finishing diets using 4 step-up diets that contained progressively greater proportions of concentrate. Final diets provided 14% CP, 0.7% Ca; 0.5 mg/d melengestrol acetate, 300 mg/d monensin, and 90 mg/d tylosin. Zilpaterol was included in the diet starting 23 d before harvest, and fed for 20 d, and cattle were harvested on d 125. Data were analyzed using the Mixed procedure of SAS, with treatment as a fixed effect and weight strata as a random effect. Removing salt from glycerin-based diets did not impact finishing performance ($P \geq 0.50$). Glycerin did not influence ADG ($P \geq 0.3$), but resulted in a linear decrease in DMI (12.4, 11.8, and 11.3 kg/d for 0, 7.5, and 15% glycerin, respectively; $P \leq 0.01$) and a linear improvement in gain efficiency (0.148, 0.151, and 0.158; $P \leq 0.05$). Carcass weight, USDA yield grade, LM area, and % KPH were unaffected ($P \geq 0.10$) by diet. Twelfth rib fat thickness was less for heifers fed 15% glycerin without salt compared with other treatments ($P \leq 0.05$), but the remaining treatments did not differ ($P \geq 0.10$). Marbling was less for heifers fed diets containing glycerin compared with heifers fed the control diet (linear effect of glycerin, $P \leq 0.01$; quadratic effect, $P \leq 0.05$). Including glycerin in byproduct-based diets improves feed efficiency by decreasing feed intake, but also depresses marbling score and quality grade.

Key words: byproducts, glycerin, salt

125 Use of corn or crude glycerol as energy source to supplement holstein calves fed with sorghum silage ad-libitum. P. Chilibroste*[1], A. Elías[2], and J. P. Marchelli[1], *[1]Agronomy Faculty, EEMAC, Paysandu, Uruguay, [2]Instituto de Ciencia Animal, San Jospe de las Lajas, La Habana, Cuba.*

An experiment was conducted to determine the BW and DMI of Holstein calves fed sorghum silage as the only fiber source and supplemented or not with a concentrate based either in corn grain or crude glycerol as energy source. The experiment took place between October 26 and December 21 of 2010 at the Experimental Station M. A. Cassinoni, Agronomy Faculty of the Republic University in Uruguay. Data were analyzed in a completely randomized block design with a repeated measurement in time model. Twenty-four 6.6 ± 1.2 mo old Holstein female dairy calves were randomly assigned to one of the following 3 treatments: TS = whole crop sorghum silage fed ad-libitum, TSC = TS plus a corn based supplement (10g/kg LW), TSG = TS plus a glycerol based supplement (10g/kg LW). Chemical composition of sorghum silage, corn and glycerol based supplement are shown in Table 1. BW of calves at the beginning of the experiment was 181.5 ± 14.2 kg. Feeds were offered once a day and orts were collected, weighed and sampled daily before the new offer. Animals were weighed every 15 d with overnight fasting. Average daily gains (kg/day) were significantly higher ($P < 0.01$) for TSC (0.518) and TSG (0.571) than TS (0.189) while TSC and TSG were not significantly different between them. Mean silage intake (as fed) was 16.6 ± 2.84 kg/day with no significant difference between treatments neither in the mean value nor in the slope heterogeneity test . We conclude that both supplements (TSC and TSG) can be used to feed Holstein calves with similar efficiency.

Table 1. Feeds chemical composition

Fraction	Sorghum silage	Corn based supplement	Glycerol based supplement
CP %	7.0±0.67	31.6±3.2	30.3±5.6
NDF %	73.9±1.62	22.3±2.3	16.5±0.7
ADF %	45.9±2.5	9.15±1.2	9.05±2.76

Key words: corn, crude glycerol, Holstein calves

126 Substitution of distillers grains and glycerin for steam-flaked corn in finishing cattle diets on performance and carcass characteristics. J. Jaderborg*, D. M. Paulus, G. I. Crawford, and A. DiCostanzo, *University of Minnesota, St. Paul.*

This study was designed to determine the effect of substituting modified distillers grains (DGS) or soy glycerin for steam-flaked corn (SFC) in finishing diets on performance and carcass characteristics of yearling cattle. Forty-eight crossbred yearling cattle (21 steers and 27 heifers) averaging 380 kg initial BW were blocked by sex and allotted to one of 48 individual feed bunks. Nine animals were removed from the study; one for health reasons, and the others were confirmed outliers resulting from feed stealing. Cattle were fed one of 4 dietary treatments once daily at 0800. Treatments resulted from the 2 × 2 factorial arrangement of DGS at 0% or 35% of diet DM and glycerin at 0% or 10% of diet DM in SFC (0.47 kg/L flake density) and grass hay (10% of diet DM) diets: 1) DGS and no glycerin, 2) no DGS and no glycerin, 3) DGS and glycerin, 4) no DGS and glycerin. Diets contained 16.5% CP, 1.48 Mcal NEg/kg DM, 0.75% Ca, 0.47% P, and from 0.17% to 0.25% S. Dry matter intake was greater ($P < 0.003$) for cattle fed diets containing DGS than for those fed diets without DGS (9.97 vs. 8.43 kg/d). Carcass-adjusted ADG (1.41 ± 0.24 kg) was not affected ($P > 0.10$) by feeding either co-product. A tendency ($P = 0.06$) for greater carcass-adjusted G:F (0.171 vs. 0.145) was observed for cattle consuming diets without DGS . Carcass-adjusted G:F was similar ($P > 0.10$) for cattle fed glycerin and those fed no glycerin (0.157 vs. 0.159). Hot carcass weight (370 ± 28 kg), LM area (82.6 ± 6.45 cm2), 12th rib fat depth (1.40 ± 0.37cm), yield grade (2.74 ± 0.64) and marbling score (530 ± 60) were not ($P > 0.10$) affected by dietary treatment. However, KPH was greater ($P < 0.01$) for cattle fed DGS diets than for those fed diets without DGS (2.71% vs. 2.42%). Iterated ME values of diets containing DGS were 13% lower ($P < 0.05$) than those without DGS. At the inclusion levels in this study, soy glycerin had a similar energy value and DGS a lesser energy value than SFC.

Key words: cattle, distillers grains, glycerin

127 Effect of linoleic acid supplementation to Holstein dams and calves on immune measures of calves. M. Garcia*, L. F. Greco, 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 immune measures. Cows (n = 96) were fed a basal diet formulated to supply a minimum amount of LA and supplemented without fat, with saturated fatty acids (SFA at 1.75% of dietary DM, or with Ca salts of primarily unsaturated fatty acids enriched in LA (EFA; 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; LLA) or high concentration of LA (1.78% LA; HLA, DM basis) for 60 d. Milk replacer 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 was offered in ad libitum amounts starting at 31 d of age. The effect of feeding HLA-MR to calves was not influenced by fat supplementation of their dams (interaction of MR by dam diet was not detected). Calves born from cows fed fat tended ($P = 0.06$) to have a greater plasma concentration of haptoglobin (1.05 vs. 0.94 OD x 100). Blood neutrophils from calves born from cows fed EFA had greater ($P = 0.04$) mean florescence intensity for phagocytosis of *E. coli* (122 vs. 113). Concentration of WBC was not affected by diet of cows or calves, but calves fed HLA-MR had greater ($P = 0.04$) concentration of blood lymphocytes (4608 vs. 4201/uL) and tended ($P = 0.07$) to have greater concentration of eosinophils at 7 and 14 d than calves fed LLA-MR. Mean plasma concentration of acid soluble protein was lower ($P = 0.01$) for the HLA-MR group (94.3 vs. 106 ug/mL). Production of interferon-gamma by isolated peripheral blood mononuclear cells stimulated with Con-A in vitro tended ($P = 0.13$) to be increased (27.8 vs. 17.6 pg/mL) in calves fed HLA-MR. Supplementing LA to pregnant cows and to newborn calves appeared to have some pro-inflammatory effects in the calves.

Key words: calves, fat, immunity

128 Effect of replacing solvent-extracted canola meal with high-oil traditional canola, high-oleic acid canola, or high-erucic acid rapeseed meals on milk production and milk fatty acid composition in lactating dairy cows. A. N. Hristov*[1], C. Domitrovich[1], A. Wachter[1], T. Cassidy[1], C. Lee[1], K. J. Shingfield[2], P. Kairenius[2], J. Davis[3], and J. Brown[3], *[1]Pennsylvania State University, University Park, [2]MTT Agrifood Research Finland, Jokioinen, Finland, [3]University of Idaho, Moscow.*

The objective of this experiment was to investigate the effects of replacing solvent-extracted conventional canola meal (Control) with high-oil content, mechanically-extracted conventional canola meal (Canola), high-oleic, low-polyunsaturated fatty acids (FA) canola meal (HOLL), and high-erucic acid, low-glucosinolate rapeseed meal (Rape) on milk production, rumen function, digestibility, and milk FA composition in lactating dairy cows. The experiment was a replicated 4 × 4 Latin square design with 8 lactating dairy cows (109 ± 15.1 DIM). Oilseed meals were included at 12 to 13% of dietary DM. Fat and CP concentrations (% of DM) of the meals were: 3.1 and 43%, 16.1 and 32.8%, 13.7 and 45.2%, and 17.9 and 34.3%, respectively. Relative to the control, inclusion of high-oil seed meals in the diet lowered ($P = 0.006$) ruminal acetate concentration and decreased DMI (30.9 vs. 28.8 kg/d, respectively; $P = 0.001$). Milk yield was lower ($P = 0.047$) for Canola and Rape than the Control (44.9, 45.0, and 47.1 kg/d, respectively). Treatments had no effect on milk composition, other than an increase ($P < 0.001$) in MUN for HOLL. Urinary urea N losses and ammonia emission from manure were increased ($P = 0.03$) by HOLL. Replacing solvent-extracted canola meal with the high-oil meals decreased milk fat 12:0, 14:0, 16:0 and total saturated FA content and enhanced cis-9 18:1 and total monounsaturated FA concentrations ($P < 0.05$). Relative to the control, Canola increased ($P = 0.03$) total trans FA in milk, while inclusion of HOLL increased ($P = 0.009$ and 0.003) trans-11 18:1 and cis-9,trans-11 CLA content. Rape increased milk fat cis-13 22:1 content from 0.07 to 2.33 g/100 g FA. In conclusion, high-oil canola or rapeseed meals, which are likely to come from small-scale biodiesel plants where oil is cold pressed without hexane extraction, fed at levels at or above 12 to 13% of dietary DM may decrease feed intake and milk production, but can be used to alter milk FA composition in lactating dairy cows.

Key words: canola meal, rapeseed meal, dairy cow

129 Chain length of dietary saturated fatty acids affects meal patterns and plasma metabolite and hormone concentrations of cows varying in milk yield. M. Hollmann*, M. S. Allen, and D. K. Beede, *Department of Animal Science, Michigan State University, East Lansing.*

Dietary saturated medium-chain fatty acids (FA; $\leq C_{12}$) in coconut oil (CO) often depress DMI of cows but the underlying mechanisms are not well understood. Eight cows were blocked by milk yield (HIGH: 53 to 59 kg/d; LOW: 24 to 35 kg/d) and assigned to treatment sequence in a crossover design experiment. Dietary treatments were 3.35% (dry basis) of CO or saturated long-chain FA (Energy Booster 100®, EB). Diets contained 58% forage (corn silage, and alfalfa hay and haylage), 26.3% NDF, and 14.5% CP (dry basis). Periods were 27 d, and cows were milked twice and fed once daily. Blood samples were collected before feeding and hourly post-feeding for 6 h on d 17 through 20. Feeding behavior was measured from d 21 through 24. CO reduced daily DMI by 18% ($P < 0.01$) regardless of production level (interaction: $P > 0.4$) and increased the size of the first meal following feeding (conditioned meal) as a proportion of daily DMI (33 vs. 22%; $P < 0.01$) and amount (tendency: 6.0 vs. 5.2 kg; $P < 0.13$). However, hunger ratio (meal size per preceding inter-meal interval) of the first spontaneous meal following the conditioned meal tended to be lower for cows fed CO than EB (1.7 vs. 2.6 kg/h; $P < 0.07$). CO increased plasma concentrations of insulin, NEFA, and BHBA ($P < 0.01$), but did not affect glucose and glucagon concentrations compared with EB. Concentrations of insulin and BHBA did not differ between treatments before feeding but CO increased concentrations after the first meal more rapidly than EB. The rapid elevation of BHBA following the conditioned meal is consistent with increased hepatic FA oxidation for CO compared with EB. Feeding behavior results are consistent with control of feed intake by hepatic oxidation of FA because the reduction in DMI by CO was only for spontaneous meals when plasma BHBA concentration was elevated.

Key words: feeding behavior, hepatic oxidation, DMI regulation

130 Effects of different amounts of dietary protected and unprotected niacin on responses of blood metabolites to an epinephrine challenge in dairy cows. F. C. Cardoso*[1], J. Garrett[2], and J. K. Drackley[1], [1]*University of Illinois, Urbana,* [2]*QualiTech, Chaska, MN.*

Niacin may modulate lipolytic responses in adipose tissue but is highly degradable in the rumen so that oral administration leads to unknown quantities absorbed. We determined responses to epinephrine (EPI) challenge as affected by 3 levels of protected niacin (PN) or unprotected niacin (UN) in the diet or infused abomasally. Six multiparous rumen–cannulated Holstein cows (BW = 656 kg; 128 ± 23 d in milk) were used in a completely randomized 6 × 6 Latin Square with an extra period to quantify carry-over effects. Periods consisted of 7 d for adaptation followed by 7 d for measurements. Cows were fed according to NRC (2001) recommendations. Treatments were: CON, no niacin; INF, abomasal infusion of 12 g UN; N12, 12 g UN; BN3, 3 g PN; BN6, 6 g PN; and BN12, 12 g PN. Treatments N12, BN3, BN6, and BN12 were top-dressed on the TMR twice daily. Treatment INF was divided in 5 equal portions and infused every 4 h. Cows receiving treatments other than INF were infused with the same volume of water at the same times. On d 12 cows received an i.v. infusion of EPI (1.4 μg/kg BW). Blood was sampled at −45, −30, −20, −10, and −5 min before EPI infusion and 2.5, 5, 10, 15, 20, 30, 45, 60, 90, and 120 min after. Total area under the curve (AUC) responses of NEFA and glucose concentrations in plasma were calculated. Statistical analysis was performed using the MIXED procedure of SAS. Least squares means were separated using the Tukey adjustment. A quadratic effect existed among treatments BN3, BN6, and BN12 ($P = 0.01$) for NEFA AUC. Time to peak NEFA concentration tended ($P = 0.08$) to be greater for N12 (22.1 ± 3.2 min) than for BN12 (14.8 ± 3 min). For glucose, INF resulted in greater AUC than N12 ($P = 0.04$) and BN12 tended to have greater AUC than N12 ($P = 0.07$). Glucose AUC displayed a quadratic response among treatments BN3, BN6, and BN12 ($P = 0.03$). Time to peak and peak concentration of glucose, as well as NEFA peak concentration, did not differ ($P > 0.1$). In conclusion, dietary PN unexpectedly resulted in greater lipid mobilization in response to EPI challenge compared with cows receiving equivalent dietary UN.

Key words: niacin, lipolysis, epinephrine

131 Chain length of saturated fatty acids affects intake and ruminal turnover of NDF and chewing activity in lactating cows varying in milk yield. M. Hollmann*, M. S. Allen, and D. K. Beede, *Department of Animal Science, Michigan State University, East Lansing.*

Coconut oil (CO), a source of dietary saturated (90%) medium-chain fatty acids (FA; 60% of FA ≤ C_{12}), reduces DMI and NDF digestibility. To test effects of CO compared with Energy Booster 100® (EB; 90% of FA C_{16} and C_{18}; 90% saturated) on ruminal NDF turnover and pool size and chewing activity, 8 cows were blocked by milk yield (53 to 59 vs. 24 to 35 kg/d) and fed diets containing either 3.35% (dry basis) CO or EB in a crossover design. Diets contained 58% forage (55% corn silage, 45% alfalfa hay and haylage) and 26.3% NDF (86% from forage), dry basis. Periods were 27 d, and cows were fed once daily. Feeding behavior was monitored and feed ingredients, orts, and milk were sampled d 21 through 24. Rumens were evacuated and digesta sampled 4 h after feeding on d 25 and 2 h before feeding on d 27. Reported results differed at $P < 0.05$. Cows fed CO consumed 18% less DM and NDF daily compared with those fed EB and no interaction was detected between treatment and production level. However, the conditioned meal after feeding was numerically greater for CO compared with EB (6.0 kg vs. 5.2 kg; $P < 0.13$). CO decreased NDF turnover rate (3.7 vs. 4.6%/h) and increased NDF turnover time (29 vs. 23 h) compared with EB, but ruminal NDF pool size was similar between treatments. Digesta weight and volume did not differ but digesta density was greater for CO compared with EB. CO reduced molar concentration of ruminal acetate (66 vs. 80 mM) and acetate-to-propionate ratio (2.3 vs. 3.1), but not propionate (28 mM), and decreased ruminal pH post-feeding (5.3 vs. 5.7), but not pre-feeding (6.0) compared with EB. Cows fed CO spent more time ruminating (8.9 vs. 7.4 h/d) and chewing (13.2 vs. 12.1 h/d) than those fed EB. Increased turnover time may have been because CO decreased ruminal NDF digestibility and passage rate (not measured). Although CO reduced DMI while maintaining rumen pool size of digesta, lack of interaction of treatment by production level and the numerical increase in DMI for the conditioned meal do not support rumen distention as a mechanism for lower DMI for CO.

Key words: NDF digestion, saturated fatty acid, rumination

132 Performance and milk fatty acid profile of Holstein dairy cows in response to dietary fat supplements and forage:concentrate ratio. S. Kargar[1], M. Khorvash[1], G. R. Ghorbani*[1], M. Alikhani[1], and D. J. Schingoethe[2], [1]*Isfahan University of Technology, Isfahan, Iran,* [2]*South Dakota State University, Brookings.*

The objective of this experiment was to investigate the lactation performance of dairy cows fed hydrogenated palm oil and yellow grease. The experiment was conducted with alfalfa-based diets containing whole cotton seed, with different forage to concentrate (F:C) ratios being fed supplemented with hydrogenated palm oil or yellow grease. The experiment used 8 lactating Holstein cows in a replicated 4 × 4 Latin square with 3 wk periods. Treatments were: 1) no added fat and 34:66 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); or 4) 2% yellow grease and 45:55 F:C ratio (YGHF). All data were analyzed using the MIXED procedure of SAS. 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). Feeding fat and increasing F:C ratio had no effect on milk yield but fat source influenced milk yield ($P < 0.05$). Fat supplementation tended ($P < 0.06$) to increase milk fat content and yield but were not affected by increasing F:C ratio. Feeding fat and source of fat tended ($P < 0.07$) to increase and increased ($P < 0.01$) total milk fat conjugated linoleic acid without affecting desaturase indices, respectively. Fat supplementation decreased milk short-chain FA and increased long-chain FA (LCFA) with significant changes in C18:0 and cis-9 C18:1 concentration. Furthermore, YG decreased medium-chain FA and increased LCAF and total unsaturated FA of milk fat relative to HPO. Total tract digestibility of organic matter was greater ($P < 0.05$) in the YG diet than HPO, however, it was not affected by fat compared with control and also F:C ratio. Feeding yellow grease had no detrimental effects on nutrient digestibility but increased production responses and improved milk FA profile without inducing milk fat depression. Increasing F:C ratio did not affect production performance and increased saturated FAs of milk fat.

Key words: yellow grease, forage to concentrate ratio, CLA

133 Effect of a high palmitic acid fat supplement on ruminal fermentation and milk production in high- and low-producing dairy cows. D. E. Rico* and K. J. Harvatine, *The Pennsylvania State University, University Park.*

Two experiments tested the effect of fatty acid (FA) supplements on milk production and composition. In experiment 1, 24 Holstein dairy cows were blocked by production level (High > 40 kg/d and Low < 30 kg/d) and in a replicated 3x3 Latin Square design. Treatments were control (no supplemental fat), Ca-Salts of palm FA (Ca-FA; Megalac; 2.4% of DM), and free FA high in palmitic acid (PA; BergaFat F100; 2% of DM). The statistical model included the random effect of period, cow and sequence, and the fixed effect of treatment, block and the interaction of block and treatment. There was a treatment by block interaction ($P < 0.05$) for fat percent but not for milk yield or other milk components. In high producing cows, milk fat percent was not different between control and PA, but was lower for the Ca-FA compared with PA (2.87 and 3.21%, $P < 0.01$). In contrast, in low producing cows, treatment had no effect on the concentration or yield of milk fat. Treatment did not affect milk yield or DMI (42.1 ± 2.6 kg/d and 26.3 ± 1.36, respectively) in the high producing block; concentration and yield of milk components was also no affected. For low producing cows, DMI was higher in the control compared with the PA treatment (24.1 and 22.9 kg/d, $P < 0.05$), but was not different between PA and Ca-FA. In experiment 2, 16 high producing cows (>40 kg milk/d) were used in a crossover design with 14 d periods. Treatments were Ca-FA and PA fed as described above. The statistical model included the random effect of cow nested in sequence and period and the fixed effect of treatment. Milk yield was significantly higher in the PA compared with Ca-FA treatment (45.8 vs. 44.1 kg/d, $P < 0.01$). There was no effect of treatment on DMI. Yields of fat, protein, and lactose were higher ($P < 0.05$) in PA vs Ca-FA. Our results show that Ca-FA decreases milk fat content relative to PA in high producing cows but not in low producing cows. Under some circumstances, PA can increase yield of milk and of milk components.

Key words: dairy cows, palmitic acid

134 Effect of extruded flaxseed or alfalfa protein concentrate in interaction with two levels of concentrate on milk fat production. C. Hurtaud*[1], G. Chesneau[2], D. Coulmier[3], and J. L. Peyraud[1], *[1]INRA-Agrocampus Ouest UMR[1080] Production du Lait, Saint-Gilles, France, [2]Valorex, Combourtillé, France, [3]Desialis, Paris, France.*

Increasing milk omega-3 fatty acids (FA) content is desirable for human health. Our objective was to study the effect of 2 supplements rich in omega-3 in interaction with the proportion of concentrate in the diet on milk FA composition. The 2 sources of omega 3 were extruded flaxseed (FLAX, 1 kg.d^{-1}) and alfalfa protein concentrate (APC, 2 kg.d^{-1}) supplying respectively 115 and 49 g.d^{-1} omega-3 per cow. The cows were fed a corn silage based diet with 30% (C0) or 65% (C+) cereal based concentrate. The trial was carried out according a nested reversed design using 24 dairy cows averaging 117 ± 14 DIM with 2 periods of 14 d. Data were analyzed according a split plot design using proc mixed procedure. There was no significant interaction between the level of concentrate and the form of omega-3. C+ largely decreased milk fat content (−1.15 %) and yield (−301 g.d^{-1}), the proportion of saturated FA (especially C16:0, C18:0, C4:0, C6:0 and C8:0) and increased trans C18:1, (especially t9, t10 and t12). Compared with FLAX, APC increased milk fat content (0.33 %), saturated FA (especially C4 to C12, C14:0 and C16:0) and decreased cis and all trans C18:1 isomers. Actually, FLAX induced high levels of cis and trans C18:1 isomers, c9t11CLA and C18:2 isomers. Transfer rate of C18:3 from feed to milk was much higher for APC (15.3 vs 4.7%) and increased with C+ when FLAX was fed. Decrease in milk fat content with C+ is classical and is due to the large amount of concentrate that had probably increased rumen propionic acid and t10 FA. It seems that these nutrients could have had a negative additive effect on milk fat content and yield. Especially, t10 FA could have inhibited FA synthesis in mammary gland. Decrease in milk fat content with FLAX is a consequence of heat seed treatment that increases oil release in the rumen, limiting ruminal biohydrogenation and inducing more trans FA. Positive effect of APC on transfer rate could be due to its manufacturing process inducing a lipid-proteic coagulum protecting FA. The effect of nature and protection of lipids on biohydrogenation depends on level of concentrates.

Key words: concentrate, lipids, milk fatty acids

135 Abomasal infusion of butterfat during CLA induced milk fat depression in lactating dairy cows. D. Vyas*[1], U. Moallem[2], B. B. Teter[1], P. Delmonte[3], and R. A. Erdman[1], *[1]Department of Animal and Avian Sciences, University of Maryland, College Park, [2]Agriculture Research Organization, Bet Dagan, Israel, [3]U.S. Food and Drug Administration, Center for Food Safety and Applied Nutrition, College Park, MD.*

During diet induced milk fat depression (MFD), the short and medium chain fatty acids (SMCFA), which are synthesized de novo in the mammary gland, are reduced to a much greater extent than the long-chain fatty acids(LCFA) which originate from the diet. Our hypothesis was that increased availability of SMCFA might rescue conjugated linoleic acid (CLA) induced MFD in lactating dairy cows. To test that hypothesis, 4 rumen fistulated lactating Holstein cows (128 ± 23 DIM) were used in 4 × 4 Latin square design with 3 wk experimental periods. Treatments were applied in 2 × 2 factorial arrangement during the last 2 wk of each period and included abomasal infusion 3X daily of a total of: 1) 230 g/d of long chain FA (LCFA, blend of 59% cocoa butter, 36% olive oil and 5% palm oil); 2) 420 g/d butterfat (BF); 3) 230 g/d LCFA with 27 g/d CLA (LC-CLA) containing 10 g/d of t10, c12 CLA and 4) 420 g/d butterfat with 27 g/d CLA (BF-CLA). Data were analyzed using Mixed procedure in SAS using treatments as fixed whereas period and cows as random factors in the model. $P \leq 0.05$ was considered statistically significant. Butterfat provided 50% of C16:0 and similar amounts of C18 FA as found in LCFA such that the difference between the BF and LCFA treatments were 190g/d SMCFA. No effects were observed on DMI or milk yield. Milk fat content was significantly reduced ($P = 0.001$) by 41% with LCCLA and 32% with BF-CLA and milk fat yield was reduced ($P < 0.001$) by 41% and 38% with LCCLA and BF-CLA compared with their respective controls. Milk FA composition showed significant reduction of de-novo synthesized FA (DNFA) with CLA infusion. Milk fat percent and DNFA yields were greater for BF-CLA compared with the LC-CLA ($P = 0.09$). In conclusion, the increased availability of SMCFA from BF during CLA induced MFD was able to rescue 21% and 7% of milk fat content and yields, respectively but differences were not significant. Milk fat responses suggest potential limitation of SMCFA however increased availability of the respective FA might not completely rescue MFD.

Table 1.

Item	BF	BF-CLA	LCFA	LC-CLA	SEM
DMI (kg/d)	24.9	24.0	25.4	22.6	1.26
Milk yield (kg/d)	49.2	46.0	47.9	46.9	5.84
Milk fat (%)	3.38[a]	2.30[b]	3.36[a]	1.99[b]	0.21
Milk fat yield (g/d)	1640[a]	1013[b]	1600[a]	937[b]	169.7
De-novo FA (%)	43.27[a]	38.64[b]	42.57[a]	36.07[b]	1.52
De-novo FA (g/d)	710[a]	396[b]	686[a]	344[b]	82.5

Key words: milk fat, de novo synthesis, lactation

136 The partial replacement of soya and rapeseed meal with urea or a slow release urea source (Optigen) and its effect on intake, performance and metabolism in dairy cows. L. A. Sinclair*, P. Griffin, G. H. Jones, and C. W. Blake, *Harper Adams University College, Newport, Shropshire, UK.*

The objectives of the study were to determine the effect of partially replacing soya and rapeseed meal with urea or a slow release urea source (Optigen; Alltech UK) on the intake, performance and metabolism in dairy cows. Forty-two Holstein-Friesian dairy cows were allocated to one of 3 treatments in each of 3 periods of 5 wk duration in a Latin square design. The first 28 d of each period allowed adaptation to the dietary treatments with measurements during the final 7 d. Cows receiving the control treatment (C) received a mixed ration that included (DM basis) 38% corn silage, 18% grass silage, 29% concentrates and 15% of a 60:40 mix of soya and rapeseed meal. Cows on the Urea (U) or Optigen (O) treatments received the same basal ration but with the replacement of 1.1 kg/cow/d of the soya/rapeseed meal mix with either 100 g of feed grade urea or 110 g of Optigen respectively. There was no effect ($P > 0.05$) of treatment on dry matter intake or milk yield (mean values of 22.5 and 33.9 kg/d respectively). There was a trend ($P = 0.09$) for cows fed U or O to have a higher milk fat content (average of 40.1 g/kg for U and O vs. 38.9 g/kg for C). Milk true protein concentration and yield were not affected by treatment ($P > 0.05$) but milk urea content tended to be lower ($P = 0.07$) in cows fed C compared with U or O. Hourly plasma urea concentrations were higher ($P < 0.05$) in cows fed U and lowest in C, but there was no effect ($P > 0.05$) of treatment on plasma ammonia levels. Cows fed O had a higher ($P < 0.01$) efficiency of N use (kg milk N/kg N intake) and food conversion ratio (kg fat-corrected milk/kg DM intake) ($P < 0.001$) and tended ($P = 0.07$) to have a higher live weight gain than those fed C, with cows receiving U having intermediate values. In conclusion, the replacement of a mixture of soya and rapeseed meal with feed grade urea or Optigen can be achieved without affecting milk performance, with N and feed efficiency being higher and live weight gain tending to be higher in animals fed Optigen compared with a soya/rapeseed meal mixture.

Key words: dairy cow, slow release urea, performance

137 Effect of added fat to diets for dairy cattle on production performance and dry matter intake. A. R. Rabiee[1], K. Brienhild[1], W. Scott[1], H. M. Golder[1], E. Block[2], and I. J. Lean*[1], *[1]SBScibus, Camden, New South Wales, Australia, [2]Church & Dwight Co. Inc., Princeton, NJ.*

It was hypothesized that effects of different dietary fats on production performance of dairy cattle differ and are influenced by diet composition. Literature provided 39 studies containing 86 comparisons of control diets to diets with different fat sources. Only randomized controlled trials were included, if these provided: information on fat treatment and diet, data on outcomes of interest and a measure of variance. Fats were evaluated in 5 groups; tallow and greases; oilseeds (cotton, soy, sunflower), Ca salts of palm fatty acids (Capalm), other Ca salts (fish, linseed, flaxseed and others), and prilled fats. Statistical evaluation used a random effects analysis to estimate the effect size (ES) and 95% confidence interval (95% CI) for milk, fat and protein yields and DMI. The ES in milk production was increased 0.265 (95%CI = 0.101 to 0.429; $P = 0.002$) and the weighted mean difference (WMD) was 0.659 kg per day (95% CI = 0.115 to 1.203). Increase in ES for Capalm, oilseeds and other Ca-salts were significant ($P < 0.1$). Milk fat yield ES was 0.144 (95% CI = −0.010 to 0.298; $P = 0.07$) and the WMD was 0.03 kg per day (95% CI = 0.004 to 0.051). ES for fat yield was positive ($P < 0.05$) for CaPalm and Oilseeds, ES for milk protein yield was −0.004 (95% CI = −0.198 to 0.191; $P = 0.971$) and the WMD was −0.006 kg per day (95% CI = −0.022 to 0.010). The ES for DMI was −0.335 (95% CI = −0.467to −0.202, $P < 0.0001$). The WMD for DMI was −0.571 kg per day (95% CI = −0.851to 0.290). These results, were heterogenous ($P < 0.002$), indicating that responses were not consistent across trials. Responses among different fat sources varied. All fat sources negatively affected DMI. The largest effects on WMD were from Tallow and other Ca-salts at −0.8 and −1.7 kg/d, respectively. Univariate meta-regression analysis showed that the different fat sources were not sources of heterogeneity for milk yield ($P = 0.658$), and milk protein yield ($P = 0.681$), but were for milk fat yield ($P = 0.002$) and DMI ($P = 0.052$). This study provides good evidence that use of fats improves the efficiency of milk production performance, but results are influenced by types of fat used and other factors.

Key words: dietary fats, meta-analysis

138 Effect of dietary fat blend and monensin supplementation on dairy cattle performance, milk fatty acid profiles and milk fat depression. M. He[1], K. L. Perfield[2], H. B. Green[2], and L. E. Armentano*[1], *[1]Department of Dairy Science, University of Wisconsin-Madison, Madison, [2]Elanco Animal Health, Greenfield, IN.*

The effect of feeding increasing levels of $C_{18:1}$ and $C_{18:2}$ both independently and together, with or without monensin, was evaluated. Fifty-six Holsteins were blocked by parity. Pairs of cows (1 high and 1 low production) of the same parity were assigned to a single feeding station and cow pair was the experimental unit. Cow pairs were assigned to monensin (15.9 g/ton DM) or control as main plot. The 7 cow pairs in each of the Monensin/Parity groups were further assigned to a sequence of fat blend diets as split plot. Seven fat blend treatments in the split plot 7 × 7 Latin Square were no added fat (NoFAT), or diets with increasing levels of $C_{18:1}$ or $C_{18:2}$: 1.0% $C_{18:1}$, 1.5% $C_{18:2}$ (LOLL); 1.0% $C_{18:1}$, 2.7% $C_{18:2}$ (LOML); 1.0% $C_{18:1}$, 3.9% $C_{18:2}$ (LOHL); 2.1% $C_{18:1}$, 1.5% $C_{18:2}$ (MOLL); 2.2% $C_{18:1}$, 2.7% $C_{18:2}$ (MOML); 3.3% $C_{18:1}$, 1.5% $C_{18:2}$ (HOLL). Each period had 21 d with last 4 d for sample collection. Data reported were analyzed using the mixed model of SAS (Y = covariate + monensin + parity + monensin × parity + fat + fat × monensin + fat × parity + period + period × monensin + period × parity + production). Monensin feeding did not affect milk fat concentration and yield but decreased the proportion of $C_{<16}$ (21.0 vs. 22.9%), increased the proportion of total C_{18} (49.7 vs. 47.7%), increased the proportion of t-10, c-12 CLA (0.07 vs. 0.05%), and increased the proportion and yield of t-10 $C_{18:1}$ (5.2 vs. 3.5% and 40.0 vs. 28.1 g/d, respectively) in milk FA. As either $C_{18:1}$ or $C_{18:2}$ increased beyond these 2 FA present in LOLL, milk fat concentration and yield and milk $C_{<16}$ yield decreased, and milk t-10 $C_{18:1}$ yield increased. When dietary total FA and FA other than $C_{18:1}$ and $C_{18:2}$ were similar,

$C_{18:2}$-rich diets decreased milk fat yield compared with $C_{18:1}$-rich diets (LOML vs. MOLL; LOHL vs. HOLL), indicating that $C_{18:2}$ is more potent than $C_{18:1}$ on milk fat depression. Increasing dietary FA content from NoFAT to LOLL, which increased primarily $C_{18:1}$ and $C_{18:2}$, reduced the yield of $C_{<16}$ while increasing total C_{18} yield in milk. Few significant monensin × fat interactions were detected on milk composition parameters analyzed.

Table 1. Effect of fat blend on dairy cattle performance and milk FA profiles

	NoFAT	LOLL	LOML	LOHL	MOLL	MOML	HOLL	SEM
DMI, kg/d	23.8^{ab}	24.1^{a}	23.3^{ab}	22.6^{b}	23.9^{ab}	23.5^{ab}	23.5^{ab}	0.5
Milk yield, kg/d	33.7^{abc}	35.8^{a}	34.0^{ab}	30.6^{c}	35.2^{ab}	32.5^{bc}	33.6^{abc}	1.4
Fat yield, kg/d	1.17^{a}	1.13^{a}	0.84^{cd}	0.74^{d}	0.98^{b}	0.79^{d}	0.91^{bc}	0.04
Fat %	3.50^{a}	3.17^{b}	2.54^{de}	2.47^{e}	2.88^{c}	2.46^{e}	2.76^{cd}	0.08
Milk FA yield, g/d								
$C_{<16}$	364^{a}	289^{b}	164^{d}	116^{e}	216^{c}	135de	172^{d}	15
Total C_{18}	334^{c}	423^{ab}	416^{ab}	393^{bc}	460^{a}	424^{ab}	466^{a}	22
t-10, c-12 CLA	0.3^{d}	0.4^{cd}	0.5^{bc}	0.8^{a}	0.4^{cd}	0.6^{ab}	0.5^{bcd}	0.1

$^{a\text{-}e}P < 0.05$.

Key words: oleic, linoleic, monensin

ADSA-SAD Dairy Foods Undergraduate Competition

139 Milk fats in the American diet. R. Pomeroy*, *North Carolina State University, Raleigh.*

The USDA-FNS [United States Department of Agriculture - Food and Nutrition Services] has recently proposed a rule to revise the Nutrition Standards in the National School Lunch and School Breakfast Programs, this revision is based on the 2005 USDA - HHS [Health and Human Services] Dietary Guidelines for Americans, and consistent with the recently released 2010 edition. One of the rulings requires schools to include either fat-free or 1% milk instead of the variety of milk fats offered currently as part of reimbursable meals. Compiled information from many scientific reviews, USDA abstracts and primary sources examine the potential health benefits of milk fats and the health concerns of whole milk. The USDA suggests 3 servings of fat-free or low fat dairy products per day; this suggestion is consistent with the objective to decrease obesity and blood cholesterol levels in Americans, which could contribute to cardiovascular disease. The opposing concern on this issue relates to the potential health benefits of milk fats; such as anti-carcinogen effects and the availability of good unsaturated fatty acids. There are many differing opinions for the nation's health at large, and the implications of this research shows that while some individuals may benefit from the extra energy provided from the fats in whole milk, most Americans do not need these extra calories in their daily food pattern.

Key words: skim milk, whole milk, milk

140 Fortification of omega-3 milk. K. C. Smith*, D. R. Winston, B. A. Corl, and K. M. Waterman, *Virginia Polytechnic Institute and State University, Blacksburg.*

Omega-3 fatty acids (n3) are polyunsaturated fatty acids essential to the human diet. Omega-3 fatty acids have been proven to play major roles in various functions of the body, such as brain development, prevention of cardiovascular disease, Alzheimer's disease and depression. Examples of n3 fatty acids include docosahexaenoic acid (DHA), docosapentaenoic acid (DPA), eicosapentaenoic acid (EPA), eicosatetraenoic acid (ETA) and stearidonic acid (SDA). Adequate intakes of n3 fatty acids (g/d) for adults consuming a 2000 kilocalorie diet are 6.67 for α-linolenic acid and approximately 0.22 for both DHA and EPA. These n3 fatty acids cannot be made by consuming α-linolenic acid, an essential fatty acid only synthesized by plants. Very long chain n3 fatty acids are also obtained from fish including tuna or salmon. Milk can be fortified with n3 fatty acids by fortifying at the plant or by supplementing the cow's diet. However, both these processes have complications. Marine oil additions to processed milk often add an off-flavor and smell, and consumers tend to shy away from a product that is not sensually stimulating. Marine oils or genetically modified soybeans supplemented into the diet of the dairy cow can supply n3 fatty acids, but rumen microbes tend to biohydrogenate unprotected polyunsaturated fatty acids, resulting in absorption of saturated fatty acids. Long chain n3 fatty acids also have poor transfer into milk fat reducing total absorption into milk. Fortifying milk with n3 fatty acids may not be as beneficial as enriching other agricultural commodities such as eggs or chicken because of off flavors, expense of rumen-protected feeds, and lack of transfer efficiency into milk.

Key words: omega-3, fortification

141 The promise of bovine lactoferrin for breast cancer prevention. E. Schaffel* and J. Fain, *Clemson University, Clemson, SC.*

Studies have shown the numerous benefits of milk and other dairy products on human health. In particular, bovine lactoferrin (bLF), an iron-binding whey protein, has been discovered to act as an antiviral, antifungal, anti-inflammatory, antioxidant, and antiparasite agent. In addition to milk, lactoferrin can be found in other tissues or secretions, such as tears, saliva, and blood. In the past several years, researchers have encountered the protein's ability to inhibit the growth of certain tumors and metastasis. Cancer is a result of several alterations in normal cells: the ability to be self sufficient in growth signals; to avoid antigrowth signs and apoptosis; to obtain an endless ability to replicate; to maintain angiogenesis; to evade tissues; and to form metastases. In one research trial, rodents receiving oral administration of bovine lactoferrin experienced significantly reduced tumorigenesis in varying organs (esophagus, tongue, lung, liver, colon, and bladder). This shows promise for future human health benefits as last year, over one million people were diagnosed with breast cancer and 460,000 people died of breast cancer worldwide, making it the second leading cause of cancer death in women and on the top 10 causes of death in high income countries worldwide. In a recent study, lactoferrin's tumor suppressing properties were observed on 2 types of human breast cancer cells: HS578T and T47D, the more aggressive form being the HS578T cells. The cells were either treated or untreated for varying periods of time with differing lactoferrin concentrations, which ranged from 0.125 μM to 125 μM. Researchers studied cell viability, apoptosis, migration, and proliferation. Although the specific results from each of these areas differed and the exact mechanisms are not completely understood, overall results highlight the whey protein's disruptive effects on vital steps in cancer development. Increasing research on the benefits of bovine biologically active food components have helped scientists better predict preventative methods to inhibit the spread of chronic diseases and show promises for combating the breast cancer epidemic.

Key words: bovine lactoferrin, breast cancer, prevention

142 Market research to boost dairy product demand. A. N. Waldeck*, *University of Kentucky, Lexington.*

Market research can provide dairy processors with knowledge to boost dairy product sales. Asking consumers about new products, improved products, and product positioning helps to generate more dairy industry revenue. Over the past 25 years, total dairy product consumption has increased while fluid milk consumption has decreased. The dairy checkoff program creates new partnerships to increase dairy product demand. The dairy industry has partnered with other corporations to boost sales through mutually beneficial marketing arrangements. Starbucks, Yoplait, and McDonald's all have incorporated dairy processing technology to ensure that dairy products remain a prominent ingredient in each of these company's product lines. The dairy industry has also partnered with Domino's and McDonald's to increase cheese consumption. For example, 2 slices of cheese are included on each McDonald's Angus Third Pounder. This item was only supposed to be on the menu for a limited time, but the product was popular enough that it is now on the menu permanently. An estimated 532 million pounds of milk is used annually for this product alone. Pizza companies purchase 25 percent of the cheese produced in the United States (DMI 2009 Annual Report). Domino's was the first pizza chain to add

extra cheese to their pizzas. As other pizza chains have observed the increase in sales resulting from this change, the number of chains offering and promoting extra cheese on the menu has increased. Market research also allows dairy processors, such as Dean Foods, to generate valuable information about targeted market segments. This information can be used to refine and focus advertising, promotion, and new product launches to these targeted populations to increase revenues. This research may also be helpful in communicating human nutrition benefits of dairy products. Market research is a multi-step process that requires considerable planning to ensure that effective information is collected and used. Market research has and will continue to contribute to dairy product consumption through product innovations, corporate collaborations, and marketing campaigns.

Key words: market research, dairy product demand, consumer

143 Dairy super foods: Antioxidants could make the difference. S. B. Weimer* and D. R. Olver, *Pennsylvania State University, University Park.*

Antioxidants are substances that reduce oxidative damage caused by free radicals, which are highly reactive molecules or atoms that attack and modify the chemical structure of cells. Because of the damages they prevent, antioxidants have been linked to fighting cancer, heart disease, and even aging. Foods naturally rich in antioxidants and those fortified with antioxidants are becoming more popular. Dairy foods are entering the antioxidant race. Fortifying dairy products such as yogurt with antioxidants has the potential to bolster sales by providing an even more appealing value-added product. Foods such as yogurt may be excellent carriers for antioxidant extracts because dairy products have the ability to mask the bitter taste of certain antioxidants. In a Uruguayan study (Ares et al., 2009), researchers compared sucrose, sucralose, polydextrose, and milk for their abilities to reduce the bitterness, astringency, and characteristic flavors of antioxidant extracts from 2 native plants. The study found that each reduced the strong flavors of the antioxidants, but that effectiveness was dependent on the type and concentration of the antioxidant extract being considered. For one of the plant extracts, milk was most effective at masking bitterness and astringency; however, for the other plant extract, sucrose was the best inhibitor of strong flavors. As a result, the study concluded that "sweetened dairy products could be interesting carriers for the development of functional foods containing polyphenolic-rich antioxidant extracts." Development of antioxidant enhanced food products is rapidly increasing. Mintel, a market research company, reported an increase of 1,616 products in the antioxidant-enhanced food and beverage category between 2005 and 2009. Companies from across the world and in the United States are beginning to offer dairy products with added antioxidant benefits.

Key words: antioxidants, dairy product innovation

144 What you don′t know can hurt you: Unlocking the secrets of milk. T. Hippman*, *Louisiana State University, Baton Rouge.*

Milk and milk products are an excellent source of vitamins and minerals. Vitamins in milk include vitamin A, thiamin, riboflavin, niacin, and vitamin B6. Minerals contained in milk include calcium, phosphorous, potassium, copper, iron, and zinc. A lack of these in the diet can cause a variety of problems such as paralysis, osteoporosis, hypertension, blindness, skin problems, irritability, and fatigue. Milk is an ideal source of these vitamins and minerals, not only because it is rich in them, but also because it contains them in the proper ratios to facilitate absorption. Of these vitamins and minerals, research has shown calcium and vitamin D to be extremely important in the diet. Research shows that vitamin D deficiency and rickets are re-emerging as health problems in infants and children. Therefore it is extremely important to maintain a healthy intake of milk and milk products on a daily basis to reduce the risk of a vitamin or mineral deficiency and thus the potential occurrence of disease.

Key words: vitamins, minerals, milk

Graduate Student Competition: ADSA-ASAS Northeast Section

145 The effect of an exogenous amylase on performance and total tract digestibility in lactating dairy cows. M. M. McCarthy*[1], M. A. Engstrom[2], E. Azem[3], and T. F. Gressley[1], *[1]University of Delaware, Newark, [2]DSM Nutritional Products Inc., Parsippany, NJ, [3]DSM Nutritional Products, Ltd., Basel, Switzerland.*

The objective of this trial was to determine performance and digestibility response of lactating dairy cows to a reduced starch diet containing a commercial amylase product. Twenty-six Holstein cows (82 ± 60 DIM) were blocked by parity and DIM and assigned to treatments in a 3 × 3 Latin square design, with 28-d periods. Treatments were normal starch TMR (NS), reduced starch TMR (RS), and reduced starch TMR with exogenous amylase (RSE). The hypothesis was that RS would decrease milk production and diet digestibility compared with NS and that RSE would alleviate some of this decrease. Rations were 41% concentrate and the NS TMR contained 12.8% corn grain, 2.9% soyhulls, and 2.9% citrus pulp. The RS and RSE TMR contained 6.0% corn grain, 6.9% soyhulls, and 6.9% citrus pulp. Starch concentrations in NS, RS, and RSE TMR were 27.5, 23.2, and 22.4%, respectively. Milk production and DMI were measured daily and milk composition was measured weekly. Fecal grab samples were collected at the end of each period and digestibility of DM and nutrients were determined. Data were analyzed using a mixed model containing the fixed effects of treatment, week, period, and their interactions, and the random effects of cow and block. Contrast statements were used to evaluate effects of dietary starch (NS vs. RS + RSE) and enzyme (RS vs. RSE). There was no effect of starch or enzyme on DMI, milk composition, or starch digestibility ($P > 0.10$). Increased dietary starch increased yields of milk (47.6 vs. 46.2 kg/d, $P = 0.03$), protein (1.38 vs. 1.34 kg/d, $P = 0.03$), and lactose (2.25 vs. 2.18 kg/d, $P = 0.02$) and tended to increase fat yield (1.33 vs. 1.28 kg/d, $P = 0.02$). Addition of amylase did not affect any production parameters. Increased starch reduced NDF digestibility (41.4 vs. 47.0%, $P < 0.01$). Addition of amylase increased digestibility of DM (72.1 vs. 70.1%, $P = 0.02$) and CP (73.4 vs. 71.1%, $P = 0.05$), and tended to increase OM digestibility (73.4 vs. 72.0%, $P = 0.10$). Although addition of exogenous amylase increased nutrient digestibility in a low starch TMR, this was not reflected by improved animal performance.

Key words: amylase, starch, by-product feeds

146 Spoilage yeasts in silage have the potential to directly impact rumen fermentation. M. C. Santos*[1], A. L. Lock[2], G. D. Mechor[3], and L. Kung Jr.[1], *[1]University of Delaware, Newark, [2]Michigan State University, East Lansing, [3]Elanco Animal Health, Greenfield, IN.*

Yeasts associated with aerobic spoilage of high moisture corn (HMC) and corn silage (CS) were isolated and characterized to determine their potential for direct effects on rumen fermentation. Samples were obtained from 21 US dairy farms; HMC averaged 6.3 and CS averaged 5.4 $\log_{10}$ cfu of yeasts/g of fresh forage. *Candida valida* (CV) was the most predominant species accounting for 35 and 31% of total isolates in HMC and CS, respectively. One isolate of CV was added to in vitro culture tubes containing TMR, buffer and rumen fluid at theoretical concentrations of 0, 4.4, 6.4 and 8.4 $\log_{10}$ cfu/ml; the 6.4 dose was equivalent to a cow consuming 30 kg of fresh CS with 7.0 $\log_{10}$ cfu/g. After 12 and 24 h of incubation at 39°C, samples were analyzed for pH, yeast number, NDF-D, volatile fatty acids (VFA) and fatty acids (FA). Culture pH declined from 6.8 at 0 h to 6.4 and 6.3 after 12 and 24 h, respectively ($P < 0.01$). After 24 h, numbers of viable yeasts for the control treatment decreased from 2.4 to 0.4 $\log_{10}$ cfu/ml. For the other levels, the measured numbers at time 0 decreased from 4.0, 5.9 and 8.1 to 2.2, 3.9 and 5.3 $\log_{10}$ cfu/ml after 24h, respectively. Inoculation with CV caused a linear decrease in NDF-D at 12 and 24 h ($P < 0.01$). After 12 h, NDF-D for the highest CV addition was 34 vs 44% for control and after 24h NDF-D was 52 vs 58%. At 24 h, the concentration of total VFA, acetate and propionate was 106, 57 and 29 mM for the highest CV dose whereas for control the concentrations were 98, 53 and 25 mM, respectively ($P < 0.05$). FA analysis of CV indicated that it contained ~25% SFA, 60% cis MUFA, and 15% cis PUFA. Overall, the biohydrogenation of unsaturated FA was not altered across treatments and declined over time with an increase in the accumulation of SFA, especially stearic acid; under the conditions tested, CV did not alter the formation of BH intermediates. The results of this study indicate that addition of CV, especially in high levels, can decrease NDF-D and may alter the concentration of propionate and acetate. However, no changes in the production of BH intermediates were detected under the in vitro conditions tested.

Key words: *Candida valida*, NDF-D, biohydrogenation

147 The effects of PPAR-gamma agonist and conjugated linoleic acid on mammary and hepatic lipid metabolism in lactating mice. D. Vyas*[1], B. B. Teter[1], P. Delmonte[2], and R. A. Erdman[1], *[1]Department of Animal and Avian Sciences, University of Maryland, College Park, [2]U.S. Food and Drug Administration, Center for Food Safety and Applied Nutrition, College Park, MD.*

Previous studies have demonstrated the antagonizing effects of PPAR-gamma agonists on conjugated linoleic acid (CLA) induced hepatic steatosis and adipose tissue lipodystrophy. We hypothesized that the PPAR-gamma agonist, Rosiglitazone (ROSI), might also antagonize the CLA induced reduction in milk fat synthesis in lactating mice. Our objective was to investigate the interaction of ROSI and CLA on mammary and hepatic lipid metabolism in lactating C57Bl/6J mice. Nineteen lactating mice were randomly assigned to one of 4 treatments (n = 4–5 per treatment) applied from Day 6 to 10 postpartum. Treatments included: 1) Control (C) diet; 2) Control plus 1.5% dietary CLA (CLA); 3) Control plus intra-peritoneal (IP) ROSI injections (10 mg/kg BW) (ROSI); and 4) CLA plus ROSI (ROSI-CLA). Mice on the C and CLA diets received IP phosphate buffered saline (PBS). Day 6 values were used as covariates for milk fat and pup body weight in the 2 × 2 factorial analysis of covariance. Food intakes were similar among treatments although there was a trend ($P = 0.09$) for increased intake with ROSI. Milk fat was depressed 42% by CLA ($P < 0.001$). ROSI significantly reduced milk fat ($P = 0.05$) and the depression was greater with ROSI-CLA. Liver weights were increased by CLA ($P < 0.001$) and reduced ($P = 0.005$) by ROSI. Pup weight gain was reduced 44% by CLA ($P < 0.001$) but not affected by ROSI. Rosiglitazone corrected the apparent steatosis effect of CLA but had no effect on CLA induced milk fat depression. As ROSI is an insulin sensitizing agent, reduced liver lipid accumulation and increased fat oxidation, along with increased glucose uptake by adipose tissue might explain reduced liver weights with ROSI treatment. Since glucose is used as a precursor for de novo fatty acid synthesis in rodents, the reduction in milk fat with ROSI-CLA could have been due to increased glucose utilization in peripheral tissues thereby reducing glucose availability for triglyceride synthesis in the mammary gland.

Table 1.

Item	Control	ROSI	CLA	ROSI-CLA	SEM
Dam food intake, g/d	6.76	7.73	5.61	6.69	0.62
Milk fat (%)	35.47[a]	34.42[a]	21.94[b]	18.48[c]	1.02
Liver weight, % of BW	8.54[b]	7.46[c]	10.54[a]	8.72[b]	0.51
Pup weight gain, g/d	0.44[a]	0.38[a]	0.23[b]	0.23[b]	0.03

Key words: CLA, PPAR-γ, milk fat

148 Expression of T-box (Tbx) 3 in bovine mammary epithelial cells. M. L. Procopio*, A. C. Lopez, K. M. McFadden, T. A. Hoagland, G. W. Kazmer, and K. E. Govoni, *Department of Animal Science, University of Connecticut, Storrs.*

Development of the bovine mammary gland is a complex process that is regulated by several hormones, growth factors and transcription factors. Tbx3 is a transcription factor that is required for mammary gland development in humans, regulates cell cycle, and is overexpressed in many breast cancer cell lines. We recently demonstrated that growth hormone (GH) treatment increases the mRNA expression of Tbx3 in osteoblast cells independent of insulin-like growth factor (IGF)-I. Based on the critical role of Tbx3 in mammary gland development and its response to GH, we hypothesize that GH treatment will increase Tbx3 expression in bovine mammary epithelial cells (MEC). Primary bovine MEC were isolated from lactating cows at slaughter and cultured in Dulbecco′s Modified Eagle Medium (DMEM) supplemented with fetal bovine serum. In addition, MAC-T cells, a well established MEC line, were cultured under similar conditions. Prior to treatment, cells were serum starved in phenol red free media for 24 h. Cells were treated with control (CON) media (DMEM + 0.2% BSA), and GH (500 ng/μL) or IGF-I (200 ng/μL) for 24 h and RNA was extracted. mRNA expression was determined by real-time RT-PCR and data were analyzed using students *t*-test. Expression of Tbx3 was similar between MEC and MAC-T cells ($P = 0.7363$), therefore the primary MEC were used for additional experiments. Surprisingly, we did not observe a significant change in Tbx3 expression in cells treated with GH ($P = 0.10$). However, IGF-I treatment reduced Tbx3 expression 1.5-fold compared with CON ($P < 0.05$). In summary, we did not observe any effect of GH on Tbx3 expression in MEC, however a slight decrease was observed with IGF-I treatment. These findings are in contrast to the role of Tbx3 in mediating GH in the osteoblast, thus demonstrating that Tbx3 action may be cell and/or tissue specific.

Key words: mammary epithelial cells, growth hormone, transcription factors

ADSA-SAD Dairy Production Undergraduate Competition

149 Colostrum replacers in neonatal dairy calf management. E. Eckelkamp*, *Louisiana State University, Baton Rouge.*

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 main concern with colostrum in general is its concentration of immunoglobulins, particularly IgG. A colostrometer is used to measure colostrum quality, with a 50 g/L concentration of IgG considered the benchmark for good quality colostrum. Maternal colostrum varies in quality, and not all colostrum is good enough to feed to a calf to provide adequate immune protection. Colostrum replacers provide alternatives to feeding maternal colostrum. Colostrum replacers are intended to contain the same amount of IgG as good maternal colostrum. When comparing colostrum replacers and maternal colostrum, it is important to consider serum IgG and total protein concentrations in the calf as well as the incidence of failure of the passive transfer of immunity. There are advantages to each type of colostrum product, and these must be carefully evaluated when determining which to use. Colostrum replacers are uniform, with an adequate amount of IgG present for the calf. Maternal colostrum is already present on the dairy and does not have to be purchased. In addition it contains IgG for diseases that are endemic to a specific dairy. There are 2 primary methods of obtaining the immunoglobulins in colostrum replacer. The first is by drying bovine maternal colostrum with a high IgG content, and the second is obtained from dried bovine serum. Several studies have compared the effectiveness of maternal colostrum and colostrum replacers. The colostrum replacers varied in their ability to provide adequate immune protection depending on the concentration of globulin fed. In conclusion, when fed in the correct amounts, colostrum replacers and maternal colostrum are comparable in quality for providing passive transfer of immunity in neonatal dairy calves.

Key words: colostrum, colostrum replacers, dairy calves

150 Genomics: A tool for commercial dairy producers. L. Ellison*, *University of Florida, Gainesville.*

Vigorous, high-producing cows are what dairy producers look for everyday to keep their herds healthy and productive. Cattle have been selected based on best productive traits for centuries, first with observations of phenotypic traits, then with Predict Transmitting Ability data from pedigrees and progeny data. With today's technology, we now have Genomics. Genomics was officially established as a form of genetic selection in January 2009 after a group of researchers developed the bovine genome by sequencing all DNA markers that compose dairy genetics. From 2003 to 2006, geneticists have strove to identify gene sequences within an animal's DNA that directly influence certain traits such as milk production or productive life. Genomics testing currently comes in the form of 3 tests: 3k, 50k, or 800k SNP (single nucleotide polymorphism) tests. For commercial producers, there is a great advantage in using 3k SNP tests in determining future production. Dairy producers can rank animals at an early age assisting them in keeping their best animals for future production and worst ranked animals for culling, or potentially breed to a higher ranked bull for improvement. Producers can make more accurate mating decisions with their heifers and young bulls and use genetically superior bulls with even more reliability. With this knowledge, producers can make better decisions for higher profitability.

Key words: genomics, genetic selection

151 Implementing an accelerated heifer program: Is it worth the risk? S. E. Fraley* and E. L. Karcher, *Michigan State University, East Lansing.*

Increasing feed costs and lower than average milk prices are inhibitory factors making it increasingly difficult for dairy producers to make a profit. With 15–20% of expenses on farms linked to heifer programs (Whitlock et al., 2002), many producers are considering accelerated growth programs for heifers to minimize costs and maximize profits. Our objective was to determine the effect of accelerated growth programs on mammary development and milk production later in life. Increasing dietary energy in prepubertal heifers inhibits mammary growth relative to body growth in a time-dependent manner (Rincker et al., 2008). Brown et al., (2005) observed increases in mammary parenchyma in calves fed milk replacer with 4.4 kcal of ME/g DM and 30.3% CP as well as a starter grain that was 25% CP from 2 to 8 wk of age. Rapid somatic growth after puberty and associated reduced mammary development, are associated with lifetime milk production. Heifers grown at a faster rate than 680 g/d produced 5–10% less milk than heifers not grown at an accelerated rate (Van Amburgh et al., 1998). Heifers on an accelerated growth program would cost the producer less in overall feed and labor because of the decrease in nonproductive day. However, the potential loss in milk production could result in a negative profit, especially if that loss occurred over the complete productive life (Vandehaar, 2001). Although accelerated heifer growth may be an effective tool to reduce replacement heifer costs, the potential loss in income makes this a risky program for dairy producers. Before deciding to implement an accelerated growth program on farm, producers need to weigh all the options and decide if the benefits offset the risks.

Key words: heifer, accelerated growth

152 Genomic testing as a tool for herd development. L. Krueger* and J. Robison, *California State University-Fresno, Fresno.*

The need for an efficient method of herd development has been made apparent through the difficulties in maintaining profitability after a sizeable herd expansion. Breeding programs on herds nationwide have utilized the potential transmitting abilities of sires available for artificial insemination by selecting animals for production based on pedigree. The artificial insemination industry increased efficiency by moving from selection based on pedigree and performance to selection based on genetic potential, determined through genomic testing. Since the beginning of this movement in 2004, the ability to accurately project genetic potential has improved, with a 3000 single-nucleotide polymorphism (SNP) genomic test offered as an alternative to a 50,000 SNP test for practical purposes, at 20% of the cost. The practicality of this technology has also improved with the combination of ear tissue collection and identification establishment. For the producer, genomic testing means the ability to act on advance information that would otherwise take 3 years (heifer development and one lactation) to discover. Due to the availability and practicality of these developments, genomic testing is on the verge of becoming commonplace in the rearing of replacement herd animals as a tool in increasing efficiency and profitability.

Key words: genomics, test, herd development

153 Impact and control of claw lesions in dairy cattle. T. A. Reiter* and J. M. Bewley, *University of Kentucky, Lexington.*

Untreated claw lesions, a leading cause of dairy cattle lameness, are a growing problem for the dairy industry. The cost of a clinical case of lameness has been estimated to be $128 to $627. Although producers may only consider the economic impact of lameness, it is also important for dairy cow welfare. Drendel et al. (2004) reported that 74.5% of heifers had claw lesions before they were 12 mo old and 85.7% had lesions a month before calving. Heifers that had lesions before calving were more likely to have lesions during lactation. Heifers that had lesions during their first lactation had significantly lower milk yields (2,496 kg less per lactation), even if they were not showing signs of lameness. Additionally, claw lesions increase the rate of premature culling and reduce estrus expression and reproductive performance. The claw is softer during lactation causing it to be more susceptible to lesions. Lesions can be categorized as infectious or noninfectious. Infectious lesions include digital dermatitis, heel erosion, and foot rot. Noninfectious lesions include white line lesions, sole ulcers, and sole hemorrhages. In establishing a prevention plan for claw lesions, dairy producers should consider environmental exposure risks. Wet environments with excessive mud and manure lead to soft and worn hooves and increase the spread of infectious agents. Housing or management conditions that result in excessive standing times cause the claw to weaken because the supportive tissue begins to break down and the horn changes shape. Nutritional factors may also contribute to claw lesions including high levels of ruminally available carbohydrates, lack of fiber, inadequate trace minerals, ration sorting, and inconsistent feeding schedules. Footbaths, typically placed in parlor exit alleys, can be used for prevention and treatment of infections using chemical solutions. Producers should work with their veterinarians and hoof trimmers to understand the cause of lesions in their herd to establish herd-specific prevention and treatment plans.

Key words: claw lesions, lameness, hoof care

154 Bacteriophages as a potential treatment for mastitis. E. G. Sumners*, D. R. Winston, and I. K. Mullarky, *Virginia Polytechnic Institute and State University, Blacksburg.*

Mastitis is the most costly disease in dairy cattle. With consumer preferences against the use of antibiotics, the dairy industry needs to identify alternatives treatments for mastitis. Bacteriophages may be an effective alternative method for treating mastitis. The use of bacteriophages has been studied in humans, mice, and dairy cattle. Bacteriophages are viruses that attack and lyse specific bacteria. However, they do not affect normal microflora. Specific bacteriophage isolates have been studied that lyse an important mastitis pathogen, Staphylococcus aureus. A study that compared multiple bacteriophage isolates ability to lyse specific strains of S. aureus in milk. The study also implied that some bacteriophages may lyse at all stages of bacterial growth and others lyse at particular stages of growth. However, another study examined the efficacy of treating S. aureus infected quarters with bacteriophages and found a 16.7% cure rate. Thirteen cows and 18 quarters where treated with bacteriophage isolates for 5 d. The results for the latter study do not support the use of bacteriophage therapy at this time. Future studies should be conducted evaluating different treatment periods and other bacteriophage isolates. Benefits that bacteriophages have over antibiotics include: no affect on microflora; ecologically purity; no side effects; and natural enemies of bacteria. With the use of bacteriophages dairy producers may have a better way to treat mastitis without concern about potential residues and consumer preferences.

Key words: bacteriophages, mastitis, antibiotic-resistant bacteria

155 Heat. C. Hoffner*, *North Carolina State University, Raleigh.*

Providing a comfortable atmosphere for high-producing animals is a necessity. The Southeastern United States is notorious for having hot and humid summer days, which can drastically affect dairy cows and their milk production. Because of this, heat stress is a huge concern among dairy farmers in our area. Cows subjected to heat stress have reduced feed intake, lower activity, higher respiratory rate, increased peripheral blood flow, and higher water loss. These behaviors have a harmful result on the milk production and the physiologic standing of the animal (J.W. West, 2002). Through observation and research, scientists have determined that a balance of environmental changes, genetic enhancements, and proper nutrition will be the answer for maintaining high milk producing dairy cows in this climate. One experiment concluded that shaded cows yielded 10% more milk than non-shaded cows (J.W. West, 2002); results of another study indicated that cows increased milk yield by 11.6% when sprayed with water for 90 s every 15 min (Strickland, et al., 1988). Genetic adjustments can be altered by monitoring cows of different hair colors. A Florida- based study specified that light-haired cows have a lower body temperature and a greater milk yield than those who are dark-haired (Hansen, 1990). Currently, more research is being conducted to determine if a heat tolerant gene can be used in dairy breeding in the future (J.W. West, 2002). Nutritional advances are emerging for boosting milk production from cows in these environments. It has been reported that providing chilled water to dairy cows improves milk yield by dropping the body temperature through absorbed heat energy (Milam, et al. 1986). Overall, heat stress can adversely affect milk production and also be harmful to the health of dairy cows. With moderate adjustments over time, cows in hot and humid climates can be more comfortable leading to more money in farmers' wallets.

Key words: heat stress, milk production, humid environment

156 Direct-fed microbials: Decreasing scrutiny and increasing productivity. A. Sassard* and J. Fain, *Clemson University, Clemson, SC.*

With increasing concerns regarding safety of the US food supply, producers are increasingly under scrutiny to reduce the use of antibiotics and growth hormones throughout the dairy industry, from calf to cow. Producers are taking the right steps forward with novel health management practices focusing on prevention of problems and promotion of animal welfare while increasing economic productivity. Direct-fed microbials (DFMs), which are biologically active microorganisms that may be used as supplements, have the potential to replace antibiotics in health management programs. Microorganisms utilized as DFMs can be either bacteria, such as *Megasphaera elsdenii*, or fungal, such as *Saccharomyces cerevisiae*. Current methods of using DFMs for dairy cattle range from treating sickly calves to stabilizing the rumen of dairy cows in lactation. Studies investigating the usage of DFMs in adult dairy cattle confer their ability to decrease metabolic problems associated with transition cattle and those receiving a high concentrate ration. It appears that DFMs affect the cow through many complex methods of action, which are dependent on the microbe used and its method of delivery. Research has found that transition cows gain the most benefit from supplementation, with DFMs reducing both sub

acute rumen acidosis (SARA) and helping to protect the cow against an acute rumen acidosis challenge. SARA can cost the dairy industry up to $1.12 per cow per d, causing permanent losses in productivity and building a foundation for additional challenges such as laminitis. DFMs provide a non-medicated method of supplementing cattle to effectively tolerate dietary changes; tempering rumen bacteria to the presence of lactate and modifying fermentation while increasing productivity by as much as 2.3 kg/d with more effective utilization of fermentation products, namely propionate. Ultimately DFMs have the potential to become a new option to combat current issues plaguing the dairy industry, from food safety concerns to animal welfare, while at the same time making production more efficient and improving a producer's profit margin.

Key words: DFMs, acidosis, food safety

157 Genetic selection for feed efficiency in dairy cows. A. M. Yeiser* and C. D. Dechow, *Pennsylvania State University, University Park.*

Feed costs are the single largest expense on dairy farms, and profitability of dairy farms has been limited by rapidly rising feed prices. Collections of dry matter intake (DMI) from a large number of individual cows can be cost prohibitive, but genetic markers for feed intake could be developed from fewer cows and allow selection for feed utilization. Feed efficiency is defined in different ways. Gross feed efficiency (GFE) is the amount of energy corrected milk produced per unit of DMI. Heritability estimates for GFE range from 0.14 to 0.37. However, GFE does not consider other cow factors such as body tissue mobilization which could inflate GFE estimates. Residual feed intake (RFI) is DMI adjusted for yield and body weight change. RFI has been considered by some researchers because it was thought to reflect differences in basal metabolic rate. Heritability estimates for RFI vary widely (0.01 to 0.69). Some evaluations of genetic variation for RFI consider change in body weight (BW) and body tissue composition, whereas others consider only change in BW. Studies that account for body tissue composition tend to find less genetic variation in RFI. This suggests that basal metabolic rate might not be changed by selection for RFI. BW and body condition score had unfavorable correlations with feed efficiency in one study, with genetic correlation estimates ranging from −0.64 to −0.70. Cows with a smaller body size were more efficient than larger and fatter cows at equivalent levels of production due to the dilution of maintenance requirements. More recently, researchers have suggested evaluating residual yield, which identifies cows with high yield at similar intake and body tissue mobilization of less efficient cows. Regardless of how feed efficiency is defined, there is evidence that genetic selection can allow dairy producers to increase the efficiency of feed utilization in dairy cows.

Key words: feed efficiency, heritability

ADSA-SAD Original Research Undergraduate Competition

158 Assessment of ruminal fermentation characteristics under normal or high fermentative temperature in continuous cultures. C. C. King*[1], C. M. Dschaak[1], J.-S. Eun[1], V. Fellner[2], and A. J. Young[1], *[1]Department of Animal, Dairy, and Veterinary Sciences, Utah State University, Logan, [2]Department of Animal Science, North Carolina State University, Raleigh.*

A dual-flow continuous culture system was used to investigate effects of ruminal temperature and forage-to-concentrate (FC) ratio in lactation dairy diets on ruminal fermentation. The experiment was a 4 × 4 Latin square design with a 2 × 2 factorial arrangement of treatments (n = 4). Diets based on alfalfa hay and corn silage as forage sources were formulated to maintain different FC ratios (60:40 or 40:60, DM basis) in the high forage (HF) or the low forage (LF) diet, respectively. Four treatments were tested: HF under normal ruminal temperature (NRT; 39°C), LF under NRT, HF under high ruminal temperature (HRT; 41°C), and LF under HRT. Each independent run lasted 10 d (7 d of treatment adaptation and 3 d of data collection). The temperature of the HRT treatment was chosen to mimic ruminal fermentative environment when cows are under heat stress. Increasing ruminal temperature increased ($P < 0.01$) culture pH from 5.73 to 5.82 on average, but decreasing forage proportion in the diets decreased ($P < 0.01$) culture pH regardless of ruminal temperature. Total VFA concentration decreased ($P = 0.05$) in the HRT compared with the NRT, however, ruminal temperature did not affect molar proportion of VFA. Digestibilities of DM and NDF were not affected by ruminal temperature, whereas the HRT tended to decrease ($P = 0.14$) OM digestibility compared with the NRT (66.6 vs. 67.4%). The HRT increased ($P < 0.01$) methane production (mmol/d and mmol/g NDF digested) and ammonia-N concentration and flow. The HRT treatment also increased the concentration of C18:0, but decreased that of the C18:1 trans-11. Overall results suggest that during HRT as experienced by cows under heat stress nutrient digestion, energy utilization, and microbial protein synthesis are altered.

Key words: ruminal temperature, microbial fermentation, continuous culture

159 Supplemental butyrate does not enhance selective permeability of ruminal epithelia in sheep. D. J. Wilson*, T. Mutsvangwa, and G. B. Penner, *University of Saskatchewan, Saskatoon, SK, Canada.*

The aim of this study was to determine if increasing the intra-ruminal butyrate concentration would improve the selective permeability of ruminal epithelia. Suffolk wether lambs (n = 18) fed a common diet were randomly assigned to 1 of 3 in vivo butyrate supplementation levels: 0% (CON); 1.25%; and 2.50% butyrate as a proportion of DMI. After a 14-d feeding period, lambs were killed and ruminal epithelia from the ventral sac was prepared for mounting in Ussing chambers with separate mucosal (pH 6.2) and serosal (pH 7.4) buffer solutions. 1-^{14}C butyrate and D-1-^{3}H mannitol (both 74 kBq/10 mL) were added to the mucosal side and used to measure mucosal to serosal flux (J_{ms}) over 2 60-min flux periods with simultaneous measurement of transepithelial conductance (G_t). For the first (challenge) flux period, the mucosal buffer solution was either acidified to pH 5.2 (ACID) or used as a control (pH 6.2; SHAM). Buffer solutions were replaced for the second flux period (recovery). In vitro data were analyzed as a split-plot design with in vivo treatment as the main-plot, in vitro treatment as the sub-plot, and flux period as a repeated measure. Ruminal VFA was higher ($P < 0.001$) in lambs fed 2.50% compared with CON or 1.25% (31.3, 36.2, and 52.4 mM, respectively). Feeding supplemental butyrate increased ($P = 0.001$) ruminal butyrate by 6.3 and 20.8 mM for lambs fed 1.25% and 2.50% compared with CON (butyrate = 5.6 mM). The $J_{ms\text{-}butyrate}$ was lower ($P = 0.013$) for lambs fed 1.25% and 2.50% butyrate (3.00 and 3.12 μmol/(cm^2 × h), respectively) than CON (3.91 μmol/(cm^2 × h)). However, no differences ($P = 0.33$) were observed for $J_{ms\text{-}mannitol}$ and G_t with average values of 0.30 nmol/(cm^2 × h) and 3.99 mS/cm^2. There was an in vitro treatment × flux period interaction ($P = 0.003$) for $J_{ms\text{-}butyrate}$, where $J_{ms\text{-}butyrate}$ was not different during the challenge period for ACID and SHAM (3.84 vs 3.39 μmol/(cm^2 × h)), but $J_{ms\text{-}butyrate}$ was lower for ACID relative to SHAM (2.70 vs. 3.44 μmol/(cm^2 × h)) during the recovery period. These results indicate that increasing intraruminal butyrate concentration does not enhance the selective permeability of ruminal epithelia.

Key words: butyrate, ruminal epithelia

160 Effect of feeding a C16:0-enriched fat supplement on milk fatty acid composition. K. E. DeLand*, C. L. Preseault, M. S. Allen, and A. L. Lock, *Michigan State University, East Lansing.*

Dietary C16:0 has been reported to increase milk fat (MF) concentration and yield. This study evaluated the effect of a dietary C16:0-enriched fat supplement on the fatty acid (FA) composition of MF, in particular saturated FA (SFA) composition and concentration, in a crossover experiment with 21 d periods. The hypothesis was that an increase in MF yield would be due to an increase in C16:0 incorporation into MF, which would increase the MF concentration of SFA. Sixteen midlactation Holstein cows (249 ± 33 DIM) were assigned to treatment sequence; treatments were a C16:0-enriched (~85% C16:0) fat supplement (FAT, 2% DM) or a control diet (CON) containing no supplemental fat. Milk samples were collected on d 18 to 21 of each period. FAT increased MF concentration and yield by 7.6 and 8.1%, respectively ($P < 0.001$). This was due to a 26% increase in FA yield (mmol/d) of C16 FA (C16:0 + C16:1 cis-9, $P < 0.001$); the yield of de novo (<C16) and preformed (>C16) FA were not different between treatments (both $P > 0.25$). On a concentration basis, the FA profile (g/100 g FA) of MF for CON and FAT was 26.8 and 23.4 < C16 FA, 36.7 and 43.5 C16 FA, and 36.5 and 33.1 > C16 FA, respectively (all $P < 0.001$). The C16:0 concentration of MF increased 19% (35.4 to 42.1 g/100 g FA, CON vs. FAT, $P < 0.001$). This only resulted in a 3% increase in total SFA (70.2 to 72.1 g/100 g FA, CON vs. FAT, $P < 0.01$) because concentrations of SFA from C6:0 to C14:0 were reduced (all $P < 0.01$). There was a reduction in MF cis polyunsaturated FA concentration (2.8 to 2.5 g/100 g FA, CON vs. FAT, $P < 0.01$), and a trend for a reduction in total cis monounsaturated FA concentration (22.8 to 21.8 g/100 g FA, CON vs. FAT, $P = 0.08$). Total trans C18:1 concentration and yield was lower with FAT (17 and 10%, respectively, $P < 0.05$), with lower concentrations of all major trans C18:1 isomers ($P < 0.01$). Results demonstrate that although FAT increased the concentration and yield of C16:0, changes in other FA resulted in minimal differences in the concentration of total SFA in MF. Overall, the FA profiles of MF from CON and FAT were within recently published survey values for currently available dairy products.

Key words: milk fatty acids, palmitic acid, saturated fat

161 Impact of water intake on dairy cattle reticulorumen temperature. M. Cornett*, D. Ray, and J. Bewley, *University of Kentucky.*

Concerns remain about the effect of water intake on temperatures collected within the reticulorumen. The dramatic drop in reticulorumen temperature (RT) following water intake has been well documented; however, the time required for RT to return to pre-drinking baseline temperature (BT) has not been quantified. The objective of this study was to quantify the relationship between water intake quantity and BT. Four mid-lactation, multiparous, Holstein-Friesian dairy cows were equipped with SmartBolus transponders (TenXSys, Eagle, ID) set to record RT at 2-min intervals. Cows were housed in a tie-stall barn at the University of Kentucky Coldstream Dairy Research Farm. A TMR ration was provided ad lib at 05:30 and 14:00. One Poly Water bowl (SMB MFG, Wallenstein, ON) equipped with a range water meter Recordall Badger Meter (Badger Meter, Milwaukee, WI) was assigned to each tie stall to assess water intake. Drinking behavior was monitored by 2 observers for 48 consecutive hours. The termination of a drinking bout was established when 30 min elapsed without another drink. Quantities consumed within each drinking bout were used for analysis. Mean (±SD) volume of water consumed per drinking event was 0.27 ± 0.31 L. Mean (±SD) temperature drop (TD) across all drinking events was 2.29 ± 1.82°C. Mean (±SD) RT at the beginning of the drinking event was 39.76 ± 0.49°C (n = 84), while mean water temperature (WT) 15 min before the drinking event was 3.63 ± 3.14°C. Mean (±SD) BT, identified in 50 drinking events (59.5% of total drinking bouts), was 57.75 ± 38.70 min. The BT was moderately correlated with pre-drinking RT (r = 0.57, $P < 0.01$), TD (r = 0.49, $P < 0.01$), and WT (r = −0.28, $P < 0.05$).The TD was moderately correlated with the pre-drinking RT (r = 0.57, $P < 0.01$), the amount of water consumed (r = 0.53, $P < 0.01$), and BT (r = 0.49, $P < 0.01$). Regression was performed with the GLM procedure of SAS (SAS, Cary, NC) to assess factors influencing BT ($r^2 = 0.36$). The quantity of water consumed ($P = 0.03$), and the RT before a drinking bout affected BT, while WT did not ($P = 0.92$).

Key words: temperature monitoring, reticular temperature, water intake

162 Genotype and breed trend influences on citric acid and coagulation times of raw milk. M. Looney*[1], A. Laubscher[1], J. Medrano[2], R. Jimenez-Flores[1], and G. Rincon[2], *[1]California Polytechnic State University, San Luis Obispo, [2]University of California, Davis, Davis.*

Citric acid or citrate in milk plays a very important role while processing milk to produce cheese or yogurt. The objective of this study was to determine if citric acid levels measured in milk was related to genetic variants of various genes identified in Holstein and Jersey cows and its effect on gel formation. We collected milk samples from both Holstein and Jersey cows from the Cal Poly Dairy Farm, San Luis Obispo. Citric acid levels, protein, fat, lactose, and minerals were measured using FTIR methods with the FOSS Milkoscan FT2 on each sample. Genotypes were obtained for the DGAT 1, β-LG, ACLy and ACO1 loci using polymerase chain reaction and an enzymatic digestion using primarily the MwoI restriction enzyme. This procedure distinguishes the A and G variants of DGAT 1, A and B variants of β-LG gene and several variants of the other genes. Results from Holstein and Jersey cows indicated that citric acid level, as a percentage, was higher for the Jersey than for the Holstein cows–0.18 and 0.14, respectively. Protein and percent fat were included as independent variables in the statistical model, the difference between Holstein and Jersey for citric acid level was then considered for the different loci variants. Our preliminary data indicates the differences due to gene variants. All the samples were tested for gel forming kinetics using the ReoRex system. These experiments show the influence that citrate levels have on gel formation induced by chymosin.

Key words: citrate, DGAT, gel formation

163 Effects of different flooring options in outside pens of hutches on dairy calf growth. K. A. Hoeing*[1], M. A. Laws[1], T. S. Dennis[1], M. M. Schutz[1], S. D. Eicher[2], and T. D. Nennich[1], *[1]Purdue University, West Lafayette, IN, [2]USDA-ARS, West Lafayette, IN.*

Growth rates of dairy calves may vary due to many different factors, including housing. The objective of this study was to determine if calf growth was affected by different flooring options in the outside pen area of a calf hutch. For this study, 33 hutches were blocked in groups of 3 by location and the outside pen area was randomly assigned to 1 of 3 treatments: soil and lime (CONTROL), solid black rubber mats (SOLID), and black rubber mats with 2.5 cm holes (HOLES). Thirty-three heifer calves in the study were assigned sequentially by birth date to the next available hutch. The study was conducted during the summer of 2010 at the Purdue Dairy Research and Education Center. Calves were fed according to standard protocols and received 2 L of milk replacer per day and ad libitum access to calf starter and water. Body weight, heart girth circumference, hip height (HH), wither height (WH), and body temperature (TEMP) were measured when the calves entered the study and every 2 wk until weaning or 8 wk of age. Calves were observed 2 times/wk to determine behavior, calf cleanliness, flooring cleanliness, and hutch bedding cleanliness. Flooring temperature was determined using infrared temperature guns. Data were analyzed with Proc Mixed of SAS using repeated measures. Two calves, on treatments SOLID and CONTROL, died for reasons unrelated to treatment and were removed from the study. At 8 wk of age, BW was greater ($P < 0.05$) for HOLES and CONTROL than for SOLID (72.5, 69.2, and 64.0 kg, respectively), and HH and WH were greater for HOLES ($P < 0.05$) than for CONTROL and SOLID. Heart girth circumference and TEMP were similar among treatments ($P > 0.20$). Mat temperatures were similar for SOLID and HOLES (46.5 and 46.0°C, respectively) and were greater ($P < 0.001$) than CONTROL (37.7°C). Calf and bedding cleanliness were similar among treatments, though flooring tended ($P < 0.10$) to be dryer for HOLES at the beginning and dirtier in the middle of the study. Flooring options in the outside pen of calf hutches affected calf BW, HH, and WH at weaning, with rubber mats with holes improving calf growth compared with a lime and soil mixture or solid mats.

Key words: dairy, calf, housing

164 Alterations in the rate of progesterone clearance induced by insulin-like growth factor-I in the mouse hepatocyte. C. L. Varela*, K. D. Baldock, W. G. Squire, and D. L. Smith, *Eastern New Mexico University, Portales.*

Circulating concentrations of progesterone are at least, a critical indicator of potential embryonic survival, or maybe more importantly, contribute directly to pregnancy retention. In our previous research, we have shown insulin reduces the clearance of progesterone; thus potentially increasing embryonic survival. Further, the reduction in progesterone clearance was due to an insulin-mediated reduction in the cytochrome P450 enzymes that catabolize progesterone. It has been shown Insulin-like growth factor-I (IGF-I), produced by the hepato-

cytes, has no receptors in the liver, however there are insulin receptors. Insulin-like growth factor-I has been shown to bind to insulin receptors but with a lower affinity than insulin binding to its own receptor. The objective of this experiment is to determine the effect of different concentrations of IGF-I on the rate of progesterone clearance by hepatocytes. To determine the rate of progesterone clearance in response to challenge with different concentrations of IGF-I, mouse hepatocytes (10^5 per well) were plated in 10, 12 well plates with 5 ng/ml of progesterone added to the culture medium. To calculate the fractional rate of decay for progesterone, media was harvested at 0, 1, 2, 3 and 4 h following the addition of treatment. Cells were cultured in the presence of IGF-I (0, 6.25, 12.5, 25, 50, 100, 200 and 400 ng/ml). The conditioned media concentrations of progesterone were determined by enzyme-linked immunosorbent assay. Progesterone clearance was increased ($P < 0.05$) with the addition of 12.5 ng/ml IGF-I compared with control. Furthermore, there was a greater increase ($P < 0.05$) in progesterone clearance in response to 25, 50, 100, and 200 ng/ml IGF-I compared with the control, 6.25, and, 400 ng/ml IGF-I. These results indicate that hepatocytes in the presence of increasing concentrations of IGF-I, increase progesterone clearance and consequently could potentially reduce embryonic survival.

Key words: insulin-like growth factor-I, progesterone, hepatocyte

165 The effects of protease enzymes and storage on the ensiling and nutritive value of corn silage. K. M. Young*, M. C. Der Bedrosian, J. M. Lim, A. P. T. P. Roth, S. A. Santos, and L. Kung Jr., *The University of Delaware.*

The objective of this study was to evaluate the effects of adding protease enzymes to chopped whole plant corn on silage fermentation and nutritive value after varying lengths of storage. Chopped and processed whole plant corn (Mycogen TMR2W726, Dow AgroScience, Indianapolis, IN) was harvested (36.3% DM) and ensiled without enzymes or treated with one of 2 different proteases (E85 or E86; AB Vista, Wiltshire, UK) at one times (1X) or one hundred times (100X) the manufacturer's recommended dosage. The enzymes were mixed with a phosphate buffer and applied to chopped forage while mixing. Replicated-treated piles of forage were prepared for each enzyme treatment. Four bags of forage were vacuumed and heat-sealed for each enzyme treatment and storage time and allowed to ensile at 23 ± 2°C for 45 and 150 d. The hypothesis was that in the silo, proteases would liberate starch and increase starch digestibility (Starch-D). The statistical analysis included the main effects of enzyme treatments, days of storage and their interactions. When compared with untreated silage, there was no effect of protease or length of storage (45 vs. 150 d) on pH, concentrations of CP, ADF, NDF, or starch. At 45 and 150 d, treatment with proteases did not affect NDF-D or the concentrations of lactic acid, acetic acid or ethanol when compared with untreated silage. Ammonia-N and soluble-N (% of CP) contents increased after ensiling compared with levels at harvest and were greater ($P < 0.01$) for the 100X enzyme doses when compared with untreated silage at both storage times (45 and 150 d). Starch-D (ruminal in vitro, 7 h) was 66.3% for freshly chopped corn plants. After 45 d of ensiling, treatment with E86 100X had greater ($P < 0.01$) starch-D (80.6%) than all other treatments except it was similar to E85 100X. After 150 d of ensiling, E85 1X (81.9%), E85 100X (82.9%) and E86 100X (88.6%) had greater ($P < 0.01$) starch-D than untreated silage (74.0%). Effects of the proteases on amino acid content and for longer periods of storage will be determined. The data obtained to date suggests that exogenous proteases could be used to improve in vitro ruminal starch-D in corn silages.

Key words: corn silage, protease

166 Differences in the rumen methanogen population exist between Jerseys and Holsteins. E. King*, R. Smith, and A.-D. Wright, *University of Vermont, Burlington.*

Holstein and Jersey breeds account for the vast majority of cows within the dairy industry. While the population of rumen methanogens has been sequenced and analyzed in the Holstein, to our knowledge, a direct comparison has not yet been done between Holsteins and Jerseys. The molecular diversity of rumen methanogens in Holstein and Jersey dairy cows were investigated using 16S rRNA gene libraries prepared from pooled PCR products from the rumens of 9 Holsteins and 10 Jersey cows from Vermont. A total of 365 clones were generated, 180 clones from the Holsteins and 185 clones from the Jerseys. Approximately 99% of all clones identified belonged to the genus *Methanobrevibacter*, with 43% of these clones closely related to *Methanobrevibacter ruminantium*. Based upon 98% sequence identity, these 365 clones were assigned to 55 different OTUs. Twenty OTUs (85% of the clones) were common in both breeds. However, the Holstein cows revealed 23 OTUs not found in the Jersey cows, and the Jersey cows revealed 12 OTUs not found in the Holsteins. Shannon index and Libshuff analysis indicate that significant differences exist between the composition ($P = 0.01$) and diversity ($P < 0.05$) of the methanogens recovered from the 16S rRNA gene libraries from these 2 dairy breeds. These results suggest that breed and differences in feed utilization efficiency may account for the different rumen methanogen populations from these 2 dairy breeds.

Key words: methanogens, *Methanobrevibacter*, dairy cows

167 The association of electrical conductivities and California Mastitis Tests on a robotic dairy farm. A. M. Brigham*[1], C. D. Dechow[1], and B. Carter[2], *[1]Pennsylvania State University, University Park, [2]Keseca Veterinary Clinic, Geneva, NY.*

With the introduction of robotic milking systems there is less daily handling of each cow and producers must rely on computer generated udder health reports. The objective of this study was to determine if measures of electrical conductivity (EC) could be used to define a more sensitive and specific report. Over the course of 4 weeks, 227 cows from one farm were evaluated with a California Mastitis Test (CMT) after being flagged by the herd's software system. The robotic system recorded EC separately for each quarter. A list of cows suspected of having mastitis was generated daily and included cows with EC deviations of greater than 21% from their baseline. Cows were also flagged if there was an abnormal milk color or extreme deviation in milk yield from the previous day. In total, 20% of cows on the automatically generated report had a negative CMT result and the false positives create an unnecessary management burden for the herd. The association of CMT scores with quarter EC and the ratio of a quarter's EC to the cow's lowest quarter EC, or inter-quartile ratio (IQR), was determined using the mixed procedure in SAS. Least-squares-means for cows with a negative CMT result were 70.1 and 1.04 for EC and IQR, respectively, which were significantly ($P < 0.0001$) lower than results for cows that were strong positives (95.3 for EC and 1.37 for IQR). Subsequent analysis indicated that IQR had higher sensitivity than EC, whereas EC and IQR were similar for specificity. Milk cultures were also conducted for 53 quarters with positive CMT, and bacteria were isolated for 64 percent of samples. Least squares means for IQR and EC were not higher for CMT positive quarters with a positive

bacteria culture than CMT positive quarters with a negative bacteria culture. Measures of EC are helpful in identifying cows with mastitis in robotic milking herds, but need further development to create more management friendly reports with higher sensitivities and specificities.

Key words: electrical conductivity, California Mastitis Test

168 Effects of shade on heat stress reduction in Holstein dairy calves. S. S. Thibeau*[1], L. B. Sage[1], C. C. Williams[2], B. F. Jenny[2], and A. H. Dolejsiova[2], *[1]Louisiana State University, Baton Rouge, [2]LSU AgCenter, Baton Rouge, LA.*

Heat stress, a particular concern to southern dairy producers, can cause a variety of homeostatic alterations that can inhibit optimal calf development and prohibit full production potential. Therefore the objective of this study was to determine the effect of shade on performance and metabolic indicators of heat stress in neonatal dairy calves. Sixteen (n = 16) neonatal Holstein heifers were assigned to either a non-shaded (NS) or shaded (SS) hutch for an 8 week period. Rectal temperatures, surface temperatures and respirations were measured at 0830 h and 1600 h 3 times per week. Average daily starter intake (ADI), water intake and fecal scores were measured twice daily. Body weight, hip and wither height were measured at birth and at wk 1, 2, 4, 6, and 8. Blood was collected at birth and then weekly for analysis of plasma urea nitrogen (PUN) and packed cell volume (PCV). As expected for a normal growing calf, ADI, body weight, hip height, and wither height increased ($P < 0.01$) with age while fecal scores decreased ($P < 0.05$) over time. However, there were no observable treatment effects ($P > 0.1$) on these parameters. Calves in NS hutches drank more ($P = 0.1$) water than shaded calves. Calves also drank more water ($P < 0.01$) as they aged. A treatment by time interaction ($P = 0.05$) was observed for rectal temperature, with afternoon measurements being higher in NS calves. A treatment by time interaction ($P < 0.01$) was also observed for surface temperature with lowest values in the SS calves in the morning. Likewise, there was a treatment by time interaction for respiration rates, with afternoon values for NS calves and morning values for SS calves being the highest. Surface temperature and respiration rates decreased ($P < 0.01$) as calves aged. There was no significant ($P > 0.1$) treatment effect on PUN, although PUN levels increased ($P < 0.05$) as calves aged. There was treatment by week interaction ($P < 0.05$) on PCV, with NS calves having greater values after wk 3. While differences were observed in physiological parameters, there were no improvements in performance of these calves with addition of shade as a management practice.

Key words: heat stress, shade, dairy calves

169 Xylose absorption in dairy calves supplemented with sodium butyrate in milk replacer. N. M. Larson*[1], S. I. Kehoe[1], S. Moreland[2], and D. Shields[3], *[1]University of Wisconsin-River Falls, River Falls, [2]Nutriad, Inc., Elgin, IL, [3]Merrick's, Inc., Union Center, WI.*

Sodium butyrate has been reported to enhance intestinal development in neonates during growth. The objective of this research was to evaluate whether sodium butyrate supplementation in milk replacer would enhance intestinal absorption in growing dairy calves thereby improving production and health parameters. Seventy 2 bull calves were fed 280 g/d DM of milk replacer twice daily and treatments consisted of no supplementation (C), 0.44% sodium butyrate supplementation (L) and 0.88% sodium butyrate supplementation (H; Nutriad, Inc.). Growth (body weight, withers height, hip height, and heart girth) and health parameters (fecal scores, treatments, milk refusals) were monitored and blood was obtained from half of the calves and analyzed for glucose, blood urea nitrogen (BUN), and creatinine. At wk 3, calves were dosed with xylose and blood was taken 4 h after dosing. Least squares means were analyzed using repeated measures of the mixed procedure of SAS 8.2 with week as a repeated effect. Growth measurements at arrival and blood measurements during wk 0 were used as covariates for growth and blood analyses. Plasma xylose concentrations were not significantly different between treatments (27.6, 24.2, and 17.19 mg/dl, for C, L, and H, respectively). There were no significant differences between treatments in glucose, BUN, and creatinine concentrations. Growth parameters were also not different however heart girth tended to be lower for H calves. Average daily gain was not different, however, feed efficiency was significantly lower for C calves (1.6, 0.96, 0.97 kg feed/kg gain, for C, L, and H, respectively). Health parameters were not different between treatments. The supplementation of sodium butyrate did not appear to enhance any growth, health or metabolic parameters in this model.

Key words: calves, sodium butyrate, intestinal health

ADSA Southern Section Symposium: Producing Quality Milk in Hot, Humid Climates

170 Extension programming in Kentucky to address somatic cell count challenges and opportunities. J. M. Bewley*, *University of Kentucky, Lexington.*

Recent market changes have renewed interest in lowering bulk tank somatic cell counts (SCC), particularly in the southeastern US states where the highest SCC in the country are observed. Extension programming efforts focused on SCC reduction increased around the country in 2010 and 2011. In Kentucky, we have implemented a multifaceted approach to extension programming for SCC reduction. The University of Kentucky Dairy Extension team has worked closely with the Kentucky Dairy Development Council in a farm-based program entitled M.I.L.K. Counts. The intent of the program is to provide direct, on-farm technical assistance to producers struggling with SCC through evaluation of DHIA records, milking procedures, management protocols, animal hygiene and housing, and dry cow treatment and handling. The M.I.L.K. Counts program incorporates a team-based problem solving approach with emphasis on the economic impact of resulting recommendations. Microbiological culturing is performed by the University of Kentucky Veterinary Diagnostic Livestock Laboratory. Approximately 25 producers have participated in the program with SCC reductions as high as 400,000 cells/mL. YouTube videos were developed (http://www.youtube.com/user/UKAgriculture) to demonstrate recommended milking procedures and to provide virtual tours of farms that consistently maintain low SCC. A visual analytics dashboard (http://tinyurl.com/UKMilkBonus) was created to illustrate the potential for increased income through SCC reductions. Kentucky herds with annual mean SCC < 250,000 were surveyed to summarize management practices employed by farms successful at maintaining low SCC. When asked to identify the management practice that contributed the most to their low SCC level, the most frequently cited practices were (1) keeping cows and facilities clean (n = 31), (2) maintaining dry, clean bedding (n = 14), (3) adhering to a consistent milking routine (n = 10), (4) forestripping (n = 7), and (5) pre and post dipping (n = 6). Lastly, a series of SCC reduction workshops were conducted across the state working with county extension agents and milk cooperative field people.

Key words: extension, SCC, milk quality

171 Dairy producer adoption of mastitis control technologies for reducing herd somatic cell counts. S. C. Nickerson*, *University of Georgia, Athens.*

Mastitis continues to be a major livestock disease affecting the dairy industry. In the US alone, this disease results in economic losses approaching $2 billion annually due to reduced milk production, milk discard, veterinary services, antibiotic use, increased labor, and reduced cow sale value. As the industry strives to improve milk quality to meet consumer as well as exportation demands, the legal limit for the somatic cell count (SCC) will likely be reduced from 750,000/mL to 400,000/mL in the near future. It is estimated that between 10 and 20% of US dairy farms, mostly located in the south, are currently at or above the 400,000/mL SCC limit and will have to adopt stricter methods for controlling mastitis in their milking herds, dry cows, and heifers. The 5-point plan of mastitis control has provided the basics of managing this disease for over 4 decades, and includes 1) teat dipping, 2) dry cow therapy, 3) functionally adequate milking machines, 4) therapy of clinical infections, and 5) culling of chronic cows. However, additional measures of control will have to be implemented to reduce mastitis prevalence and the associated elevation in SCC. Such management practices include vaccination, dietary supplementation, and mastitis control in heifers. The adoption of both the proven traditional methods and the more novel technological approaches toward mastitis management by dairy producers is dependent on several factors, and is based on what motivates the implementation of mastitis prevention and control practices.

Key words: dairy producer, mastitis, somatic cell count

172 Effect of micronutrients on the regulation of the immune system and its role in milk quality. W. Weiss*, *OARDC/The Ohio State University, Wooster.*

All cells and tissues require micronutrients to function properly, however immune cells and the immune system are particularly sensitive to the supply of many micronutrients. Stimulated neutrophils and macrophage produce prodigious quantities of free radicals, and metallo-enzymes (containing copper, selenium, or zinc), B-carotene and vitamin E have direct major antioxidant functions that are needed to control those radicals. Marginal deficiencies of Cu, B-carotene and vitamin E reduce the killing ability of bovine neutrophils and these affects are probably caused by impaired antioxidant status. A marginal deficiency of Se reduces both the migration and killing ability of bovine neutrophils. The Se effect on killing ability is probably via antioxidant status but migration effects may be via non-antioxidant selenoproteins. A marginal deficiency of Zn has not been shown to affect killing ability of neutrophils but has reduced migration and phagocytic activity in humans and rodents. Experiments with bovines are limited or lacking, but studies with humans and rodents have shown that Cu, Se, Zn, and vitamins A, D, and E affect gene expression of pro- and anti-inflammatory cytokines and their receptors resulting in altered immune cell function, cell populations, and acquired immune response. Experiments measuring gross lymphocyte responses in bovines generally has found enhanced proliferation of cytotoxic T-cells when chromium is supplemented; increased lymphocyte proliferation with supplemental Se; little effect on lymphocyte proliferation with supplemental Cu; and highly variable lymphocyte responses to supplemental vitamin A, B-carotene and vitamin E. Many micronutrients have profound effects on immune function, however, effects on mammary gland health and milk quality are often less evident. This is likely because control diets may not have been low enough in the nutrient of interest to impair immune function. Diets that are adequate (but not excessive) in Cu, Se, Zn, B-carotene, and vitamins A and E are necessary for good mammary gland health and most studies indicate current NRC recommendations are appropriate for those nutrients.

Key words: vitamins, trace minerals, mastitis

173 Use of records to investigate and monitor mastitis in dairies. M. W. Overton*, *University of Georgia, Athens.*

Mastitis is an infection of the mammary gland that can occur in both clinical and subclinical states and with each, somatic cell counts (SCC) rise and milk quality declines. Changes in SCC that occur as a result of infection can be used to track changes across time. It is helpful to

remember that a herd's SCC is largely the result of 2 things: 1) How many cows get mastitis? 2) How long do cows maintain mastitis? This presentation will demonstrate how SCC and clinical mastitis history can be used to investigate and monitor mastitis issues within a dairy herd. One approach is to identify the herd's clinical mastitis risk by month and by parity to assess the impact of seasonality and age on clinical case risk. Many herds do not accurately or consistently record clinical cases but do utilize monthly DHIA testing. As such, one can use the monthly data to examine changes within a cow and within a group relative to a cut-point of 200,000 SCC. This approach is illustrated in the following table and can give a quick assessment of udder health status and potential sources for further investigation.

Table 1. Common metrics for monitoring mastitis

Item	Description	Goal
Monthly clinical mastitis incidence	% of all milking cows each month that are recorded with one or more cases of clinical mastitis	< 2%
Heifer new infection risk	% of fresh heifers >200,000 SCC at first test	<15%
Dry cow new infection risk	% of cows <200,000 SCC at the last test before dry off that calve and have a first test SCC >200,000	<15%
Dry cow cure risk	% of cows with an SCC >200,000 at the last test of the prior lactation that calve with a first SCC test <200,000	>75%
New mastitis case risk	% of cows that were <200,000 SCC at the previous test but now have SCC >200,000	<9%
Cure risk	% of cows that were >200,000 SCC at the previous test but now have an SCC <200,000	>30%
Chronic cow risk	% of cows with the last two consecutive, monthly tests of >200,000 SCC	<12%
Chronic cow attributable risk	% of current cows >200,000 SCC that were also >200,000 SCC at the previous test	<65%
Uninfected cows	% of cows that with 2 consecutive tests that were <200,000 SCC at both tests	>70%

Key words: mastitis, somatic cells, monitoring

174 Advancing mastitis research: Using proteomics to identify biomarkers and evaluate adjunctive therapies. J. L. Boehmer*, *U.S. Food and Drug Administration Center for Veterinary Medicine, Laurel, MD.*

Mastitis remains a major focus of dairy cattle disease research due largely to associated economic losses and the limited availability of effective treatment options. Coliform mastitis caused by gram-negative bacteria is particularly problematic because of the fever, pain, and profound host inflammatory response induced by lipopolysaccharide (LPS), a cell wall component of gram-negative bacteria released into the mammary gland following pathogen invasion. The bovine innate immune system is very effective at eliminating gram-negative bacterial species, but a need exists to identify effective adjunctive therapies to treat the secondary local and systemic inflammatory responses caused by LPS. To facilitate new veterinary drug approvals, the Food and Drug Administration (FDA) Center for Veterinary Medicine (CVM) is looking to biomarker discovery, or the identification of a biological marker that can be measured in a fluid such as milk, and that could serve as an indicator of health or disease, or of responses to drug treatment. Historically, characterization of the bovine host response to LPS has been attempted using enzyme-linked immunosorbent assays (ELISAs), but reliance on antibodies can hinder biomarker discovery because the commercial availability of bovine-specific antibodies is limited. Proteomic strategies, including liquid chromatography coupled to mass spectrometry (LC-MS/MS) have emerged as one of the most promising approaches to identifying biomarkers of disease and novel drug targets, primarily because proteomics affords large-scale protein identification, and is not reliant on antibody availability. At CVM, the latest proteomic methodologies are being utilized to identify potential biomarkers of inflammation in bovine milk. The identification of biomarkers of inflammation related to coliform mastitis could advance current knowledge of the disease; biomarkers could also provide the regulatory criteria needed to evaluate the efficacy of potential adjunctive therapies for coliform mastitis, including non-steroidal anti-inflammatory drugs (NSAIDs).

Key words: mastitis, proteomics, inflammation

175 Effects of oxytocin administration in early life on the behavioral and physiological stress response of swine. J. L. Rault*[1], C. S. Carter[2], J. P. Garner[1], J. N. Marchant-Forde[3], B. T. Richert[1], and D. C. Lay[3], *[1]Department of Animal Sciences, Purdue University, West Lafayette, IN, [2]Department of Psychiatry, University of Illinois at Chicago, Chicago, [3]USDA-ARS-Livestock Behavior Research Unit, West Lafayette, IN.*

The swine industry is moving toward the group-housing of sows. However, group-housing can result in increased aggression and social stress, with detrimental effects on swine health and productivity. In contrast, positive social relationships can reduce the adverse effects of social stress. This could be mediated by oxytocin (OT), a neuropeptide underlying social behavior, possibly by buffering the hypothalamic-pituitary-adrenal (HPA) axis. We hypothesized that stimulating the oxytocinergic system of piglets early in life, by chronic postnatal OT administration, could provide long-term protective effects against social stress. In each of 6 litters, 2 piglets per litter received 0.25 mL (24 IU or 50 µg) of OT intranasally (OT) and 2 control littermates received 0.25 mL of saline (SAL) on postnatal d 1, 2 and 3. Each piglet was weaned at d 19 and mixed into a pen with 4 unfamiliar piglets. This social mixing was repeated from the nursery to growing phase at 8 wk of age. On each occasion, we collected videos to analyze behavior and blood samples to analyze cortisol, adrenocorticotropic hormone (ACTH), and immunological parameters over 3 d post-mixing. The pigs were then submitted twice to a resident-intruder test at 10 wk of age, and finally to a dexamethasone-corticotropic releasing hormone (Dex-CRH) challenge at 11 wk of age. Results were analyzed using a mixed model in SAS. Pigs given OT had higher ACTH concentrations than SAL pigs 24 h after weaning ($P < 0.05$) and mixing at 8 wk ($P < 0.1$). Yet, cortisol concentrations did not differ between treatments ($P > 0.1$). The Dex-CRH challenge revealed that OT pigs were less responsive to dexamethasone than SAL pigs ($P < 0.05$). At 24 h after weaning, OT barrows had a higher neutrophil:lymphocyte ratio compare with other pigs ($P < 0.05$). The behavior of OT pigs did not differ from SAL pigs after mixing ($P > 0.1$), nor did weight gain from birth to slaughter ($P > 0.1$). Administrating OT in early life modified the HPA axis. Contrary to our prediction, OT may have dysregulated the negative feedback loop of the HPA axis, leading to detrimental consequences in coping with social stress.

Key words: group-housing, oxytocin, behavior

176 Flavor preferences in sucking piglets conditioned by prenatal flavor exposure through the maternal gestation diet. J. Figueroa*, D. Solà-Oriol, R. Davin, X. Manteca, and J. F. Pérez, *Universitat Autònoma de Barcelona, Bellaterra, Barcelona, Spain.*

Volatile compounds of the maternal diet are known to be transmitted to the gravid uterus during pregnancy. Such uterine experience may affect later olfactory preferences. The aim of this study was to examine the influence of prenatal flavor exposure via mother's diet in the flavor preferences on sucking piglets. During late gestation (14d) 20 sows were assigned to one of 2 treatments; a flavored diet (Anis, 0.075% or Vanilla, 0.15%; n = 10) and an unflavored diet (n = 10). Eighty male/female piglets coming from these 20 sows (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 at d 14, 21 and 26 (2-postweaning days) after farrowing. Olfactory cues tested included strips impregnated with anis, vanilla, and water in the middle as negative control. The mother's gestational feed flavor (MFF) and control flavor (CF) were identified in each sow depending on the flavored pregnancy diet. The position of MFF and CF were rotated in each test. Piglets were tested in litter-pairs. Each test lasted 7 min, during which, the time spent by piglets in nasal contact with each strip was measured by direct observation. The average of the 2 couples per sow was analyzed using the GENMOD procedure of SAS. Piglets born to flavor-treated sows showed preferential responses toward MFF at d 14 (3.6 s/couple), 21 (3.8 s/couple) and 26 (2.9 s/couple) as compared with CF (0.7, $P < 0.001$; 0.55, $P < 0.001$ and 0.11, $P < 0.01$ s/couple) and water (0.3, $P < 0.001$; 0.95, $P < 0.01$ and 0.2, $P < 0.001$ s/couple). No different preferences were observed among flavors for control piglets. These results show that prenatal exposure to flavors via maternal diet influences piglet's preferences, probably through a positive association between the flavor and the hedonic power of the uterine experience. These preferences acquired before birth are highly resistant to extinction. This may help to spark interest for novel feeds by reducing neophobia, such as during sucking or weaning period occurs.

Key words: amniotic fluid, flavors, preference

177 Preference in weanling pigs for sweet or umami taste after in utero exposure. S. J. Chavez*[1], E. van Heugten[1], I. Ipharraguerre[2], and G. B. Huntington[1], *[1]North Carolina State University, Raleigh, [2]R&D Feed Additives, Lucta S.A., Barcelona, Spain.*

Weaning is a very stressful time transitioning the pig from a milk diet to solid feed. The addition of familiar flavors to the piglet diet has reduced stress and improved animal performance during the first several days post-weaning. The objectives of the experiment were to investigate the role of taste perception associated or not with increased nutrient supply in determining preference after weaning and determine if the taste of gestation or lactation diets influence weanling preference. Twenty sows in second or greater parity were randomly assigned to 1 of 5 diets and blocked into a sweet or umami group with a control (CON) in each group. The sweet group consisted of the CON, sucrose (SU), and non-caloric sweetener (SW), while the umami group consisted of CON, monosodium glutamate (MSG), and glutamate-free umami additive (UM). The SU was added at 5.0% of the diet, SW at 0.1%, MSG at 1.5%, and UM at 0.05%. Sows were fed 2.27 kg/d of their respective treatment diet beginning on d 10 of gestation. At farrowing, sows were given a lactation diet in the same treatment, while pigs were cross-fostered across treatments within sweet or umami groups. Pigs were weaned at 21-d and placed into pens (1.73m x 0.83m) of 2–4 pigs/pen with 2 feeders/pen. Pens were given 3-d double-choice preference tests. Data were analyzed using the t-Student test with significance at $P < 0.05$. In the sweet group, when SU was provided, pigs chose SU over 75% of the time for all preference tests that included SU. In the umami group, when MSG was provided, pigs chose MSG 80% of the time for all preference tests with MSG. Pigs in the UM group preferred ($P < 0.02$) MSG over CON, preferred ($P < 0.03$) MSG over UM, but there was no preference ($P > 0.16$) for UM over CON. The SU and SW pigs preferred ($P < 0.02$) SU over CON, control pigs preferred ($P < 0.01$) SW over CON, and SU and control pigs preferred ($P < 0.02$) SU over SW. In conclusion, pigs had a stronger preference for sweet and

umami tastes associated with increased nutrient supply, which likely resulted from the expected interplay between chemosensory perception and post-ingestive effects.

Key words: preference, sweet, umami

178 Withdrawn

179 Glucosamine:chondroitin or ginger root extract have little effect on articular cartilage in swine. D. C. Lay Jr.*[1], J. N. Marchant-Forde[1], B. T. Richert[2], and K. A. McMunn[1], *[1]Livestock Behavior Research Unit; Agricultural Research Service-USDA, West Lafayette, IN, [2]Purdue University, West Lafayette, IN.*

Sows are culled at a high rate from breeding herds due to musculoskeletal problems and lameness. Research in our laboratory has shown that even first-parity sows have significant amounts of osteochondritic lesions of their articular cartilage. Glucosamine chondroitin and ginger root extract have both been proposed as cartilage building supplements. Gilts (n = 30) were assigned to receive a daily dose of 1,500 mg glucosamine + 1,200 mg chondroitin complex (GC sows); 300 mg ginger root extract; or serve as controls. All gilts started on treatments at 3 mo of age and were maintained on diets through 2nd parity. After weaning, they were slaughtered to evaluate their articular cartilage. Cartilage was scored on scale from 0 to 4, defined as smooth to severely damaged. Hooves were scored on a scale from 0 to 3, defined as minimum cracks to deep splits. Cartilage thickness was measured by weighing 4, 6 mm biopsies taken from the articular cartilage. In addition, cross sections on the head of the femur and humerus were used to measure cartilage thickness. Cortical bone thickness was measured on both the femur and the humerus. Blood samples were collected every 4 wk (3 times) during gestation to measure differential leucocyte counts and erythrocyte sedimentation rate. Cartilage on the head of the humerus was thicker ($P < 0.02$) for sows on ginger root supplement compared with sows on control diets, with GC sows being intermediate ($P < 0.05$). However, no other measures of the quantity or thickness of cartilage or bone were different between treatments ($P > 0.10$). Osteochondritic lesions were evident in 100% of the animals on study. Erythrocyte sedimentation rate only tended to be slower for control sows compared with either supplemented group ($P < 0.12$); while mean corpuscular volume was lower ($P < 0.02$) for controls compared with gingerroot sows with GC sows intermediate. These data indicate that the level and duration of these supplements used in this study are not effective in making appreciable differences in the joint health of swine, and thus will not prove effective in increasing sow longevity and soundness through 2 parities.

Key words: swine, lameness, cartilage

180 Market pig transport losses, surface temperatures and trailer air temperatures with medium or heavy bedding on the trailer. A. Sapkota*[1], B. L. Davis[1], A. Butters-Johnson[2], and J. J. McGlone[1], *[1]Texas Tech University, Lubbock, [2]Iowa State University, Ames.*

The USA Trucker Quality Assurance program calls for the use of bedding in the trailers during transport of market pigs. Level of bedding typically varies with season and weather. The amount of bedding used during transportation of market weight pigs is not based on available science. Bedding use in different quantities may be both an economic and animal welfare concern. The objective of this study was to evaluate different amounts bedding during cold weather transport of market pigs (outside air temperatures −13.4 to 13.9 C). Trailers (n = 32 loads of approximately 165 pigs each) were fit with 6 (M) or 12 (H) bales (1 bale = 0.2 m3) of wood shavings to be used in the trailers during transportation (representing depths of 16 and 26 mm). Measures included surface temp of pigs at finishing site and at packing plant, changes in temp. inside truck during loading, trip, stops during trip, wait at plant, unloading, and number of dead on arrival (DOA), killed on arrival (KOA), dead in pen (DIP), non-ambulatory non-injured (NANI), non-ambulatory injured (NAI). Pigs were transported for 225 to 450 min. Trucks were 60% to 95% boarded (vents in the sides of trailers blocked). Statistical model included effects of bedding level, observer, bedding*observer interaction, and unloading times and boarding as covariates. Trailers at times arrived at farm sites with bedding frozen. During pig loading, inside trailer temp. increased 0.32 and 0.18 C/min for H and M, respectively ($P < 0.001$). During transport, H trailers increased ($P < 0.001$) inside air temp. (0.01 C/min) while M trailers did not increase inside air temp. (−0.008 C/min). Inside trailer air temp. when trailers arrived at the plant were 9.5 ± 1.9 C warmer ($P < 0.01$) for H than M trailers. Rates of DOA+KOA+DIP were 0.5 ± 0.2 and 0.1 ± 0.1 for H and M trailers ($P > 0.05$). Surface temp. of pigs upon arrival were 20.3 ± 1.4 C and 19.7 ± 1.6 C for H and M trailers ($P > 0.05$). More data are needed to clarify effects and data collection is ongoing. More bedding may provide a warmer inside air temp. but may pose a risk of increased pig deaths during cold weather transport.

Key words: pigs, animal welfare, transport

181 Brain lesions and time to death resulting from application of a non-penetrating captive bolt to anaesthetized nursery piglets. T. M. Casey-Trott[1], R. Brooks[2], P. V. Turner[1], S. G. Nykamp[1], M. Litman[1], S. T. Millman[2], and T. M. Widowski*[1], *[1]University of Guelph, Guelph, Ontario, Canada, [2]Iowa State University, Ames.*

A previous study indicated that a non-penetrating captive bolt (NPCB) was effective for euthanasia of 100 neonatal piglets based on immediate and sustained insensibility until full cardiac arrest. The objective of the current study was to assess the brain lesions caused by a NPCB in 20 piglets in 4 weight classes (n = 5 piglets: 3, 5, 7, or 9 kg) as compared with brain lesions of the neonatal piglets from the previous study. Since this was a novel technique for piglets ≥5.5 kg, they were anaesthetized with 71.4 mg/ml ketamine, 14.3 mg/ml xylazine and 1.4 mg/ml butorphanol 0.2 mL/kg IM before NPCB application to ensure insensibility. The NPCB was placed on the frontal bone between the eyes and fired twice in rapid succession, followed by one shot to the back of the skull behind the ear. Piglets were monitored for rhythmic breathing, neuromuscular leg spasms, and heart beat until full cardiac arrest. Macroscopic, histological, and CT scans were scored post mortem to assess degree of skull fracture and hemorrhage. One piglet required an additional shot following a misfire due to presence of rhythmic breathing. Breathing was immediately absent in all other piglets. Leg spasms ceased in 148 s (±12.4 SE). An alternative method (sodium pentobarbital 100 mg/kg) was required for one piglet due to sustained heartbeat. All other piglets reached full cardiac arrest in 371 s (±17.9 SE). Moderate to severe macroscopic damage was reported in ≥90% of piglets. Histological analysis showed moderate to severe subdural (SD) hemorrhage and mild to moderate parenchymal (P) hemor-

rhage. Fracture displacement (FD) averaged 9.38 mm (±0.84 SE). In comparison to the brain lesions of neonatal piglets, damage was less severe in anaesthetized piglets (Mann-Whitney test for ordinal data: SD: $P = 0.007$; P: $P = 0.041$) despite greater FD (t-test: $P = 0.019$). Although brain damage in the anaesthetized piglets was less severe than that of the conscious neonates, the NPCB still caused parenchymal brain lesions and effectively induced cardiac arrest. The next trial will test the effectiveness of the NPCB on conscious piglets up to 9 kg.

Key words: euthanasia, piglet, brain lesion

Animal Health: Johne's Disease

182 Bayesian analysis of longitudinal Johne's disease diagnostic data without a gold standard test. C. Wang*[1], B. Turnbull[2], S. Nielsen[3], and Y. Gröhn[2], *[1]Iowa State University, Ames, [2]Cornell University, Ithaca, NY, [3]University of Copenhagen, Frederiksberg, Denmark.*

A Bayesian methodology was developed based on a latent change-point model to evaluate the performance of milk ELISA and fecal culture tests for longitudinal Johne's Disease diagnostic data. The situation where there is no perfect reference test was considered, i.e., no "gold standard." A change-point process with a Weibull survival hazard function was used to model the progression of the hidden disease status. The model adjusted for the fixed effects of covariate variables and random effects of subject on the diagnostic testing procedure. Markov chain Monte Carlo methods were used to compute the posterior estimates of the model parameters that provide the basis for inference concerning the accuracy of the diagnostic procedure. Based on the Bayesian approach, the posterior probability distribution of the change-point onset time can be obtained and used as a criterion for infection diagnosis. An application is presented to an analysis of ELISA and fecal culture test outcomes in the diagnostic testing of paratuberculosis (Johne's disease) for a Danish longitudinal study from January 2000 to March 2003. The posterior probability criterion based on the Bayesian model with 4 repeated observations has an area under the receiver operating characteristic curve (AUC) of 0.984, and is superior to the raw ELISA (AUC = 0.911) and fecal culture (sensitivity = 0.358, specificity = 0.980) tests for Johne's disease diagnosis.

Key words: Johne's disease, longitudinal, no gold standard

183 Environmental contamination with *Mycobacterium avium* ssp. *paratuberculosis* in endemically infected dairy herds. R. L. Smith*[1], Y. H. Schukken[1], A. K. Pradhan[1], J. M. Smith[2], R. H. Whitlock[3], J. S. Van Kessel[4], D. R. Wolfgang[5], and Y. T. Grohn[1], *[1]Department of Population Medicine and Diagnostic Sciences, College of Veterinary Medicine, Cornell University, Ithaca, NY, [2]Department of Animal Science, University of Vermont, Burlington, [3]Department of Clinical Studies, New Bolton Center, School of Veterinary Medicine, University of Pennsylvania, Kennett Square, [4]Environmental Microbial and Food Safety Laboratory, ANRI, USDA-ARS, Beltsville, MD, [5]Department of Veterinary and Biomedical Science, Penn State University, University Park.*

Environmental contamination with *Mycobacterium avium* ssp. *paratuberculosis* (MAP) is thought to be one of the primary sources of infection for dairy cattle. The exact link between fecal shedding of MAP by individual cows and environmental contamination at the herd level was explored with a cross-sectional analysis of longitudinally collected samples on 3 dairy farms. Composite samples from multiple environmental sites in 3 commercial dairy herds in the Northeast US were cultured quarterly for MAP, providing 898 samples (113 (12.6%) were culture-positive), and all adult animals in the herds were tested biannually by fecal culture (FC), for 6 years. Of the environmental sites sampled, manure storage areas and shared alleyways were most likely to be culture-positive. Environmental sample results were compared with FC results from either the concurrent or previous sampling date at both the herd and the pen level. At the herd level, a 1 log unit increase in average fecal shedding increased the odds of a positive environmental sample by 3.5 and increased the average amount of MAP in the sample by 2.1 cfu/g. At the pen level, the odds were increased by a factor of 3 and the average amount of MAP was increased by 1.1 cfu/g. There was no significant relationship between environmental site status and the distance between shedding animals and the site, and neighboring pens did not affect the results of the pen-level analysis. The amount of MAP in pen-level samples was positively correlated with the number of animals in the pen shedding >30 cfu/g of MAP. At least 6 environmental samples met the criteria for the US Voluntary Bovine Johne's Disease Control Program on 45 of the 65 testing dates; of these, 16 of the 42 FC-positive testing dates were positive by the 6-sample environmental testing method, resulting in a herd sensitivity of 0.38 (95% CI: 0.23 to 0.52), and 0 of the 3 FC-negative testing dates were positive by this method. Although environmental sampling can be used as a tool in understanding the level of MAP infection in a herd or pen, it does not appear to be a sensitive diagnostic method for herd positivity and should be used with caution.

Key words: Johne's disease

184 *Mycobacterium avium* ssp. *paratuberculosis* promotes rapid IL-1β release and macropahge transepithelial migration. E. Lamont*[1], S. O'Grady[1], W. Davis[2], T. Eckstein[3], and S. Sreevatsan[1], *[1]University of Minnesota, [2]Washington State University, [3]Colorado State University.*

Pathogen processing by the intestinal epithelium involves a dynamic innate immune response initiated by pathogen-epithelial cell cross-talk, which may be augmented by interactions between host pathways and/or cell types. Studies investigating *Mycobacterium avium* ssp. paratuberculosis, the causative agent of chronic enteritis in ruminants, focus solely on the macrophage and largely neglect responses within the epithelium. We show that *M. avium* ssp. *paratuberculosis* induces phagosome acidification within bovine epithelial (MAC-T) 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. 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 *M. avium* ssp. *paratuberculosis*; thereby, setting the tone for the ensuing infection. We hypothesized that *M. avium* ssp. *paratuberculosis* harnesses host responses to recruit macrophages to the site of infection to ensure its survival and dissemination. We investigated macrophage recruitment in response to *M. avium* ssp. *paratuberculosis* using a MAC-T-bovine macrophage coculture system. Within 10 min of infection, macrophages were recruited to the apical side of MAC-T cells. Inhibition of phagosome acidification and IL-1β abrogated this response, while MCP-1/CCL2 blocking had no effect. IL-1β processing was dependent upon Ca^{2+}uptake from the extracellular media and intracellular Ca^{2+}oscillations as determined by EGTA and BAPTA-AM treatments. Thus, *M. avium* ssp. *paratuberculosis* guidance of phagosome-acidification enlists IL-1β processing in an extracellular calcium dependent manner to efficiently transverse the epithelium and into its niche—the macrophage.

Key words: *Mycobacterium avium* ssp. *paratuberculosis*, interleukin 1 beta, macrophage recruitment

185 Real-time estimation of the lacto-presence of *Mycobacterium avium* subspecies *paratuberculosis* in milk and milk products originating from goat and cattle herds endemic for Johne's disease. S. V. Singh*[1], T. Raghuvanshi[1], R. B. Sharma[1], B. Singh[1], A. V.

Singh[1], P. K. Singh[1], A. Kumar[1], and A. Srivastav[2], *[1]Central Institute for Research on Goats, Mathura, Uttar Pradesh, India, [2]College of Veterinary Sciences, Mathura, Uttar Pradesh, India.*

Mycobacterium avium subspecies paratuberculosis (MAP) is the cause of Johne's disease in ruminants and is endemic in countries where investigated including India. Live MAP has been recovered from raw and pasteurized milk and milk products. Information on the status of MAP in the milk and milk products is extremely limited. Real time estimate of lacto-presence of MAP were studied in milk and milk products originating from herds endemic for Johne's disease. Forty eight and 23 individual milk samples were collected from two goat farms (Farm A. and Farm B) and a cattle farm (Farm C) in Mathura region of North India. Eighteen pooled goat milk samples from the Farm A. and B. and 24 paneer (raw cheese from pooled milk) samples were collected. Samples were screened using microscopy, indigenous ELISA kit and IS900 PCR to estimate lacto-presence of MAP. Tests showed variable lacto-presence of MAP in milk and milk products. Using microscopy, 25, 4.2, 5.6 and 12.5%, of milk samples of Farm A. and B, pooled milk and paneer samples were positive, respectively. In milk-ELISA, 25% of individual milk samples of Farm A. and B. were positive, whereas, none of the pooled milk samples were positive for MAP. Screening of 9 and 3 individual milk samples of Farm A. and B, 3 pooled milk samples and 2 samples of paneer by IS900 PCR, one milk sample of Farm A. was positive. Lacto-presence of MAP was higher in milk samples originating from cattle herds and of 23 milk samples, 56.5, 86.9 and 30.4% were positive in microscopy, ELISA and PCR, respectively. Lacto-presence of MAP in the two goat farms was low to moderate and was high in the cattle herd. Load of MAP in livestock herds had significant correlation with presence of MAP in milk and milk products originating from herds endemic for JD, thereby posing serious health risk to human population.

Key words: milk and milk products, lacto-prevalence, *Mycobacterium avium* subspecies *paratuberculosis*

186 Association of Bsa I polymorphism of MHC Class II DRB gene with *Mycobacterium avium* ssp.*paratuberculosis* bacterimia in Jamunapari breed of goats. S.V. Singh, P. Rai, P. K. Singh*, A. V. Singh, M. K. Singh, and J. S. Sohal, *Central Institute for Research on Goats, Mathura, Uttar Pradesh, India.*

Johne's disease (JD) caused by *Mycobacterium avium* subspecies *paratuberculosis* (MAP) is responsible for huge economic losses in livestock productivity worldwide. Failure to detect early infection and lack of effective vaccine hamper control of disease. Studies on variations in host genetics that contribute to resistance or susceptibility to disease may potentially help to control disease effectively. Polymorphism in exon-2 of caprine MHC Class II DRB region further elucidated the effect of genetic variation in this region on MAP bacteremia in Jamunapari goats. Blood samples from 38 adult goats of Jamunapari farm (Central Institute for Research on Goats in Mathura) endemic for JD were analyzed to detect MAP infection using IS900 PCR and characterize MHC class II DRB region using Bsa I. PCR-RFLP. Of 38 goats 26 (68.4%) were positive for presence of MAP in blood. Three genotypes for Bsa I, namely BB, Bb and bb (with genotypic frequency of 0.711, 0.025 and 0.265, respectively) and two alleles B. and b (with allelic frequency of 0.843 and 0.157, respectively) were observed in the DRB second exon region of Jamunapari goats. Non-significant effect of Bsa I. MHC class II alleles with MAP bacteremia was found ($\chi^2 = 1.950$, df = 2, $P = 0.005$). There was no significant difference in distribution of all three genotypes (BB, Bb and bb) between goats positive or negative for MAP DNA in blood. Distribution of homozygous BB alleles was approximately significant ($\chi^2 = 3.779$, $P = 0.052$) in MAP positive group of goats. Genetic variation of MHC Class II DRB region may regulate MAP infection; therefore, a comprehensive study on substantial goat population is needed to get some conclusive impact of BsaI based single nucleotide polymorphism and others of DRB region alleles on JD susceptibility and / or resistance.

Key words: paratuberculosis, MHC class II DRB gene, polymorphism

187 Johne′s program—Impact on education and outreach activities. K. E. Olson*, *KEO Consulting, Schaumburg, IL.*

Federal investment in the Voluntary Bovine Johne′s Disease Control Program declined from $21m in 2003 to $6.8m in FY09. Primary metrics have included number of herds in the program and samples tested in approved labs; however, it is anticipated that program investments have produced other activities that will enhance efforts to address the disease. State Designated Johne′s Coordinators (DJCs), Dairy Herd Improvement Association (DHIA) service units and, dairy and beef producer organizations were surveyed to document program participation changes and identify current activities that will affect the producer′s ability to deal with the disease. Responses were received from 32 DJCs, 16 beef organizations, 5 dairy cooperatives, 12 DHIA organizations and 3 dairy records processing centers. The following program impacts resulting from funding reductions were reported by DJCs: 25 ran fewer individual samples; 25 had fewer Risk Assessments and Management Plans (RAMPs) completed; 24 certified or re-certified fewer veterinarians; 22 conducted fewer educational events; 19 had fewer committee meetings. The DJC survey quantified activities not measured in program metrics that affect producer knowledge and ability to deal with the disease including: 1,434 Johne′s certified veterinarians available to work with producers; 56 meetings with 9.721 participants; 10,720 copies of 27 publications distributed; 13 internet sites devoted to Johne′s information delivery; 12 reported articles in trade publications reaching 9,656 readers. Producer organizations reported:1 beef meeting with 250 producers; 20 dairy meetings with 975 producers; 6 DHIAs trained technicians and 4 met with producers; 207,033 milk ELISA samples run by DHIA, a 10% increase. Research is currently funded by one breed association and JDIP is providing competitive grants that have leveraged additional outside funds. A concern identified is the need for additional communication between program leadership and producers relative to program operation with reduced funding. Program resources have developed a strong infrastructure to assist producer efforts, but additional planning is needed to find ways to maintain needed resource and make them available to producers.

Key words: Johne's, JDIP

188 Mathematical modeling of *Mycobacterium avium* subspecies *paratuberculosis* infection transmission in dairy cattle: Current status and future directions. Z. Lu*[1], R. Mitchell[1], R. Smith[1], Y. Schukken[1], Y. Gröhn[1], K. Ahmadizadeh[2], M. Teose[2,3], T. Damoulas[2], and C. Gomes[2], *[1]Department of Population Medicine and Diagnostic Sciences, College of Veterinary Medicine, Cornell University, Ithaca, NY, [2]Department of Computer Science, Cornell University, Ithaca, NY, [3]Center for Applied Mathematics, Cornell University, Ithaca, NY.*

The objective of this presentation is to review the current status and to outline the future research directions of mathematical modeling of *Mycobacterium avium* subspecies *paratuberculosis* (MAP) infections

in dairy cattle. As one of the most important infectious diseases in dairy cattle, MAP infections cause considerable economic losses in the dairy industry and pose a potential threat to public health. Control of MAP is difficult due to the long incubation period and poor diagnostic tests for early MAP infections. To have a better understanding of MAP transmission dynamics and to evaluate the effectiveness of MAP control strategies in dairy cattle, several within-herd mathematical compartment models on the basis of MAP infection history have been developed using deterministic and stochastic modeling approaches. We reviewed these mathematical models and examined their usefulness and limitations. Subsequently, we identified 4 potential research directions in mathematical modeling of MAP infection at different levels of organization. The first is to investigate how MAP is transmitted between herds in a large spatial region. In the United States, studies showed that at least 70% of dairy herds were infected with MAP. To understand this high herd-level MAP prevalence and find effective control strategies for MAP at herd level, construction of a network structure of animal movements will be necessary. The second research direction is to continue modeling the within-herd level of MAP infection, considering more challenging problems such as MAP strain competition, co-infection, and the importance of environmental transmission. The third research direction is to study the infection process of MAP and host immune response at the individual animal level. Mathematical models at this level will be particularly helpful for understanding the potential mechanism of MAP vaccines. The fourth direction is to build individual-based economic optimization models and to find optimized MAP control strategies within a herd.

Key words: paratuberculosis, mathematical modeling, dairy cattle

189 Vertical transmission or increased susceptibility to MAP? E. Knupfer[1], R. M. Mitchell*[2], A. K. Pradhan[2,3], A. Kramer[1], J. Dieguez[4], R. H. Whitlock[5], T. Fyock[5], and Y. H. Schukken[2], *[1]Utrecht University, Utrecht, the Netherlands, [2]Cornell University, Ithaca, NY, [3]University of Maryland, College Park, [4]Universidade de Santiago de Compostela, Spain, [5]University of Pennsylvania, New Bolton Center.*

MAP-infected dairy cattle are assumed to be a high risk for transmitting infection to their daughters. Alternatively, if both dam and daughter are genetically more susceptible to MAP, they may be both infected but not necessarily due to vertical transmission. Using strain typing techniques including multi locus short sequence repeat (MLSSR) typing allows a potential distinction between vertical transmission and genetic susceptibility. Analyzing strain diversity in longitudinal data sets provides additional insight into within-herd infection dynamics, including the transmission of MAP from dams to daughters. To investigate the importance of vertical transmission, we identified 12 pairs of dams and daughters for which both animals are known MAP infected from the Regional Dairy Quality Management Alliance (RDQMA) study herd in NY. All adult animals were tested for MAP via fecal culture semi-annually for seven years. Tissue samples were available on a subset of cull animals. Animals were considered MAP-infected if they ever cultured positive or if any of their tissues cultured positive at slaughter. Cultures were performed at University of Pennsylvania on HEYM solid media. Positive cultures were substreaked and processed for MLSSR typing. Following genotyping, isolates from each dam-daughter pair were compared to determine whether they shared the same MAP genotype. Environmental MAP burden at birth was assessed via typing of MAP-positive environmental samples (collected four times a year) and known MAP-infected animals present on the farm during the high-risk first year of life. Of the 12 infected dam-daughter pairs, 9 had identical strains shared between the dams and daughters. In addition, 2 daughters had the dam's strain as well as another circulating strain. Overall, there were 7 strains represented in the daughters that did not come from dams (2 daughters had multiple strains which did not originate from the dam). These results lend additional importance to the impact of genetics on susceptibility, as 5 of 12 daughters carried different strains of MAP than their dams, even when concurrently infected with the dam's strain.

Key words: *Mycobacterium avium* subspecies *paratuberculosis*, vertical transmission, strain typing

190 MAP co-infection or evolution? R. M. Mitchell*[1], E. Knupfer[2], A. K. Pradhan[1,3], A. Kramer[2], J. Dieguez[4], R. H. Whitlock[5], T. Fyock[5], and Y. H. Schukken[1], *[1]Cornell University, Ithaca, NY, [2]Utrecht University, Utrecht, the Netherlands, [3]University of Maryland, College Park, MD, [4]Universidade de Santiago de Compostela, Spain, [5]University of Pennsylvania, New Bolton Center.*

Co-infection is important in human tuberculosis (Htb), especially in high prevalence environments where multiple exposures increases likelihood of infectious progression. This phenomenon is not often studied in bovine mycobacterial infections, partially due to the lack of differentiation between host-specific strains of MAP. However, as illustrated by recent research on cull animals and longitudinal sampling on dairy farms which includes tissue samples at slaughter, cattle live in a very high prevalence environment. If the many subclinically infected animals which are in close contact with herdmates are intermittently shedding throughout their lives, this will result in multiple exposures. We examined whether animals shed the same MAP strain throughout their lifespan. All animals on the NY farm in the Regional Dairy Quality Management Alliance (RDQMA) were tested for MAP using fecal sampling semi-annually for seven years. Tissue samples were available on a subset of cull animals. Cultures were performed at University of Pennsylvania on HEYM solid media. All positive fecal cultures and one or more positive tissue sample from each animal were evaluated by multilocus short sequence repeat typing (MLSSR) for each animal. Strain types were assigned based on number of repeats at each MLSSR locus selected. In the 96 animals with at least one positive fecal or tissue culture over the course of the longitudinal study, there were 13 strain types identified. Of the 59 animals with only one sample processed, 4 (7%) had mixed infections (clear evidence of two sequences of differing repeat lengths) when analyzed. Of the 37 animals with more than one sample analyzed, 19 (51%) had more than one MAP strain throughout life including 17 with mixed infections. This close study of within-farm dynamics reveals that it is not uncommon for animals to be infected with multiple strains of MAP. The often close relationship between strains in multiple infections brings to mind the possibility that what we are seeing in MAP is really within host evolution of MAP strains rather than (mixed) co-infection in a portion of multiply infected animals.

Key words: *Mycobacterium avium* subspecies *paratuberculosis*, strain typing, multiple infections

191 Towards understanding endemicity of MAP infection in dairy herds. R. M. Mitchell*[1], G. F. Medley[2], and Y. H. Schukken[1], *[1]Cornell University, Ithaca, NY, [2]Warwick University, Coventry, UK.*

Maintenance of MAP infection on dairy farms is non-trivial in terms of infectious dynamics. Indeed a large portion of animals do not shed MAP throughout their lifetimes despite being truly infected when their tissues are cultured at slaughter. In this study we incorporate the

infection biology of MAP into a mathematical model which takes into account age and dose dependent infectious progression. The model incorporates a large proportion of truly infected but never shedding animals which are observed as MAP positive in tissue culture studies but not in fecal shedding. We modified our current models of MAP in Matlab to incorporate a slow-progressing latent category based on previously published data on dose and age dependent infection probabilities. In this model, animals either shed shortly following exposure and enter an early shedding compartment, or do not shed early and enter a slow-progressing latent state- where they remain for an extended period of time. Animals which shed early have a shorter duration of latency following this early compartment and progress to late shedding. Infectious progression is modeled differently for animals which receive high or low initial doses of MAP. Animals which receive high doses of MAP spend a longer period of time in the early shedding compartment and are therefore more likely to come into contact with susceptible young animals during this time of increased infectiousness. Model output indicates that endemic MAP infection is possible at transmission rates that would not allow successful entry of MAP in a fully susceptible population. Indicating that MAP endemicity is driven by different infection dynamics than the initial establishment of MAP in a dairy herd. Our model indicates that there are 2 sustainable MAP infection equilibria at relative contact rates of less than one between adult animals and calves. This structure appears to be unique to dairy cattle, and may explain why endemically MAP infected herds occur frequent. Our findings explain why slaughter samples show a dramatically higher prevalence of MAP infection in tissue samples compared with MAP fecal shedding.

Key words: *Mycobacterium avium* subspecies *paratuberculosis*, endemicity, models

192 *Mycobacterium avium* subspecies *paratuberculosis*-infected macrophages have different protein and transcriptome profiles than control or uninfected culture mates. E. Kabara* and P. Coussens, *Michigan State University, East Lansing.*

Previously, our group presented evidence that *Mycobacterium avium* subspecies *paratuberculosis* (MAP)-infected macrophages are significantly less apoptotic than uninfected, culture mates (bystander macrophages) found in a MAP-infected culture. This mirrors the apoptotic status of Mycobacterium tuberculosis (TB)-infected macrophages and bystander cells found in TB-infected cultures. Currently, little published work has been done studying apoptotic pathway regulation in TB and MAP-infected macrophages. Therefore, our goal was to investigate the mycobacterial specific mechanism and corresponding host reactions that are employed to prevent apoptosis in mycobacterium-infected macrophages. We hypothesize that MAP-infected macrophages have differential expression of several apoptotic when compared with bystander macrophages. Two distinct methods were undertaken to test this hypothesis. First, we used flow cytometry with fluorescent labeling of MAP bacteria and antibody labeling of host proteins to study the expression and phosphorylation status of host proteins of MAP-infected, bystander, and control macrophages with and without stimulation. Among our many observations, we saw no significant differences in MAPK protein expression and phosphorylation in unstimulated control and MAP-infected macrophages which is in agreement with previous publications on this subject. Second, we isolated RNA from control and MAP-infected macrophages cultures where over 90% of the cells are infected to study a population of MAP-infected macrophages without bystander cells. These samples were used in RT-qPCR testing of apoptosis pathway transcripts. We observed significant upregulation of Caspase 3 and 9 mRNA expression in MAP-infected macrophages as compared with controls while seeing no significant difference in caspase 8 expression between the 2 samples (P-value <0.05).

Key words: Johne's, apoptosis, pathway

193 Effect of changes in management practices on the risk of Johne's disease in Minnesota Johne's disease demonstration dairy herds. L. A. Espejo*, S. Godden, and S. J. Wells, *University of Minnesota, Department of Veterinary Population Medicine, St. Paul.*

Certain management practices have been recommended to minimize transmission of Johne's disease between infected and susceptible cattle. The objective of this study was to evaluate the risk of testing positive and its association with changes in recommended management practices in different birth cohorts. Eight dairy herds and approximately 6,000 cows were enrolled in the Minnesota Johne's Disease Demonstration Herd Program. Herds were monitored for a period between 5 to 10 years. Annual testing for *Mycobacterium avium* ssp. *paratuberculosis* was performed for all cows that calved, using bacterial culture and serum ELISA. Risk assessments were performed annually to measure the level of implementation of the recommended management practices. Eight birth cohorts were defined based on the date of cow enrollment in the program. Birth cohorts −2 and −1 corresponded to cows that were born 2 and 1 year before the beginning of the program, respectively, and cohorts 0 to 5 corresponded to cows that were born 0 to 5 years after the beginning to the program. The annual risk assessment score was used to quantify the level of exposure by birth cohort and herd. A time dependent Cox's regression model was used to model the time to test positive, explained by herd, birth cohort and birth cohort exposure level. Compared with birth cohort −2, there was a reduction of the hazard ratio (95%CI) of bacterial culture positivity of 0.65 (0.49 to 0.85), 0.56 (0.42 to 0.73), 0.66 (0.48 to 0.90), 0.38 (0.26 to 0.58), 0.22 (0.14 to 0.35), 0.22 (0.14 to 0.34), and 0.20 (0.13 to 0.32), for birth cohorts −1, 0, 1, 2, 3, 4, and 5, respectively. Similar results were obtained for serum ELISA. The instantaneous hazard of testing positive for both tests increased with the level of exposure, however, the strength of this association decreased over time. There was a reduction in the transmission of Johne's disease associated with the level of implementation of the recommended management practices.

Key words: Johne's disease, disease control

194 Zinc-finger nucleases: Innovations in custom-designed modification of the swine genome. J. J. Whyte*, J. Zhao, K. D. Wells, M. S. Samuel, K. M. Whitworth, E. M. Walters, M. H. Laughlin, and R. S. Prather, *University of Missouri, Columbia.*

Genetically modified swine hold great promise in the fields of medicine and agriculture. Pigs are similar to humans in anatomy and physiology and they reproduce rapidly to provide a reliable source of research animals. By combining emerging gene modification technologies with the completion of the swine genome, custom-designed pigs will provide urgently needed organs and therapeutic proteins for patients, realistic models of human disease, and high quality, efficiently produced food to meet the nutritional demands of the ever-expanding world population. Conventional gene targeting (adding foreign DNA via homologous recombination) is highly inefficient in mammalian somatic cells and provides little control over the site of transgene integration. The landscape of gene modification has recently changed with the use of zinc-finger nucleases (ZFNs) to enhance targeting efficiencies up to 10,000-fold. ZFNs consist of a nonspecific endonuclease domain and a sequence-specific zinc-finger DNA binding domain. Custom pairs of ZFNs heterodimerize upon binding DNA at predetermined gene loci to form a catalytically active nuclease complex. The resulting cleavage triggers DNA repair pathways that can be exploited to either disrupt gene coding or enhance insertion of exogenous DNA constructs. ZFNs have been used to genetically alter organisms such as plants, insects, zebra fish and rats. Recent publication of the first genetic modification in pigs by combining ZFN technology with somatic cell nuclear transfer has opened the door to genome targeting with a precision that was not previously possible in a large animal model. A preliminary report describing ZFN-based knockout of the α1,3-galactosyltransferase gene in porcine fibroblast cells raises the possibility of model pigs with selective knockout of endogenous genes without introducing any transgenic sequence into the genome. This presentation will provide an overview of ZFNs, emphasizing their potential to accelerate the production of genetically modified pigs of agricultural and biomedical importance. Current methods of ZFN design, important considerations for their safe and effective use in modification of the swine genome, and future innovative applications of this technology in pigs will be discussed.

195 Improved RNA quantitation and applications to animal science. C. D. Haudenschild*, *Illumina Inc., Hayward, CA.*

In the past few years we have seen numerous significant changes in the way we approach the study of organism development and the biology of diseases in model and non model organisms. What was mostly a gene-centric method that relied on following simple expression patterns is now largely a statistically based science. With the introduction of next generation sequencing methods to the study of gene expression, we can now rely on whole genome views of the transcriptome leading to ever increasing data volumes and compare large sample numbers. Due to the variety of information sources we can now interrogate, we are able to start appreciating the true complexity of cells and the significance of the variables involved. In the study of gene expression, one now considers temporal expression in conjunction with what particular alleles are transcribed in what tissue and which splice variants are predominant. The analysis of translation state also became available and can provide essential pertinent information. Analyzing whole genome sequences in conjunction with sequence based expression profiles on large segregating populations should also allow for better QTL characterizations. The data permits the enhancement of usability of newly assembled genome by better defining gene structure annotation and thus allowing for better comparison across closely related species. Numerous protocols are available and examples of applications will be described.

196 Informatics-driven biological research: Infectious diseases as an example. B. Sobral*, *Virginia Bioinformatics Institute at Virginia Tech, Blacksburg.*

Infectious disease researchers have to deal with diverse types of data to develop hypotheses about candidate macromolecules that can be used to design countermeasures (diagnostics, vaccines and therapeutics). Even considering only molecular data, it is a challenge to access all the public information available to them and implement workflows that support their analysis needs. I will use the example of *Brucella* spp. to illustrate how public, open, freely available resources can be designed, developed, and implemented in support of such infectious disease research and development goals. There are now 40 genomes of *Brucella* (Alphaproteobacteria; Rhizobiales) sequenced, sampling all known species and biovars of this facultative intracellular pathogen. A phylogenomic analysis of these genomes united all *Brucella* when they were compared with outgroups including *Ochrobactrum*, *Bartonella*, *Mesorhizobium* and *Agrobacterium*. Although the *Brucella* genomes are united, there is some interesting diversity. A well-studied group of *Brucella* species are united in a clade separated by a long branch. This large clade has little phylogenetic depth, but species within this group are known to have specific host preferences. Sub-branching patterns within this group reflect these host preferences and specific protein families unique to, and absent from, these groups were identified. Two novel strains, *Brucella inopinata* BO1T and BO2, were recently identified and isolated from human patients. Genomes from these strains, as well as 2 new isolates isolated from Australian rodents (*Brucella* spp. NF2653 and 83/13), are quite unique and separated from the rest of the *Brucella*. Although they share many similarities with the other *Brucella* species, they are missing many large areas of their genomes that can be seen in other *Brucella*. Analyses of these areas using new bioinformatic tools and data resources have shown that some of these missing areas include previously identified genomic islands and virulence factors, and there are novel findings as well that impact biochemical pathways and unique changes in the synthesis of lipopolysaccharide.

Breeding and Genetics Symposium: Really Big Data: Processing and Analysis of Very Large Datasets

197 High performance computing and really big datasets: Overview and best practices. F. Foertter*, *Genus plc, Hendersonville, TN.*

More often than not, researchers today find themselves overwhelmed with increasingly large data sets. It has become difficult to develop efficient workflows to edit and then analyze large data sets to extract meaningful results. Whereas desktop computers have sufficed in the past, data sets involving high density SNP or sequence data are growing so large that new high performance computing (HPC) methods are under development to allow efficient data housing, searching and analysis. This presentation will provide scientists an insight on how Genus is using HPC to manage large data sets in both research and genomic evaluation. Topics will include a review of hardware choices, including power/temperature and scalability considerations, and data storage and density. Also important are the financial and security considerations between owned clusters, university and national laboratory clusters, and commercial options such as pay-as-you-go clouds. Software issues will also be addressed, including the advantages and disadvantages of commercial versus Open Source and discussion on building in-house codes. Relevant setup scenarios and industry best practices related to Genus' implementation will also be presented. Finally we will demonstrate how Genus is currently leveraging HPC to decrease time-to-results in research, increase accuracy in genomic evaluations, and therefore increasing the rates of genetic improvement.

Key words: computation, genomics, analysis

198 Data structures and visualization. J. B. Cole*, *Animal Improvement Programs Laboratory, ARS, USDA, Beltsville, MD.*

Genomic tools for genetic improvement have been rapidly adopted in many livestock species over the past few years. This presents new challenges for data collection and management, as well as opportunities for analysis and presentation. The US national dairy database currently includes genotypes for 83,117 bulls and cows and 2,620 imputed dams representing 3 different densities and 4 chip versions. Storage requirements for these genotypes are modest, even when high-density (>500,000K) genotypes are imputed from lower densities. However, storage requirements for intermediate and results files for genetic evaluations are much more substantial, particularly when multiple runs must be stored for research and validation studies. Full-sequence data will be available at reasonable cost in the near future, and will require much more storage. The greatest gains in accuracy from genomic selection have been realized for traits of low heritability, such as fertility and longevity, and there is increasing interest in new health and management traits. In addition to data on novel traits, potentially useful economic and demographic information is being collected by on-farm computer and analytical systems. There is increasing interest in traits such as feed efficiency and resistance to climate change, but the collection of sufficient phenotypes to produce accurate evaluations may take several years, and high-reliability proofs for older bulls are needed to precisely estimate marker effects. As traits proliferate and the number of genotyped animals continues to grow increasingly sophisticated analytical approaches will be tractable. Machine learning algorithms may be useful in identifying previously unrecognized relationships among traits, and the analysis of genetic (co)variances among loci could help identify important gene networks. Improved visualization tools, particularly those capable of processing very large volumes of data in a reasonable amount of time, are needed to help better understand the results of analyses. The challenges and opportunities presented by growing amounts of phenotypic and genomic data are generally similar regardless of the species in question.

Key words: genomics, data structures, visualization

199 Computational challenges in genetic evaluation with really big datasets. I. Aguilar*[1] and I. Misztal[2], *[1]Instituto Nacional de Investigación Agropecuaria, INIA Las Brujas, Canelones, Uruguay, [2]Animal & Dairy Science Department, University of Georgia, Athens.*

Genomic selection poses new computational problems. Genotypes for each individual require a large amount of storage and this amount will increase with larger SNP chips and eventually with individual genome scans. Computations in genomic selection using this data seem to require even more computing power especially when large fractions of population will be genotyped. Looking back in the history of animal breeding, 2 choices exist, brute force or new theoretical developments. For example, storing large A matrices required massive computers and inverting those seemed impossible. Rules to create A^{-1} explicitly by Henderson made these computations trivial. Even with A^{-1}, creating the mixed models explicitly required large resources. The iteration on data algorithm decreased the required resources drastically. Developments in sparse matrix inversion and of the AI algorithm made fast REML a reality. The genomic selection is most likely no different. While the genomic data seems huge, use of larger SNP chips results in limited gains. Sampling for best subset of SNP as in BayesX is time consuming, but methods based on the genomic relationship matrix G seem as efficient especially with larger data sets. In fact, given G the genomic selection may be another BLUP in the form of single-step GBLUP where computations are not much greater than in regular BLUP. The limiting factor in ssGBLUP is constructing and inverting G for many genotypes. Careful programming makes these operations much less expensive. For example, a regular algorithm for creating G for about 14k genotyped individuals required about a day. After using custom libraries and exploiting parallel computing via OpenMP, the computing time was reduced to 15 min. It is possible that G can be made sparse for large number of genotypes and that the number of useful genotypes for prediction will be limited. Hardware improvements have resulted in machines with multiple cores, with much faster speed and bigger cache memory and with more memory. Nevertheless, for successful implementations of large genetic evaluations, improvements in methodology were as important as advances in computer power.

Key words: genetic evaluation, computing methods, genomic selection

200 The implementation of analysis of large data. M. Coffey*, *Scottish Agricultural College, Penicuik, Midlothian, UK.*

Developments in DNA based technologies have led to large amounts of genotype data being available for farmed livestock. This has created great excitement among those engaged in research since data equals papers. However, for those engaged in national genetic evaluations

the logistics of handling so-called large data sets creates unique challenges that generate little scientific interest. These challenges must be overcome to exploit these new technologies and must be overcome in a way that does not create disruption during the transition from conventional evaluations to genomic EBVs (GEBVs). What constitutes large is ill defined but data in the terabytes is now routinely available. It is impractical to throw out existing systems at a whim and business development must take place to generate revenue that stimulates adoption. Thus genetic evaluation centers need to adopt different computing strategies to account for genotype data within systems that run routinely month after month. Data storage cost is not a real issue but processing time is, especially as systems are developed that run in real time for farmers to decide which animals to genotype via web based services and receive GEBVs as a result. This paper will highlight the practical aspects of implementing genomic evaluations.

Key words: genomic breeding value, genetic evaluation

Dairy Foods: Filtration and Drying

201 Impact of annatto color and bleaching of whey and microfiltration permeate on ultrafiltration processing characteristics during production of 80% protein concentrates. M. Adams[1], J. Zulewska*[2], and D. M. Barbano[1], [1]*Cornell University, Ithaca, NY,* [2]*University of Warmia and Mazury, Olsztyn, Poland.*

Our objective was to determine if annatto color or bleaching had any influence on ultrafiltration (UF) flux during production of 80% whey protein concentrate (WPC) or 80% serum protein concentrate (SPC). Cheddar cheese whey (18 vats using 900 kg of whole milk each) and microfiltration (MF) permeate of skim milk (18 processing runs using 1000 kg of skim milk each) were produced. The 18 runs were divided into 3 replicates with 6 different treatments within each replicate. The 6 treatments within either the whey or MF permeate replicates were: 1) no annatto (NA), 2) NA + benzoyl peroxide (BPO), 3) NA + H_2O_2, 4) annatto (A), 5) A + BPO, and 6) A + H_2O_2. Approximately 700 kg of separated, treated whey or treated MF permeate was heated to 50°C and processed with the UF system in batch recirculation mode using a polyethersulfone spiral wound UF membrane (Model 3838, GEA NIRO Inc., Hudson, WI) with a nominal pore size of 10,000 Da. Addition of annatto color had little or no effect ($P > 0.05$) on UF flux. Bleaching separated Cheddar cheese whey or MF permeate with or without added color improved ($P < 0.05$) UF flux during processing to produce 80% protein concentrates. Generally, H_2O_2 produced higher fluxes than BPO treatments ($P < 0.05$) and BPO increased SPC production fluxes to a lesser extent ($P < 0.05$) than it did WPC production fluxes. Relative to the flux of unbleached whey (about 15 L/m^2h), the bleached whey had a flux of about 20 to 23 L/m^2h. Water flux before processing, after processing, and after final cleaning were measured at 50°C. The water flux after cleaning restored flux to the level before processing whey or permeate. The flux after processing (i.e., fouled water flux) demonstrated differences in fouling and loss of water permeability that were consistent with differences resulting from the bleaching treatments. Little, if any, effect of the annatto on fouled water flux was observed.

Key words: whey bleaching, ultrafiltration flux, annatto

202 Functional properties of milk serum protein concentrates with varying levels of β-casein. L. Coppola*[1], S. Rankin[1], M. Molitor[2], and J. Lucey[1], [1]*University of Wisconsin-Madison, Madison,* [2]*Wisconsin Center for Dairy Research, Madison.*

Microfiltration (MF) can isolate serum proteins (MSP) from milk. The dissociation of β-casein from casein micelles at <8°C in combination with MF is a means to create MSP concentrates (MSPC) with varying levels of β-casein. MF permeates were produced at ~23°C (MSPC1) and ~5°C (MSPC2) using polymeric, cross-flow MF, concentrated and spray dried (~85% protein). Composition, browning, volatile profiles, and sensory characters of MSPC before and after accelerated storage (50°C for 28d) were compared with whey protein concentrate (WPC) and WPC samples. Significant effects were declared at $P \leq 0.05$. MSPC1 and MSPC2 contained different levels of β-casein (1.0 vs 20% of the total solids composition, respectively). WPC samples contained more fat than both MSPC. Browning was determined by colorimetry (CIELAB) of powders and optical density of rehydrated samples. Pre-storage L* values were not different between samples, but a* and b* values of MSPC were lower than WPC. After storage, MSPC had higher L* and lower a* values than WPC. Rehydrated MSPC exhibited smaller changes in browning during storage than WPC. SPME/GC-MS of rehydrated samples showed fewer types of volatiles were present pre-storage and that fewer types increased in intensity following storage for MSPC samples compared with WPC. Descriptive sensory analysis indicated that turbidity, odor, and astringency were not affected by storage and were higher in WPC. MSPC2 had lower sweetness than other samples pre-storage but not post-storage. Pre-storage, WPC samples had higher levels of cardboard and residual flavors. With storage, MSPC1 had a trend toward increased milkfat flavor and MPSC2 had an increase in cucumber flavor while WPC increased in salty, acid, sweet, milkfat, cooked, cabbage, and cucumber flavors. Principal component analysis (PCA) indicated marked differences between MSPC and WPC samples both pre-and post-storage, with WPC described by more off-flavor descriptors. MSPC differed in browning, volatiles, composition, and sensory properties compared with WPC samples, likely to make them attractive in food applications where fewer off-flavors and increased storage stability are desired.

Key words: milk serum protein, β-casein, whey

203 Impact of microfiltration temperature on the composition and functionality of casein concentrates. J. R. Koch*[1], J. A. Lucey[1], K. J. Burrington[2], and M. Molitor[2], [1]*University of Wisconsin, Madison,* [2]*Wisconsin Center for Dairy Research, Madison.*

Microfiltration (MF) is used to separate serum proteins from caseins. There is a trend of performing membrane filtration at cold temperatures to reduce microbial growth. Our objective was to investigate if performing MF at cold or warm temperatures impacted the protein composition and functionality of casein concentrates. Five samples were produced using polymeric spiral wound MF (~0.08 μm) - 2 samples of warm (24°C) temperature MF (WMF) and 3 of cold (5°C) temperature MF (CMF). At cold temperatures β-casein dissociates from casein micelles, which could result in more β-casein in the serum phase. Retentates were concentrated to attain powders with ~80% protein. A milk protein concentrate (MPC) was also produced using ultrafiltration. Reverse-phase HPLC was used to determine the protein composition. The casein to whey ratio was 17:1 and 11.5:1 in the WMF and CMF concentrates, respectively. The β-casein to αs-casein ratio was 4:5 and 5:7 in the WMF and CMF concentrates, respectively. A low concentration of κ-casein was found in all MF permeates likely due to heat-induced complexation of κ-casein with β-lactoglobulin. Solubility of casein concentrates increased with an increase in the temperature of hydration and with the time of hydration. Foams were made from 5% protein solutions, and physical properties (over-run and stability) and rheological properties (vane geometry) were determined. There was no significant difference ($P < 0.05$) in over-run for all samples. Both WMF and CMF concentrates had higher foam stability compared with foams made with MPC. Samples with a higher proportion of β-casein had greater foam stiffness. The foam made from WMF concentrate had significantly higher foam stability and foam stiffness compared with CMF concentrate. Producing casein concentrates at different separation temperatures alters the protein profile. Both separation temperatures reduced the whey (serum) protein content in casein concentrates, but at cold temperature the β-casein content was also reduced. Casein concentrates separated at various temperatures had different functional properties, which could be useful for specific food applications.

Key words: casein concentrate, microfiltration

204 Spiral wound microfiltration process for production of micellar casein concentrate. C. Marella*, P. Salunke, and L. E. Metzger, *Midwest Dairy Foods Research Center, South Dakota State University, Brookings*

Micellar casein concentrate (MCC) is the retentate obtained from microfiltration (MF) of skim milk. Previous research has indicated that MF of skim milk with ceramic membranes result in improved membrane performance relative to spiral wound membranes. However, spiral wound polymeric units have an advantage in terms of capital and operating costs relative to ceramic units. Moreover spiral wound polymeric units are currently extensively used in the US dairy industry. The objective of this study was to evaluate impact of operating pressure and level of diafiltration on membrane performance during MF of skim milk using spiral wound polymeric membranes. Preliminary lab scale experiments were conducted using three levels of transmembrane pressure (TMP) and four levels of diafiltration (DF). Skim milk was microfiltered at 23.3 °C to a volume reduction of 4, using 0.5 µ Polyvinylidene fluoride membrane in a flat sheet configuration. During the experiments, process flux was maintained within 80% of the initial flux by addition of DF water at 6 intervals so as to control the viscosity of the retentate. The effect of TMP and effectiveness of DF were assessed by measuring overall flux, serum protein removal (SP removal), casein to total protein ratio (CN/TKN), casein to true protein ratio (CN/TP), and rejection of casein and serum protein. CN/TKN ratio of MCCs ranged from 0.87 to 0.96 while CN/TP ratio ranged from 0.89 – 0.96. The rejection of casein ranged from 0.97 to 1.0 while the rejection of SP ranged from 0.1 to 0.53. SP removal ranged from 35 – 81.45%. The highest ratio of CN/TKN, CN/TP, SP removal and the lowest rejection of SP were obtained with the use of 35.4 kPa TMP and 150% DF. These are the lowest TMP and highest DF used in the experiments. SP removal data were fitted into a model in which SP removal was expressed as a function of DF and square of TMP. The model predicted SP removal within 90-95% of actual SP removal obtained during pilot trials using various TMP and DF levels. With appropriate selection of TMP and DF level, the efficiency of polymeric MF membranes can be optimized for production of MCC.

Key words: micellar casein concentrate, spiral wound MF, serum protein

205 Characterization of α-lactalbumin and β-lactoglobulin powders obtained from serum whey. C. Marella*, P. Salunke, L. E. Metzger, and K. Muthukumarappan, *Midwest Dairy Foods Research Center, South Dakota State University, Brookings.*

The composition and functional properties of conventional whey protein products can vary widely due to variability in the cheese manufacturing processes. However, variations in the composition and functionality of whey protein products obtained from microfiltration (MF) of skim milk should be minimal since whey proteins are harvested before cheese manufacture. The objective of the present study was to evaluate the functional properties of α-Lactalbumin (α-La) and β-Lactoglobulin (β-Lg) enriched powders, serum protein concentrate (SPC) and a conventional WPI. The α-La, β-Lg and SPC were obtained from MF of skim milk. All the powders were produced at SDSU dairy plant using a combination MF, ultrafiltration, reverse osmosis and spray drying. Functionality testing was conducted in triplicate. Solubility (1% protein solutions); thermal aggregation (heating 1% protein solutions at pH 3 and 7 at 80 oC for 5 min, with out and with added CaCl2, gel strength and syneresis (10% protein solutions heated at 80 oC for 30 min, with and without CaCl2, NaCl); and foaming properties (5% protein solutions) were studied. All the powders were fully soluble at pH 3.0 and 7.0. Heating at pH 3 didn't cause any loss in solubility, whereas none of the solutions at pH 7 could withstand heating in the presence of added CaCl2. The α-La, β-Lg and SPC powders exhibited much higher gel strength (3.5 to 7 fold higher) and lower syneresis when compared with WPI. Among these powders, α-La powder had the lowest syneresis and β-Lg powder has the highest gel strength and moderate syneresis in the presence of added CaCl2. Foam over run (FOR) and foam stability of the α-La, β-Lg and SPC powders were higher than those of conventional WPI. The α-La powder has the highest foam over run of 1070%, which was 43% higher than WPI and about 30% higher than the β-Lg and SPC. The results of this study demonstrate that α-La and β-Lg powders may have value in applications that require high gel strength, low syneresis and high foaming properties.

Key words: α-lactalbumin, β-lactoglobulin, functional properties

206 Effects of washing/diafiltration on milk protein concentrate (MPC) functionality. J. Du* and J. A. Lucey, *University of Wisconsin-Madison, Madison.*

The production of milk protein concentrate (MPC) has grown in recent years and MPC is produced by removing some of the lactose from skim milk (by ultrafiltration, UF) before drying. However, high protein MPC powders often have low solubility and they can exhibit a decrease in solubility during storage, especially at high storage temperatures. In high protein MPC products, washing or diafiltration (DF) is required to further reduce the lactose content. We were interested in understanding if extensive washing reduces the concentration of casein-bound calcium as this could be involved in the impaired functionality of MPC. The objectives of this study were to understand the changes that occur in soluble and bound calcium during UF/DF and the effects of the calcium status on the solubility of MPC products. Four MPC samples were produced from skim milk that was subjected to between one to 4 cycles of UF/DF. We wanted to keep the lactose content constant in all the powders, as that also impacts solubility, so water with 5.4% lactose was used as the washing solution during DF instead of water. Milks were concentrated to 1.67 fold with UF membranes (10k Da) and then back diluted (washed) to the original protein solids level with lactose solution. The retentate was then freeze-dried and the calcium equilibrium and structure of casein micelles were determined. The soluble calcium levels in these retentates were significantly impacted by the protein level used for rehydration ($P < 0.05$); the lower the protein level used for rehydration, the higher the measured soluble calcium content. The ratio of bound calcium to casein decreased with the number of DF cycles but after 3 DF cycles the ratio became nearly constant. Scanning electron microscopy indicated that the casein micelles became much smaller in samples with 3 DF cycles compared with the less washed samples. Casein micelle size was determined by Malvern Zetasizer and the average size of the casein micelles was reduced with increased number of (DF) washing. Further research is investigating the impact of washing cycles on powder solubility.

Key words: milk protein concentrate, solubility, calcium

207 Effect of adding NaCl or KCl during manufacture of MPC80 on its physico-chemical properties. V. Sikand*[1], P. S. Tong[1], S. Vink[1], and J. Walker[2], *[1]Dairy Products Technology Center, Cal Poly State University, San Luis Obispo, [2]Dept. of Statistics, Cal Poly State University, San Luis Obispo.*

Milk protein concentrate (MPC) powder with equal to or greater than 80% protein concentration has been shown to have poor solubility. The poor solubility of MPC limits its potential usage in the food industry. In a previous study in our lab, we have shown that the addition of 50–150mM NaCl into diafiltration water can improve the solubility of MPC80. However, adding NaCl into diafiltration water may impact other functional properties. The objective of this study was to determine the impact of addition of 150mM KCl and NaCl during MPC manufacture on solubility and other functional properties (foaming stability, turbidity and heat stability) on the resulting MPC powders. The powder samples were reconstituted at room temperature to contain 5% total solids. Percent solubility was tested after 3 h of mixing and was calculated as total solids in the supernatant to total solids in the original solution. Percent foaming stability, expressed as collapse of foam, was tested after 5 min to initial mass of foam. Turbidity was measured in Nephelos Turbidity Units (NTU) using a calibrated nephelometer. Heat stability was determined by measuring the heat coagulation time of 2 mL samples immersed in a oil bath set at 140°C. Our results indicate that higher solubility($P < 0.001$) was found in NaCl (100%) and KCl-treated MPC80 (98.8%) than in control MPC80 (90%). Foaming stability($P < 0.001$) was found to be highest in KCl-treated MPC (21.8%) followed by NaCl-treated MPC (10.6%) and then followed by control MPC (4.6%). Higher heat stability ($P < 0.001$) was observed in control MPC80 (23.7 min) when compared with NaCl (16.5 min) and KCl-treated MPC80 (16.4 min). Lower turbidity($P < 0.001$) was observed in NaCl (129 NTU) and KCl-treated MPC (117 NTU) as compared with control MPC (564.2 NTU). Our results indicate that the functional properties of MPC80 powders are influenced by addition of KCl or NaCl in the manufacture of MPC. These results suggest that the functional properties of MPC80 powders can be modified by changing its mineral composition during its manufacture.

Key words: MPC80, functional properties

208 Determination of the drying behavior of dairy products to improve the process, energy costs and the quality of the dairy powders. P. Schuck[1,2], A. Dolivet[1,2], S. Mejean[1,2], P. Zhu*[1,3], E. Blanchard[3], and R. Jeantet[2,1], *[1]INRA, UMR1253, Rennes, France, [2]Agrocampus Rennes, UMR1253, Rennes, France, [3]Laiterie de Montaigu, Montaigu, France.*

The most frequently used technique for dehydration of dairy products is spray drying. This is an effective method for preserving biological products as it does not involve severe heat treatment and it allows storage of powders at an ambient temperature. Due to the variety and complexity of the concentrates to be dried, a more rigorous understanding of spray-drying based on physico-chemical and thermodynamic properties have now become necessary. At the same time, the current state of the art and knowledge do not allow determination of the parameters of spray-drying of dairy products. The only way to determine these parameters is to perform several complex and expensive experiments with a pilot scale spray-dryer. The aims of this study were to propose a new indirect method that determines the ratio of bound to unbound water. The results, combined with thermodynamic and physico-chemical parameters (such as absolute and relative humidity of air, total solids and temperature of concentrate, air flow rate, etc.), provide more precise determination of certain spray-drying parameters such as inlet air temperature and mass flow rate. We performed more than 50 experiments to correlate calculated and measured parameters in a pilot plant dryer (Bionov, Rennes, France) using water, skim milk, caseinate, crystallized whey and maltodextrin. The results show that the difference between the calculated and measured inlet air temperature was below 5%, the determination coefficient being close to 0.96. The economic interest of this system is obvious, because it is easy to anticipate the spray-drying parameters by using a controller integrating the water availability of the concentrate and certain thermodynamic parameters. Software based on this step was developed (SD2P®, Spray Drying Parameters Simulation & Determination) and registered.

Key words: powder, prediction, software

Dairy Foods Symposium: Technological Advancements in the Reduction of Pathogens and Spoilage Organisms in Milk

209 Technological advancements in the reduction of pathogens and spoilage organisms in milk—Introduction and challenges. D. R. McCoy*, *Dairy Research Institute, Rosemont, IL.*

The introduction of pasteurization in 1886 improved both the safety and keeping quality of milk and milk products. Newer methods like ESL and UHT treatments have further increased the safety and the shelf-life of modern dairy foods as well as allowing non-refrigerated distribution. However, there are still challenges such as further widening the distribution opportunities for milk, reducing energy requirements, and improving the flavor of longer life products. As new technologies are explored, it is important to recognize not only the science but also the regulatory requirements for successful implementation. Well-designed experimental approaches can expedite both scientific discovery and regulatory review. Finally, it should be recognized that many plant operations reduce microbial load but do not need to meet the high safety standard inherent in being an alternative to pasteurization, which may allow implementation earlier in the regulatory process.

Key words: pasteurization, milk, processing

210 Reduction of cooked and oxidized flavors in UHT milk. D. G. Peterson*, *University of Minnesota, St. Paul.*

Fluid milk is thermally processed to reduce the microbial load for both product safety and stability. Multiple thermal treatment options are available, such as pasteurization, extended shelf-life (ESL), and ultra-high temperature (UHT) processing. UHT techniques provide the longest shelf-life and allow non-refrigerated distribution. Despite these notable benefits, UHT processing negatively influences milk flavor quality due to the generation of thermally catalyzed off-flavor compounds, primarily by Maillard chemistry. This presentation will focus on the application of common food phenolic compounds (i.e., in cocoa, tea, and soybeans) to suppress off-flavor development and improve acceptability in UHT products. Optimization of the phenolic structure-reactivity to suppress Maillard-type off-flavor development in UHT milk will also be reviewed.

Key words: UHT, off-flavor, reduction

211 CHIEF/pulse electric field technology—A unique processing system. R. Ruan*[1,3], S. Deng[1], Y. Cheng[1], X. Lin[2,3], P. Chen[1], and L. Metzger[4], *[1]University of Minnesota, St. Paul, [2]Fuzhou University, Fuzhou, Fujian, China, [3]Nanchang University, Nanchang, Jiangxi, China, [4]South Dakota State University, Brookings.*

Consumers are increasingly aware of the taste, flavor, color, nutritional value, as well as safety of the foods they eat. They demand safe foods that are both fresh and natural. Therefore, food processes must be designed to render minimal adverse effects on food quality and nutrition values while ensuring safety. Conventional thermal processing not only kills spoilage and pathogenic microorganisms but also degrades the taste, color, flavor, and nutrients of the food. Non-thermal methods are alternatives which offer possibilities of preparing fresh-like, minimally processed safe foods. Among all emerging non-thermal processes, high intensity pulsed electric field (PEF) is considered the best. Nonetheless, the PEF process has few large scale industrial applications to date chiefly because PEF equipment and process are very specialized and costly. Concentrated high intensity electric field (CHIEF) developed at the University of Minnesota is a technology similar to PEF. Both of them use high intensity electrical field to inactivate the bacteria through the well accepted electroporation and other mechanisms. Compared with traditional PEF technique, CHIEF uses much cheaper power supply, and does not have electrode erosion and contamination issues. Our research on juice and milk indicates that CHIEF has a great potential of becoming a commercial process for non-thermal pasteurization of fresh liquid foods. The advantages and disadvantages of the two technologies will be compared and the potential commercialization applications in milk processing will be discussed.

Key words: PEF, CHIEF, electric field

212 UV light inactivation of bacteria and spores in milk to enhance shelf-life. J. S. Cullor*, P. V. Rossitto, J. Crook, and J. Parko, *University of California at Davis, Tulare.*

Thermal pasteurization of milk achieves safe and high quality product that is acceptable to consumers. Thermo-tolerant spoilage organisms though do survive pasteurization restricting the shelf-life of products as evidenced by code dates of 14 to 18 d. Spoilage organisms include gram-positive, gram-negative and aerobic spore-forming bacteria of the genera *Bacillus*, *Paenibacillus*, and *Geobacillus*. These spores can and do survive pasteurization, germinate, multiply and cause spoilage in milk, milk products and UHT products after processing. Delivery of germicidal UV light at 254 nm inactivates microbes in milk. Though UV light inactivation of microbes in water is an established technology that currently has many commercial applications, utilization of this technology in foods is somewhat new. Introduction of the alternative technology of UV germicidal light in milk has been validated in laboratory studies on milk with 3.5% and 2% fat and shown to increase microbial shelf life. UV log killing values or D-Values have been established for gram-positive spore forming bacteria and the pathogens *E. coli* O157:H7, *Salmonella enterica* serovar Senftenberg, *Yersinia enterolitica*, *Staphylococcus aureus*, *Campylobacter jejuni*, *Serratia marcescens*, *Aeromonas hydrophila*, and *Listeria monocytogenes*.

213 Electrical resistive heating versus conventional UHT technologies. D. J. McMahon*[1], B. Ganesan[1], M. Qian[2], and C. Brothersen[1], *[1]Western Dairy Center, Utah State University, Logan, [2]Food Science and Technology Department, Oregon State University, Corvallis.*

Electrical resistive (ER) heating involves release of heat as an electrical current is passed through a conductor such as milk. This induces very rapid volumetric heating without exposure of the milk to hot steam or metal heat transfer surfaces. Such heating provides opportunities for processing of heat-sensitive materials as well as fluids containing particulates and these are briefly reviewed. Current ultra-high temperature (UHT) processing of milk uses indirect plate (or tube) heat exchanger (PHE) or direct steam injection or infusion (DSI). In USA, pasteurized milk is preferred over UHT milk because of flavor development induced by UHT heating and exacerbated by long ambient temperature

storage. Milk was UHT-processed (140°C, 4 s) by ER, DSI and PHE and stored for 8 mo at room temperature (22°C) for flavor attributes and consumer preferences. Fresh pasteurized milk acted as control for sensory evaluation and was most preferred by consumers. The ER milk was liked more than DSI or PHE milks initially and at 1 mo. All UHT milks were equally liked at 4 mo, while at 8 mo the ER and DSI milks were liked more than PHE milk. After 8 mo, DSI and PHE milks were considered more bitter than pasteurized or ER milks, while all UHT milks were more brothy than pasteurized milk. Overall, ER milk was preferred more than DSI or PHE milks. SPE gas chromatography-mass spectrometry analysis of volatile compounds showed that volatile sulfurs generally decreased during storage, while dimethylsulfide increased by 0.5-fold in DSI milk. Dimethylsulfide was the most abundant volatile sulfur compound and was found 2 to 4-fold higher at 1 wk in PHE milk than others. Methanethiol, dimethyldisulfide, and dimethyltrisulfide highly varied over time in UHT milks. Carbonyls other than hexanal increased in ER milk during storage but remained low in DSI and PHE milks. In conclusion, we found that ER produced better-flavored UHT milk than current UHT processes, but the flavor changes did not correlate with changes in known volatile sulfur or carbonyl compounds. ER heating also has potential to rapidly heat milk to higher temperatures for UHT heating with shorter required hold times.

Key words: ultra-high temperature, milk, electrical resistance

214 Continuous flow microwave heating for pasteurization and sterilization of dairy products. J. Simunovic*, *North Carolina State University, Raleigh.*

Over the last dozen years, continuous flow microwave heating of foods has progressed from a bench top concept to an industrial scale technology used commercially in thermal sterilization and aseptic packaging of low acid vegetable purees. Feasibility testing protocols have also been developed and implemented for sterilization of a variety of dairy products ranging from milk to sour cream and cream cheese. Developed equipment, procedures and processes will be presented and anticipated future applications discussed.

Forages and Pastures: Alternative Forages and Improving Forage Quality and Characterization

215 Gain from selection for 16- and 96-h in vitro ndf digestibility of alfalfa stems. H. G. Jung* and J. F. S. Lamb, *USDA-Agricultural Research Service, St. Paul, MN.*

Alfalfa is a high quality forage, but stems are high in NDF and of limited digestibility. A gain from selection study with alfalfa populations selected for divergent in vitro NDF digestibility (IVNDFD) was planted at St. Paul and Becker, MN. Two cycles of selection were conducted starting with a base population created by mixing seed from 6 commercial varieties. Individual plants (n = 2000) were harvested twice (spring and first regrowth) at late flower for 2 years. Plants consistently low or high for 16- or 96-h IVNDFD were crossed to create 4 cycle one IVNDFD populations: low 16-h/low 96-h (LL), low 16-h/high 96-h (LH), high 16-h/low 96-h (HL), and high 16-h/high 96-h (HH). Cycle one populations were planted and harvested twice annually for 2 years to identify plants with appropriate IVNDFD combinations and crossed to create cycle 2 populations. Near-infrared reflectance spectroscopy calibrations were developed for NDF, ADL, Klason lignin, cell wall polysaccharide components, and 16- and 96-h IVNDFD based on 470 samples from the base population, cycle 2, and other experiments. Data were analyzed as a randomized complete block with 4 replicates, 2 locations and 9 populations, and 2 harvests arranged as repeated measures. The least significant difference test ($P < 0.05$) was used to compare population means when the F-test was significant. After 2 cycles of selection, 16-h IVNDFD increased from 19.3% for the base population to 20.1% for the HH population. The LL population (19.0% 16-h IVNDFD) differed from the HH population after 2 cycles, but not from the base. Both LL (50.3%) and HH (55.8%) differed for 96-h IVNDFD from the base (52.4%) after 2 cycles. The LH and HL populations did not differ significantly from the base; however, means shifted in the direction of the positive selection criterion. Selection for greater IVNDFD resulted in less NDF, cell wall, and lignin (ADL and Klason) in the cycle 2 HH than the base and cycle 2 LL populations. Cellulose and pectin increased for HH cycle 2 and hemicellulose declined in cycle 2 LL compared with the base. Genetic selection in alfalfa was successful in improving IVNDFD of stems.

Key words: alfalfa, fiber, digestibility

216 The nutritive value of mature corn silage from BMR, non-BMR and a 50:50 mix ensiled for varying lengths of time. J. M. Lim*[1], M. C. Santos[1], J. P. Riguera[1], M. C. Der Bedrosian[1], K. E. Nestor Jr.[2], and L. Kung, Jr.[1], *[1]University of Delaware, Newark, [2]Mycogen Seeds, Indianapolis, IN.*

The effects of hybrid type (H) and storage length (LEN) on the nutrient value of corn silage were studied. Hybrids were 1) brown midrib (BMR, Mycogen F2F700, Dow AgroScience, Indianapolis, IN), 2) non-BMR (NML, Mycogen TMF2W726) and 3) a 50:50 mixture (MIX). The BMR and NML were planted separately whereas MIX was produced by planting alternate rows of each H. Five replicated rows of plants (at about 40% DM) for each H were chopped (~20 mm length) and processed. Forage was ensiled (25°C) in vacuum-sealed bags and 5 replicates were opened after 200 and 400 d. All silages fermented well (pH <3.7). Ammonia-N increased for all treatments from d 0 to 200 but did not change between 200 to 400 d. Lignin content was lowest for BMR, highest for NML and intermediate for MIX and the difference ($P < 0.01$) was greater after 400 vs. 200 d of ensiling. The NDF content of BMR (42.5%) was higher ($P < 0.01$) than the NML (34.6%) and MIX (37.74%) at d 0 but this difference diminished over ensiling time. Over time, silage NDF-D did not change but was different ($P < 0.01$) among the treatments and was highest for BMR (63.7%), intermediate for MIX (59.8%) and lowest for NML (51.7%). Starch content was lower ($P < 0.01$) for BMR (36.8%) than NML (40.7%) and MIX (42.3%) from 0 to 200 d but not on 400 d of ensiling. Starch digestibility (Str-D) was lower ($P < 0.01$) for BMR (65.3%) than NML (68.5%) and MIX (68.5%) for 0 and 200 d but was not different on 400 d of storage. Str-D increased by 6% for all treatments from d 0 to 200. From d 200 to 400 of ensiling, Str-D did not change for the NML but increased by 6 and 20% more for MIX and BMR, respectively. This study showed that NDF-D of silage was influenced by hybrid type but not length of storage. Length of storage increased Str-D, which proved that prolonged storage enhanced the nutritive value of corn silage. Planting NML yielded more ($P < 0.01$) DM than BMR (22.6 vs. 17.3 t/ha). Interplanting and harvesting BMR and NML together was not detrimental to silage quality and produced an acceptable DM yield (19.3 t/ha).

Key words: silage, BMR

217 Concentrations and apparent digestibility of lignin and carbohydrate fractions in cell walls of whole-crop cereal silages. J. Wallsten* and R. Hatfield, *US Dairy Forage Research Center, Madison, WI.*

Whole-crop cereal silage (WCCS) of oats generally have lower fiber digestibility than WCCS of barley. When investigated more closely the difference seems to mainly be in the digestibility of the hemicellulosic fraction (HC), where HC is calculated as neutral detergent fiber (NDF) minus acid detergent fiber (ADF). The objective of this study was to see if the difference is true or a result of losses during analysis. A set of 27 WCCS samples of barley, wheat and oats harvested at 3 different maturity stages and 54 corresponding fecal samples (from dairy heifers fed the respective silages) were analyzed for cell wall (CW) composition. Analysis included NDF, ADF and total CW, recovered by washing the samples in different aqueous and organic solvents. The CW residues were used to analyze ash, acetyl bromide lignin and neutral sugar composition. The data were analyzed with proc reg and proc mixed in SAS. The CW concentration was higher than the NDF concentration in both forages and feces. The correlation between the 2 fiber fractions was lower in forages (R = 0.63) than in feces (R = 0.94), possibly due to soluble fiber fractions that were included in forage CW, but not in the forage NDF. The lignin concentration in the silages was higher ($P < 0.001$) in oats (111 g/kg DM) than in barley (88 g/kg DM) and wheat (91 g/kg DM). Also in the feces oats (190 g/kg DM) had higher lignin concentration ($P < 0.001$) than barley (168 g/kg DM) and wheat (168 g/kg DM). There was an apparent loss of 20–40% of the lignin during digestion and the losses were higher in more immature silages. The correlation between xylose and HC concentrations was lower than expected in both forages (R = 0.63) and feces (R = 0.65). However, the correlation between xylose and HC digestibilities was high (R = 0.91). The high apparent digestion of lignin is probably a result of losses from the feces during analysis rather than actual digestion in the animal. The trend with higher losses for more immature silages is of concern as that will overestimate fiber and possibly in vitro DM digestibility for these silages.

Key words: neutral detergent fiber, xylose, acetyl bromide lignin

218 Construction of a recombinant *Pichia pastoris* integrating a two-copy xylanase gene from *Thermomonospora fusca* and characterization of its secreted protein. Q. Wang*[1], M. Z. Ma[1], X. Y. Weng[2], J. Y. Sun[1], and J. X. Liu[1], *[1]MOE Key Laboratory of Molecular Animal Nutrition, College of Animal Sciences, Zhejiang University, Hangzhou, P.R. China, [2]College of Life Science, Zhejiang University, Hangzhou, P.R. China.*

Endo-β-1, 4-xylanases are key glycosidases in the degradation of xylan, the most abundant natural polysaccharide after cellulose. The study was designed to construct a recombinant strain expressing thermostable xylanases. Due to its good thermostability, a gene from *Thermomonospora fusca* xylanase (tfx) was employed to generate a yeast expression vector pGAPZαA-tfx. Then, the resulting vector was linearized with AvrII and inserted into *Pichia pastoris* GS115 at the locus of GAP promoter by electroporation (1500V, 5.2 ms). Transformants were spread onto YPD plates (1% yeast extract, 2% peptone, 2% dextrose, 2% agar) with 500–2000 ug/ml Zeocin. Seven putative multicopy recombinants exhibiting high resistance to Zeocin were selected to determine gene copy number. The strain GS115/33 was identified as a 2-copy recombinant by Southern blotting and real-time PCR, and used for protein expression. Subsequently, scale-up expression was achieved for 96 h in a 2-L baffled shaking flask containing 100 mL YPD medium. The recombinant xylanase TFX, driven by the GAP promoter and *Saccharomyces cerevisiae* α-mating factor, was constitutively secreted into culture medium. The specific xylanase activity in culture supernatant reached 89.8 U/mg, and purification by 6 × His tagged Ni-NTA agarose resulted in 10-fold increase in specific activity (932.5 U/mg). After being incubated at 70°C for 5 min, the residual activity retained more than 70%. SDS-PAGE analysis revealed that the molecular weight of TFX was about 43 kDa, while the unglycosylated protein was 32 kDa after treatment with Endoglycosidase H. Three potential N-glycosylation sites (N5, N183 and N230) may contribute to the extra molecular weight. A weak protein interaction was observed between TFX and rice xylanase inhibitor (RIXI), a main xylanase inhibitor in cereals, by using yeast 2-hybrid. Because of its high specific activity and good tolerance to temperature and xylanase inhibitor, TFX produced by GS115/33 would be an attractive candidate for the feed and biofuel industries.

Key words: xylanase, *Pichia pastoris*, protein expression

219 Screening exogenous fibrolytic enzyme products for improved in vitro ruminal fiber digestibility of bermudagrass. J. J. Romero*, K. G. Arriola, M. A. Zarate, and A. T. Adesogan, *Department of Animal Sciences, IFAS, University of Florida, Gainesville.*

Eighteen exogenous fibrolytic enzyme products (EFE) from 5 companies were evaluated for their effect on digestibility of a 4-week regrowth of Tifton 85 bermudagrass haylage (68.1, 34.2, 3.7 and 18.7% NDF, ADF, ADL, and CP, respectively). All EFE were evaluated with a 24-h in vitro ruminal digestibility assay using bermudagrass haylage as substrate. EFE were diluted in citrate–phosphate buffer (pH 6) and applied in quadruplicate to the substrate at the manufacturer–recommended rates. The suspensions were incubated at 25°C for 24 h before addition of buffered rumen fluid (39°C) and further incubation for 24 h. The run was repeated once (Experiment 1). Compared with the Control (buffer and substrate alone), 6 EFE had greater DMD (%) (54.2 ± 0.4 vs. 52.4 ± 0.4; $P < 0.05$), 6 EFE had greater NDFD (%; 40.8 ± 0.6 vs. 38 ± 0.6; $P < 0.05$), 4 had greater ADFD (%; 43.3 ± 0.3 vs. 40.8 ± 0.7; $P < 0.05$), 8 had greater hemicellulose digestibility (%; 38.1 ± 1.3 vs. 35.1 ± 0.6; $P < 0.05$), 5 had greater cellulose digestibility (%; 46.3 ± 0.3 vs. 44.3 ± 0.6; $P < 0.05$), 2 had lower pH (7.33 ± 0.01 vs. 7.40 ± 0.02; $P < 0.01$) and 11 had greater pH (7.5 ± 0.03 vs. 7.4 ± 0.02; $P < 0.05$). In Experiment 2, the 12 EFE with the greatest NDFD from Experiment 1 were tested using similar procedures. Compared with the Control, 5 EFE had greater DMD (55.2 ± 0.7 vs. 51.2 ± 0.8; $P < 0.05$), 10 had greater NDFD (36.4 ± 2.0 vs. 30 ± 0.9; $P < 0.05$), 8 had greater ADFD (39.3 ± 1.3 vs. 34.4 ± 1.0; $P < 0.05$), 10 had greater hemicellulose digestibility (34.8 ± 2.2 vs. 28.9 ± 0.9; $P < 0.05$), 9 had greater cellulose digestibility (42.9 ± 0.9 vs. 36.8 ± 1.2; $P < 0.05$), 11 had lower pH (6.97 ± 0.03 vs. 7.05 ± 0.01; $P < 0.05$), and 1 had lower ruminal NH_3 (mg/dl; 42.1 ± 0.76 vs. 44.1 ± 0.66; $P < 0.05$). Several promising EFE candidates to improve the digestibility of bermudagrass haylage were identified in this experiment.

Key words: forage, enzyme, screening

220 Relationships between exogenous fibrolytic enzyme product activities and in vitro ruminal digestibility of bermudagrass. J. J. Romero*, K. G. Arriola, M. A. Zarate, and A. T. Adesogan, *University of Florida, IFAS, Department of Animal Sciences, Gainesville.*

The objective was to examine relationships between exogenous fibrolytic enzyme activities (EFE) and digestibility values of bermudagrass haylage treated with the enzymes. The protein concentration (PR) and endoglucanase (EN), exoglucanase (EX), β–glucosidase, (BG), and xylanase (XY) activities of 18 EFE from 5 companies were measured using carboxymethylcellulose, avicel, cellobiose, and oat spelt xylan, as substrates, respectively. The EFE were diluted in citrate - phosphate buffer (pH 6) and applied in quadruplicate at manufacturer–recommended rates to ground (1 mm) Tifton 85 bermudagrass haylage (4–week regrowth; 68.1, 34.2, 3.7 and 18.7% NDF, ADF, ADL, and CP, respectively). Suspensions were incubated for 24 h at 25°C and for a further 24 h at 39°C after addition of buffered–rumen fluid. The run was repeated once (Experiment 1). A similar second experiment was conducted with the 12 EFE with the greatest NDFD in Experiment 1. Stepwise regressions of digestibility of DM, NDF, ADF, hemicellulose (HEM) and cellulose (CELL) on enzyme activities and protein content of 18 (Experiment 1) and 12 (Experiment 2) EFE were conducted. Experiment 1 did not yield any accurate relationships ($R^2 < 0.07$; $P < 0.01$). In Experiment 2, PR (mg/g EFE) and enzyme activities (μmol/min/mg EFE) explained ($P < 0.01$) 56, 81, 68, 82, and 47% of the variation in DMD, NDFD, ADFD, and HEM and CELL digestibility, respectively. Prediction equations were as follows: $DMD = 51.2 - 0.001XY - 3.37EX - 1.28BG + 0.^{32}PR + 0.00000204EN^2 + 0.0000000130XY^2 + 0.05BG^2 - 0.00197PR^2$; $NDFD = 30.7 + 0.00853EN - 0.0009448XY - 5.76EX - 2.32BG + 0.43PR + 0.00000167EN^2 + 0.05612BG^2 - 0.00280PR^2$; $ADFD = 34.7 + 0.01594EN - 0.00093598XY - 11.66EX - 2.6BG + 0.41PR + 1.53EX^2 + 0.06BG^2 - 0.00267PR^2$; HEM digestibility $= 29.0 + 0.01067EN^2 - 0.00113XY - 6.73EX - 3.07BG + 0.51137PR + 0.00000205EN^2 + 0.07819BG^2 - 0.00343PR^2$; CELL digestibility $= 38.2 - 0.00067827XY - 2.5EX - 0.66BG + 0.27PR + 0.00000218EN^2 - 0.00161PR^2$. Important relationships between enzymatic activities and PR concentration and enzyme effects on in vitro digestibility were developed.

Key words: enzyme, forage, regression

221 Effect of rate of application of various exogenous fibrolytic enzyme products on in vitro ruminal fiber digestibility of bermudagrass. J. J. Romero*, K. G. Arriola, M. A. Zarate, and A. T. Adesogan, *Department of Animal Sciences, IFAS, University of Florida, Gainesville.*

The objective was to examine the effects of the dose rate of 5 exogenous fibrolytic enzyme products (EFE; E1, E2, E3, E4, and E5) from 3 companies on the digestibility of a 4–wk regrowth of Tifton 85 bermudagrass haylage (66.8, 33.2, 3.7 and 18.7% NDF, ADF, ADL, and CP, respectively). Application rates were 0x (Control), 0.5x, 1x, 2x and 3x; where 1x was the respective manufacturer–recommended dose (10, 15, 2.25, 2.25, and 15 g/kg substrate). Enzymes were diluted in citrate–phosphate buffer (pH 6) and applied in quadruplicate to ground (1 mm) bermudagrass haylage. The suspension was incubated for 24 h at 25°C and for a further 24 h at 39°C after addition of buffered rumen fluid. The run was repeated once. Data for each enzyme were analyzed separately as a completely randomized block design. The model included effects of dose, run, and the interaction. Polynomial contrasts were used to determine dose rate effects and the Fisher's LSD test was used to compare EFE means. Increasing the dose rate had the following effects: produced non-linear increases in DMD (%) of E2 and E4 (cubic; $P < 0.01$) and E1 and E3 (quadratic; $P < 0.01$); increased NDFD (%) of E1, E2 and E4 (cubic; $P < 0.01$) and E3 (quadratic; $P < 0.01$); increased ADFD (%) of E2, E4 and E5 (cubic, $P < 0.05$), E3 (quadratic, $P < 0.05$), and E1 (linear, $P < 0.01$); increased hemicellulose digestibility (%) of E1 and E2 (cubic, $P < 0.01$), E3 and E5 (quadratic, $P < 0.01$), and E4 (linear, $P < 0.01$); increased cellulose digestibility (%) of E2, E3, E4 and E5 (cubic, $P < 0.05$), and E1 (linear, $P < 0.01$) and increased pH of E2 and E4 (cubic, $P < 0.01$), E1 (quadratic, $P < 0.01$) and E3 (linear, $P < 0.05$). The optimal doses (and % increases compared with the control) for improving the DMD of E1, E2, E3 and E4 were 1x (2.8), 0.5x (2.5), 1x (1.5) and 2x (1.1), respectively. Optimal doses (and % increases compared with the control) for improving NDFD were 1x (5.7), 0.5x (4.7), 1x (2.9) and 2x (2.6), respectively. Enzyme application increased the DMD and NDFD of bermudagrass haylage but the optimal application rate varied with the enzyme.

Key words: forage, enzyme, dose

222 Alternative approaches of replication for estimating in vitro starch disappearance. D. R. Mertens*[1] and R. Ward[2], *[1]Mertens Innovation & Research LLC, Belleville, WI, [2]Cumberland Valley Analytical Services Inc., Maugansville, MD.*

Measuring disappearance kinetics of starch and other substrates as they ferment is expensive and labor intensive because replicated serial measurements are needed. Assuming starch is 100% digested, rates of disappearance could be calculated theoretically from measurements at a single time by assuming that disappearance is zero at a fixed and assumed lag time. However this approach is dependent on removal of outliers and high precision in the measurement of in vitro starch digestion (IVSD). Our objective was to evaluate alternative strategies for minimizing the number of IVSD needed to measure starch disappearance rate. The IVSD of 6 samples of corn grain or silage (4-mm grind) were measured in quadruplicate on 3 consecutive days by Cumberland Valley Analytical Services, Inc. using a composite inoculum from 3 donors fed TMR. Measurements were made at 2, 4, 6, 12, 18, and 24 h. Local regression (Proc LOESS in SAS) was used to detect outliers. LOESS has the advantage that not only the observations replicated within day, but also those from repeated days and serial times can be used to detect outliers. Proc NLIN of SAS was used to fit a model with a single exponential pool with discrete lag to the results. Rate and lag estimates were generated for each replicate within day. Proc MIXED of SAS was used to test day effects with random replicates. There was no difference among consecutive days for rates ($P = 0.13$) but a 1 h difference in lags ($P = 0.04$). All 72 measurements for each feed were used to estimate the overall rate of starch disappearance, which varied from 0.114 to 0.168/h for the 6 corn sources. Deviations from the overall rate for each source were calculated by using 4 replicates within each day or 2 replicates from each of 2 d. There was no difference in deviations, absolute deviations or squared deviation for within-day or among-day rate estimates. When 2 replicates within day were compared with 1 replicate from 2 d there was no difference in replication approach. For consecutive-day in vitro, it appears that replications within day are as accurate as between day replicates for estimating rate.

Key words: in vitro, starch, kinetics

223 Microbial protein synthesis and partitioning of nutrients of native species from semiarid regions of North Mexico. M. Guerrero-Cervantes[1,3], M. A. Cerrillo-Soto*[1,3], A. S. Juárez-Reyes[1,3], H. Bernal-Barragán[2,3], and R. G. Ramírez[2], *[1]Universidad Juárez del Estado de Durango, Durango, México, [2]Universidad Autónoma de Nuevo León, Nuevo León, México, [3]Red Internacional de Nutrición y Alimentación en Rumiantes.*

The aim of this study was to determine the partitioning of nutrients and microbial protein synthesis of fruits and foliage of 3 cacti: (*Opuntia imbricata*, *O. leptocaulis* and *O. leucotricha*), fruits of 3 browse: (*Acacia shaffneri*, *Prosopis leavigata* and *Atriplex canescens*), and foliage of 4 forbs: (*Coldenia greggii*, *Dalea bicolor*, *Jatropha dioica* and *Panthenium incanum*), which are commonly consumed by range small ruminants in semiarid regions of Mexico. Foliage was obtained from 10 distinct plants at early stages of growth, dried and milled (1 mm). Triplicate samples (500 mg) were incubated in 100 mL glass syringes, using buffered rumen fluid. Gas production was recorded at 0,3,6,9,12 and 24 h. After incubation, contents of syringes were centrifuged. An aliquot from the supernatant (5 mL) was utilized for determination of volatile fatty acids (VFA = mmol/40 mL incubation medium) using gas chromatography. The solid residue was lyophilized and subjected to the determination of purine content (μmol) using spectrophotometry. Efficiency of microbial protein synthesis (EMPS) was calculated as μmol purines/mmol VFA. Incubation residues from a separate set of syringes were refluxed with neutral detergent fiber solution and the partitioning factor (PF) was calculated as the ratio of mg substrate truly degraded/ml gas produced$_{24h}$ in vitro. Data were analyzed by ANOVA using PROC GLM. Mean differences were separated using Tukey′s test. The PF and purine values were similar among groups of feedstuffs ($P > 0.05$). Total VFA were in average higher ($P < 0.05$) for the foliage of cacti (930 mmol/40 mL) and lower for forbs (657 mmol/40 mL). The EMPS for fruits of browse (9.30) was almost twice the value for Opuntia foliage (4.67; $P < 0.05$), while values for fruits and foliage of forbs were similar. These data support the potential of native species as feed resources in harsh environments. The data obtained might be utilized for the establishment of feeding systems for small ruminants in semiarid regions.

Table 1. Efficiency of microbial protein synthesis and partitioning of nutrients of native plants

Species	PF	Purines (μmol)	Total VFA	EMPS (μmol purine/mmol VFA)
Fruits of Opuntia	2.89[a]	6.25[a]	805[ab]	7.48[ab]
Foliage of Opuntia	2.98[a]	4.68[a]	930[a]	4.67[b]
Fruits of browse	3.02[a]	6.01[a]	739[ab]	9.30[a]
Foliage of forbs	2.90[a]	4.31[a]	657[b]	7.05[ab]
Mean	2.95	5.31	783	7.12
sem	0.28	2.55	245	3.01

[a,b] Means in columns with unlike letter differ ($P < 0.05$); PF=Partitioning factor; VFA=Volatile fatty acids; EMPS=Efficiency of microbial protein synthesis

Key words: native plants, microbial protein synthesis, in vitro gas production

224 Effects of species and season on chemical composition and ruminal crude protein and organic matter degradability of some multi-purpose tree species by West African Dwarf rams. O. M. Arigbede*[1,2], U. Y. Anele[1,2], K.-H. Südekum[2], J. Hummel[2], A. O. Oni[1], J. A. Olanite[1], and A. O. Isah[1], *[1]University of Agriculture, Abeokuta, Nigeria, [2]University of Bonn, Bonn, Germany.*

Seasonal chemical composition and ruminal organic matter (OM) and crude protein (CP) degradabilities were determined in 4 tropical multipurpose tree species (MTPS), namely *Pterocarpus santalinoides*, *Grewia pubescens*, *Enterolobium cyclocarpum*, and *Leucaena leucocephala*. Three West African Dwarf rams fitted with permanent rumen cannula were used for the degradability trials. Foliage samples were randomly collected from 6 plants per MPTS 4 times to represent seasonal variations: January – mid dry; April – late dry; July – mid rainy, and October – late rainy seasons. Samples were analyzed for oven DM at 60°C for 96 h, milled (2.5 mm) and weighed (5 g) into 9 × 18 cm nylon bags. Bags were incubated in triplicate for 6, 12, 24, 48, 72 and 96 h in the rumen of 3 West African dwarf rams (35 kg body weight). Another portion of the dried foliage samples and residues after in sacco incubation were milled through a 1 mm sieve and stored until required for chemical analysis and ruminal in situ OM and CP degradability estimation. All samples had high CP (161 - 259 g/kg DM) and moderate fiber concentrations (neutral detergent fiber (ash-free), 300 - 501 g/kg DM; acid detergent fiber (ash-free), 225 - 409 g/kg DM and acid detergent lignin, 87 - 179 g/kg DM as well as low contents of secondary metabolites (13.5 to 33.5, 0.8 to 11.5 and 3.0 to 17.4 g/kg DM for tannins, trypsin inhibitors, and phytic acid respectively). Interaction effects between species and season were observed for DM, CP and secondary metabolite contents except for trypsin inhibitor ($P = 0.614$). Ruminal degradability of OM and CP showed that more than 50% were degraded at 24 h and the undegraded fraction varied from 17.5 to 47.6%. This implied that the MPTS were highly degradable and their incorporation into ruminant feeding systems as dry season forage supplement is recommended.

Key words: multi-purpose tree species, chemical composition, ruminal degradation

225 Effect of land clearing and tillage methods on growth and yield of maize-cassava intercrop. A. H. Ekeocha*, *University of Ibadan, Ibadan, Oyo, Nigeria.*

One of the prevailing problems facing developing countries today is that of producing enough food to meet their ever increasing population. It is in view of this that this work was carried out to evaluate the effect of land clearing and tillage methods on growth and yield of a maize-cassava intercrop. The experiment was carried out at the International Board for Soil Research and Management, Epemakinde, Nigeria. (4° 45 ^{0} E, 6° 45° N) after 3 cropping years. The experimental design was a split-split plot in a randomized complete block design with 3 replicates. Three land clearing methods namely manual slash and burn (SB), bulldozed not windrowed (BNW) and bulldozed windrowed (BW) constituted the main treatments while 4 tillage methods namely (zero, conventional, traditional and minimum tillage) constituted the sub-treatments. There were a total of 12 treatment combinations per block. The plot size for each land clearing treatment was 20m × 30m each. Data were subjected to ANOVA and significant means separated using the least significant difference. The results indicate that maize grain yield was not different ($P > 0.05$) among land clearing and tillage methods. Traditional and minimum tillage had more grain (2.94 and 2.59 t ha^{-1}) on average, representing 22.5% and 7.9% increase in yield above conventional tillage (2.40 t/ha). Cassava fresh weight was significantly ($P < 0.05$) affected by the land clearing method, SB and BNW (21.94 and 21.20 t ha^{-1}) having higher yields than BW representing 44.1% and 39.2% increase in cassava fresh weight above BW (15.23 t ha^{-1}). Similar results were obtained under tillage practices where there were differences ($P < 0.05$) among the tillage practices and minimum tillage and zero tillage had higher fresh weight (21.31 t/ha) and (20.61 t/ha) on average representing 28.6% and 24.4% increase in fresh weight above traditional tillage (16.57 t/ha). In conclusion, SB under minimum tillage treatment and BNW under zero tillage treatment gave better maize and cassava yield and appear to be the better options.

Key words: land clearing, tillage methods, growth and yield

Graduate Student Competition: ADSA Graduate Paper Competition - Production Division - MS Students

226 Toll-like receptors expression in the gastro-intestinal tract of dairy calves. N. Malmuthuge*[1], M. Li[1], P. Fries[2], P. Griebel[2], and L. L. Guan[1], [1]*University of Alberta, Edmonton, Alberta, Canada,* [2]*Vaccine and Infectious Disease Organization, University of Saskatchewan, Saskatchewan, Saskatoon, Canada.*

Toll-like receptors (TLRs) are a family of pattern recognition receptors which sense pathogen associated molecular patterns to initiate innate immune responses and maintain intestinal homeostasis. However, the understanding of baseline TLRs expression within specific regions of the gastro-intestinal tract (GIT) of dairy calves and possible age-related expression changes are not well understood. In this study, TLRs expression patterns were investigated throughout the GIT of newborn and weaned dairy calves. Total RNA was extracted from rumen, jejunum, ileum, cecum and colon tissues of 3 weeks old (n = 8) and 6 mo old Holstein male calves (n = 8). Expression of 10 TLRs (TLR1-TLR10) was evaluated relative to β-actin expression in each region using quantitative real time PCR. Gene expression (ΔC_T) data were analyzed using MIXED procedure of SAS and statistical model include gut location and age as fixed effects. Analysis of TLRs data revealed TLR10 expression was significantly ($P < 0.01$) higher in ileum than other GIT regions of 3 week-old calves. TLRs 2, 4 and 10 ($P < 0.01$) were differentially expressed among GIT regions of 6 mo old calves and TLR10 expression was again highest in the ileum. Future studies are required to understand the biological significance of TLR10 in the bovine ileum, which is an important site for B cell development. Expression of most TLRs was lower in rumen than other GIT regions, irrespective of age, supporting the importance of intestinal epithelium in enteric immune responses. Moreover, expression of many TLRs, except TLRs 3, 5 and 6, was significantly downregulated after weaning. The observed downregulation in TLRs expression in weaned calves may reflect host mechanisms to control inflammatory responses to commensal microflora and pathogens as well as development of other immune mechanisms to regulate TLRs signaling. In conclusion, our study indicates that bovine TLRs expression varies throughout the GIT and is age-dependent. These findings are critical for understanding innate immune responses to both commensal microflora and enteric pathogens in dairy calves.

227 Soybean meal substitution by a microbial protein source in dairy cattle diets. J. A. Sabbia*[1], K. F. Kalscheur[1], A. Garcia[1], A. Gehman[2], and J. M. Tricarico[2], [1]*South Dakota State University, Brookings,* [2]*Alltech Inc., Brookings, SD.*

The objective of this study was to examine the effect of a source of microbial protein (DEMP, Alltech, Nicholasville, KY) on milk production, DMI, rumen and blood parameters on high-producing dairy cows as replacement for soybean meal (44% CP). Sixteen Holstein cows with 93 + 37 DIM were used in a 4 × 4 Latin square design. Diets contained 40% corn silage, 20% alfalfa hay, and 40% concentrate mix. Cows were fed one of 4 treatments: 0, 1.14, 2.28, or 3.41% of the diet DM with DEMP. DMI showed a cubic effect (25.9, 27.1, 25.9, 26.6 kg/day; $P = 0.04$), as DEMP in the diets increased. Milk production (41.1 kg/d) was not affected by treatment, whereas energy-corrected milk tended to respond quadratically (39.5, 41.5, 41.8, 41.0 kg/d; $P = 0.09$). Milk fat percentage (3.53, 3.66, 3.62, 3.53%; $P = 0.06$) and yield (1.35, 1.45, 1.49, 1.42 kg/d; $P = 0.07$) also tended to show a quadratic response. A similar quadratic response was shown for total solids percentage (12.3, 12.5, 12.5, 12.3%; $P = 0.02$) and yield (4.87, 5.11, 5.12, 5.03 kg/d; $P = 0.08$). Milk urea nitrogen also responded in a quadratic manner (13.4, 13.7, 13.5, 12.9 mg/dl; $P = 0.05$). There was no effect on milk protein and lactose percentage or yield, nor was there an effect on feed efficiency. NEFA concentration in plasma was similar between treatments, whereas plasma glucose (63.7 to 68.5 mg/dl; $P = 0.06$) and BHBA (11.5 to 13.1 mg/dl; $P = 0.04$) increased linearly. Inclusion of DEMP had no effect on most ruminal VFA concentration, except isovalerate which decreased linearly ($P < 0.001$). Ruminal pH was unaffected by DEMP inclusion, but ammonia concentration tended to decrease linearly from 14.1 to 11.7 mg/dl ($P = 0.09$). Ruminal N fractionation showed a cubic response in total free amino acids (12.1, 10.4, 14.1, 11.2 mg/L; $P = 0.02$). There was a quadratic response for peptides that weighed between 3 and 10 kDa (9.1, 14.9, 12.3, 12.0%; $P = 0.05$) and for those less than 3 kDa (30.8, 28.3, 27.7, 29.4%; $P = 0.03$) when expressed as percentage of total nitrogen. In conclusion, soybean meal substitution with DEMP can improve milk and total solids production in high-producing dairy cows.

Key words: microbial protein, nitrogen fractionation, milk production

228 Effect of timing of initiation of Resynch and presynchronization with GnRH on fertility of resynchronized inseminations in lactating dairy cows. G. Lopes Jr.*, J. O. Giordano, A. Valenza, M. M. Herlihy, J. N. Guenther, M. C. Wiltbank, and P. M. Fricke, *Department of Dairy Science, University of Wisconsin-Madison, Madison.*

Lactating Holstein cows (n = 1,512) were randomized to a 2x2 factorial design resulting in 4 Resynch treatments: 1) Ovsynch (GnRH–7 d–PGF–56 h–GnRH–16 h–TAI) initiated d 32 ± 3 d after AI (GPG32); 2) presynchronization with 100 μg GnRH 25 ± 3 d after AI and Ovsynch initiated 32 ± 3 d after AI at nonpregnancy diagnosis (GGPG32); 3) Ovsynch initiated 39 ± 3 d after AI (GPG39); 4) presynchronization with 100 μg GnRH 32 ± 3 d after AI at nonpregnancy diagnosis and Ovsynch initiated 39 ± 3 d after AI (GGPG39). Overall, 296 cows were inseminated to estrus between enrollment (25 ± 3 d after AI) and initiation of Resynch treatments, and 1,216 cows (GPG32 = 315, GGPG32 = 360, GPG39 = 248 and GGPG39 = 293) received TAI. Blood samples were collected from all cows at the first GnRH injection of Resynch (G1), and ovarian structures were evaluated and blood samples were collected at G1, PGF, and TAI of the Resynch protocols in a subgroup of cows (GPG32 = 105, GGPG32 = 119, GPG39 = 93 and GGPG39 = 113). Based on logistical regression analysis, pregnancies per AI (P/AI) 32 d after AI was not affected by parity and did not differ among treatments [GPG32, 33.3% (105/315); GGPG32, 36.1% (130/360); GPG39, 32.7% (81/248); GGPG39, 39.3% (115/293)]. When analyzed as main effects, presynchronization with GnRH increased ($P = 0.05$) P/AI [33.0% (186/563) vs. 37.7% (245/653) for GPG vs. GGPG], whereas timing of initiation of Resynch did not [34.7% (235/675) vs. 35.9% (196/541) for Day 32 vs. Day 39]. Presynchronization with GnRH increased ($P = 0.007$) the proportion of cows with high P4 (>0.5 ng/mL) at G1 [72.6% (403/556) vs. 79.3% (519/653) for GPG vs. GGPG], and cows with high P4 at G1 had greater ($P = 0.006$) P/AI than cows with low P4 [37.5% (346/922) vs. 28.6% (82/287)]. Ovulation to G1 decreased ($P = 0.039$) luteal regression after PGF [87.5% (121/139) vs. 78.5% (143/183)], and high P4 at G1 decreased ($P < 0.001$) ovulation to G1 [68.4% (67/98) vs. 40.9% (136/332)]. We conclude that presynchronization with GnRH

7 d before initiation of Resynch increased fertility of resynchronized dairy cows whereas timing of initiation of Resynch did not.

Key words: resynchronization, GnRH, progesterone

229 Somatic cell count and management benchmarks in Minnesota dairy herds. R. F. Leuer* and J. K. Reneau, *University of Minnesota, St. Paul.*

Dairy Herd Improvement Association (DHIA) tests provide a large amount of information about herd milk production and milk quality. Many guidelines have been given about farm SCC performance and its relationship to mastitis and milk quality, however associations are lacking. The objective of this study was to investigate the relationship between herd SCC level and performance rank for mastitis and milk quality benchmarking. Minnesota DHIA monthly average herd records were collected from January 2007 to November 2010. Herd tests without SCC information were removed and only herds with an average of 10 tests per year were included. Herds were divided into 4 categories based on average herd SCC over the collection period. Low herds (L) with less than 200,000 SCC (n = 325), medium low (ML) herds between 200,000 and 300,000 SCC (n = 547), medium high herds (MH) herds between 300,000 and 400,000 SCC (n = 470), and high herds (H) above 400,000 SCC (n = 438). Cows > 200,000 SCC were considered infected. Monthly records (n = 66,296) were analyzed using PROC GLM with significant differences determined at $P < 0.05$ using Tukey's multiple comparisons test. The 4 categories were all significantly different in average SCC (L = 157,000, ML = 251,000, MH = 350,000, H = 513,000), average of total cows on test day (L = 116, ML = 141, MH = 110, H = 86), percent infected (L = 16.4, ML = 24.7, MH = 32.9, H = 43.4), percent of current cows with new infections (L = 8.1, ML = 10.5, MH = 12.5, H = 14.2), percent of fresh cows with chronic infections (L = 6, ML = 11.2, MH = 17.6, H = 27.4), percent of current cows with chronic infections (L = 8.3, ML = 14.2, MH = 20.4, H = 29.2), percent infected <30 d in milk (L = 1.7, ML = 2.3, MH = 2.8, H = 3.3), percent infected between 30 and 220 d in milk (L = 7.7, ML = 11.7, MH = 15.4, H = 20), percent infected >220 d in milk (L = 7, ML = 10.7, MH = 14.7, H = 20.1), percent of herd >220 d in milk (L = 35.4, ML = 36.7, MH = 38.5, H = 40.5), rolling herd average (RHA) milk production (L = 10,351, ML = 9,944, MH = 9,201, H = 8,440 kg), RHA protein production (L = 315, ML = 304, MH = 284, H = 263 kg), and RHA fat production (L = 386, ML = 371, MH = 348, H = 325 kg). The 4 categories demonstrated differences that contribute to herd SCC.

Key words: benchmarking, DHIA, SCC

230 Effect of dietary trans fatty acids on selected inflammatory mediators in early lactating dairy cows. J. S. Watts*, D. L. Sevier, J. K. Kinch, S. M. Clark, M. A. McGuire, and P. Rezamand, *Department of Animal and Veterinary Science, University of Idaho, Moscow.*

Trans fatty acids (tFA) contribute to inflammation. The mechanism responsible is not well understood; however, it is thought to involve integration of tFA into cell membranes of immune cells, affecting membrane fluidity and cell signaling. The objective of this study was to investigate the effects of a ration supplemented with tFA on the fatty acid (FA) profile of peripheral blood mononuclear cells (PBMC) and the gene expression of inflammatory markers in early lactating dairy cows. tFA (Virtus Nutrition; Corcoran, Ca) was fed at 0, 1.5, and 3% of dry matter replacing (1:1 wt:wt) saturated fatty acids (sFA). Multiparous lactating Holstein cows 7 d in milk (n = 12) were randomly assigned to a treatment sequence in a 3x3 Latin square design. Each period lasted 14 d. Heparinized blood was collected on d0 (pretreatment) and on d 10 and 14 of each period. Plasma was collected and solid phase extraction was used to isolate plasma phospholipids. Additionally, PBMCs were isolated for FA analysis by gas chromatography and gene expression analysis by RT-PCR using bovine RPS9 as the endogenous control. Data were analyzed using the MIXED procedure of SAS with significance at $P < 0.05$. As dietary tFA increased, the percentage of 18:1 trans isomers increased with linear increases in the t9 and t12 isomers in plasma phospholipids ($P < 0.002$). In PBMCs, both t10 and t12 isomers of 18:1 increased linearly ($P < 0.02$). Dietary tFA had no detectable effect on mRNA expression of pro-inflammatory TNF-α or IL-6, although pretreatment expression of IL-6 and ICAM-1 differed among groups. Expression of IL-1β and ICAM-1 decreased linearly with increasing tFA and a treatment x day interaction in expression of ICAM-1 was detected. Overall, dietary tFA linearly increased the tFA present in plasma phospholipids and PBMCs; however, dietary tFA decreased PBMC expression of some of the pro-inflammatory markers in early lactating dairy cows.

Key words: trans fatty acids, inflammation, transition cow

231 Effects of physical preparation of diets and level of modified wet distillers grains with solubles on production and rumen measurements of lactating dairy cows. J. C. Ploetz*[1], W. C. Hornback[1], D. E. Beever[2], P. H. Doane[3], M. J. Cecava[3], M. R. Murphy[1], and J. K. Drackley[1], *[1]University of Illinois, Urbana, [2]Keenan Systems, Borris, Ireland, [3]Archer Daniels Midland Company, Decatur, IL.*

Our objective was to determine if methods for preparing TMR (Keenan MechFiber [KMF] technology vs. vertical auger [VA] mixer) would alter physical form of the TMR and enable increased utilization of modified wet distillers grains with solubles (MWDGS). Holstein cows (n = 24 with 12 ruminally cannulated; 144 DIM ± 31 d at start) were used in a split-plot design with mixer type as the whole plot and MWDGS levels as subplots in a 3 × 3 Latin square arrangement with 35-d periods. Inclusion rates of MWDGS were 10, 20, and 30% of diet DM, primarily replacing corn, SBM and whole cottonseed. Feed DMI tended to be less for KMF ($P = 0.06$) but was unaffected by MWDGS level ($P = 0.39$). However, a mixer x MWDGS quadratic interaction ($P = 0.14$) was observed; DMI increased as MWDGS increased when mixed using VA but not when using KMF. Milk production did not differ ($P = 0.75$) by level of MWDGS or interaction of MWDGS x mixer ($P = 0.18$). Milk protein content tended ($P = 0.09$) to decrease linearly with increasing MWDGS. Milk protein yield at 30% MWDGS inclusion decreased for KMF but increased for VA (interaction of mixer x linear effect of MWDGS, $P = 0.05$). Milk fat percentage declined with increasing MWDGS ($P = 0.003$) but the interaction between mixer wagon and MWDGS ($P = 0.006$) showed that decreases were larger with VA mixing. Cows fed the diet containing 30% MWDGS mixed with KMF averaged 3.45% (1.24 kg/d) milk fat whereas cows fed the same diet mixed with VA averaged 2.81% (1.10 kg/d) fat. Particle size of the TMR did not explain differences in milk fat. Feed conversion efficiency (FCE; energy-corrected milk/DMI) decreased linearly ($P = 0.007$) with MWDGS, but FCE tended to be maintained when higher MWDGS diets were mixed using KMF vs. VA (mixer, $P = 0.12$; mixer x MWDGS quadratic, $P = 0.13$). Ruminal pH tended ($P = 0.13$) to be greater for KMF than for VA; ruminal pH ($P = 0.05$) and ammonia concentration ($P < 0.001$) decreased linearly as MWDGS increased. Using the KMF mixer wagon resulted in better FCE with higher amounts of MWDGS primarily because milk fat content and yield were not depressed.

Key words: TMR mixer, distillers grains, milk fat

232 Modifying the double-Ovsynch protocol to include human chorionic gonadotropin to synchronize estrus in lactating dairy cows. J. A. Binversie*, K. E. Pfeiffer, and J. E. Larson, *Mississippi State University, Mississippi State.*

The objectives of this study were to determine whether conception, ovulation or presynchronization rates were altered, or follicle and CL characteristics were altered after modifying the double-Ovsynch (DO) protocol to include human chorionic gonadotropin (hCG) compared with the DO protocol. Holstein (n = 146) and Jersey (n = 37) cows were blocked by parity and randomly assigned to 1 of 2 treatments. Cows received either an injection of 100 μg of GnRH (n = 91) or 2000 IU of hCG (n = 92) at the initiation of the Pre-Ovsynch (PO) portion of the DO protocol (PO: GnRH/hCG-7d-$PGF_{2\alpha}$-3d-GnRH). After 7 d, cows started the Breeding-Ovsynch (BO) portion of the DO protocol (BO: GnRH-7d-$PGF_{2\alpha}$-56h-GnRH-16h-TAI with sex-sorted semen). Transrectal ultrasonography and blood samples were used to assess ovarian structures, ovulation, pregnancy diagnosis (at d 32 post TAI), and circulating concentrations of progesterone (P4). Conception rates were similar for cows treated with GnRH or hCG (32.2 and 25.0%; $P > 0.1$). Ovulation rates at the onset of PO were increased in cows treated with hCG compared with GnRH (77.2 and 62.2%; $P < 0.05$). Concentrations of P4 7 d post hCG/GnRH treatment for cows that ovulated were greater in cows treated with hCG compared with those treated with GnRH (LSMeans ± SEM; 5.1 ± 0.3 and 3.8 ± 0.4 ng/ml; $P < 0.05$). The size of the largest follicle 7 d post hCG/GnRH treatment for cows that had ovulated was smaller in cows treated with hCG compared with cows treated with GnRH (12.4 ± 0.5 and 13.8 ± 0.6 mm; $P < 0.05$). Luteal regression (P4 < 1.0 ng/ml) from the injection of $PGF_{2\alpha}$ of PO did not differ between GnRH and hCG treated cows (67.0 and 60.9%; $P > 0.1$). Although more cows ovulated to hCG, a greater proportion of these cows tended to fail to have undergone luteolysis by 3 d post $PGF_{2\alpha}$ compared with cows that had ovulated to GnRH (29.6 and 16.1%; $P = 0.09$). Therefore, the overall percentage of cows which were synchronized to the PO did not differ between GnRH and hCG treated cows (61.5 and 52.2%; $P > 0.1$). In conclusion, no improvement was achieved by replacing the first injection of GnRH in the DO protocol with hCG.

Key words: double-Ovsynch, hCG, presynchronization

233 Fibroblast growth factor 9 influences steroidogenesis and gene expression in ovarian granulosa and theca cells of cattle. N. B. Schreiber* and L. J. Spicer, *Oklahoma State University, Stillwater.*

Ovarian cysts result in the loss of millions of dollars to the dairy industry annually because of increased number of days open, reduced milk production, and increased culling rate. Fibroblast growth factor 9 (FGF9) is downregulated in cystic follicles versus normal dominant follicles in cattle. Therefore, experiments were conducted to evaluate the role of FGF9 in hormone-stimulated steroidogenesis, proliferation and gene expression in bovine ovarian granulosa and theca cells from antral follicles of cattle. Quantitative PCR was used to measure gene expression of side-chain cleavage enzyme (CYP11A1), aromatase (CYP19A1), 17-hydroxylase (CYP17A1), LH receptor (LHCGR) and/or FSH receptor (FSHR). Small (1–5 mm) follicle granulosa cells (SMGC), large (8–22 mm) follicle theca cells (LGTC) and large follicle granulosa cells (LGGC) were grown in vitro and treated for 48 h with 0, 3, 10, or 30 ng/mL of recombinant human FGF9 to evaluate the effects on steroid production, cell proliferation, and gene expression. In SMGC, FGF9 (30 ng/mL) decreased ($P < 0.05$) estradiol and progesterone production by 80% and 56.4%, respectively, after cells were stimulated with 30 ng/mL of FSH and IGF1. In LGTC, FGF9 (30 ng/mL) decreased ($P < 0.05$) progesterone and androstenedione production by 71% and 79%, respectively, after cells were stimulated with 30 ng/mL of LH and IGF1. In contrast, IGF1-induced SMGC and LGTC proliferation was further stimulated ($P < 0.05$) 1.8- and 1.5-fold by FGF9, respectively. FGF9 decreased ($P < 0.05$) CYP11A1 and FSHR mRNA abundance and had no effect on CYP19A1 mRNA abundance in SMGC and LGGC treated concomitantly with FSH and IGF1. FGF9 decreased ($P < 0.05$) abundance of CYP11A1, CYP17A1, and LHCGR mRNA by 97%, 77%, and 97%, respectively, in LGTC treated concomitantly with LH and IGF1. In conclusion, FGF9 regulates ovarian function in cattle by stimulating cell proliferation and inhibiting steroidogenesis of both granulosa and theca cells. FGF9 inhibition of steroid production is likely via attenuation of both gonadotropin receptor and steroidogenic enzyme gene expression.

Key words: cystic follicles, granulosa cells, theca cells

234 Relationships among temperature, moisture, bacterial counts, and animal hygiene in compost bedded pack barns. R. A. Black*, J. L. Taraba, G. B. Day, F. A. Damasceno, M. C. Newman, K. A. Akers, and J. M. Bewley, *University of Kentucky, Lexington.*

The objective of this study was to assess the relationships among temperature, moisture, bacterial counts, and animal hygiene for composted material collected from compost bedded pack (CBP) barns. Compost samples were collected from 54 CBP barns in Kentucky from October 2010 to February 2011. A composite sample was collected from 9 evenly distributed sampling areas throughout each barn for analysis of nutrient composition and bacterial counts. Compost moisture was measured using an oven at 75°C. Compost temperatures (CT) were measured 10.2 cm below the pack surface. Subjective hygiene scores were collected by the same observer for 50.4 ± 16.1 cows per herd using a 4 point scoring system described by Cook (2007, 1-clean, 4-dirty). Producers reported their most recent SCC. The MEANS procedure of SAS® (Cary, NC) was used to calculate mean (±SD) SCC (238,162.2 ± 81,701.5 cells per ml, n = 37), hygiene score (2.22 ± 0.46, n = 43), moisture (54.9 ± 12.5%, n = 51), CT (30.5 ± 11.4°C, n = 52), coliform (6.09 ± 0.63 $\log_{10}$ cfu/g, n = 54), *Escherichia coli* (5.73 ± 0.68 $\log_{10}$ cfu/g), streptococcal species (7.00 ± 0.68 $\log_{10}$ cfu/g, n = 54), staphylococcal species (7.60 ± 0.49 $\log_{10}$ cfu/g, n = 53), and bacillus species (7.30 ± 0.56 $\log_{10}$ cfu/g, n = 54). Moisture was highly correlated with ambient temperature ($r = -0.73$, $P < 0.01$). Moisture was negatively correlated with CT ($r = -0.38$, $P < 0.01$) and positively correlated with hygiene score ($r = 0.68$, $P < 0.01$). Hygiene score and CT were also negatively correlated ($r = -0.42$, $P < 0.01$). *Escherichia coli* count was moderately correlated with CT, moisture, SCC, and hygiene score ($r = 0.62$, $P < 0.01$; $r = -0.41$, $P < 0.01$; $r = 0.42$, $P < 0.01$; and $r = -0.39$, $P < 0.02$). No significant correlations between coliform, staphylococcal species, streptococcal species, and bacillus species counts and CT ($P > 0.10$) were observed. These results suggest that high CT and low moisture are important for maintaining a dry resting surface for cows and may contribute to pack bacterial counts.

Key words: compost bedded pack barn, bacterial analysis, SCC

235 Objective assessment of pain in dairy cattle with clinical mastitis. C. E. Fitzpatrick*[1], N. Chapinal[1,2], C. S. Petersson-Wolfe[3], and K. E. Leslie[1], *[1]University of Guelph, Guelph, Ontario, Canada, [2]University of British Columbia, Vancouver, British Columbia, Canada, [3]Virginia Polytechnic Institute and State University, Blacksburg.*

Clinical mastitis has negative effects on profitability and cow welfare, with significant discomfort and pain. This study was conducted to objectively assess pain in cases of experimentally induced clinical mastitis, involving 24 (12 primiparous and 12 multiparous) lactating Holstein cows enrolled in an LPS endotoxin challenge study. Each animal was challenged in one rear mammary quarter by intramammary infusion with 25 µg of *E. coli* LPS. Subsequently, a subcutaneous injection of either a placebo (n = 12) or NSAID treatment (meloxicam) (n = 12) was randomly allocated and administered using, yet to be identified, double-blind methods (Treatments A and B). The animals were monitored for 2 d before, and 2 d following, the intramammary challenge. Several behavioral, physiological and performance parameters were monitored throughout the study period, including activity, rumination, body temperature, milk weights, DMI, SCC and clinical scores of milk, udder edema, pain sensitivity of the mammary glands, serum amyloid A and haptoglobin. During the first 6 h after inoculation and treatment, cows ruminated 14.6 ± 2.1 min/2 h interval ($P < 0.001$) less compared with the same baseline time period before challenge. Overall, multiparous cows were found to ruminate 6.1 ± 1.6 min/2h ($P = 0.001$) more than primiparous cows. There was no difference in rumination between treatment groups. Using a pain pressure algometer, the difference between the pressures applied to the control quarter was compared with the challenge quarter for each sampling time period before, and after inoculation. There was an effect at hour 6 after inoculation and treatment as compared with the baseline readings. For Treatment A animals, more pressure could be applied on their challenge quarter than their control quarter (1.9 ± 0.9 lbs; $P = 0.0445$). Treatment B animals registered more pressure applied to the control quarter than the challenge quarter (2.5 ± 0.9 lbs.; $P < 0.01$). These results indicate the potential for using continuous measurement of rumination and pain pressure sensitivity for objective assessment of pain due to illness in cases of clinical mastitis.

Key words: mastitis, pain management, behavior

236 Herd reproductive performance with an automated activity monitoring system versus a synchronized breeding program in 3 commercial dairy herds. R. C. Neves*, K. E. Leslie, J. S. Walton, and S. J. LeBlanc, *University of Guelph, Guelph, ON, Canada.*

The objective of this study was to compare overall herd reproductive performance with an automated activity monitoring system relative to a synchronized breeding program. A pen-level randomized trial was performed over 1 year using 3 commercial herds in Ontario, Canada, in which cows were housed in a primiparous and a multiparous pen on each farm. Pens were randomly assigned to an automated heat detection (AHD) system based on monitoring activity levels (Heatime, SCR Engineers Ltd.) or a timed artificial insemination program (TAI; Ovsynch), and a crossover occurred after 6 mo of the trial to avoid confounding treatment with parity. Insemination based on additional detection of estrus by observation was practiced in all pens. Herds A, B, and C milked 495, 305 and 260 cows on average, respectively. Herd A had 1476 AI, herd B 781 AI, and Herd C 988 AI throughout the study period. Analyses of the 3 herds were conducted using pen as the experimental unit. The proportion of TAI in the TAI pen was 49%, 71% and 55% for herds A, B and C. The proportion of AI in the AHD group after a heat signaled by the AHD system was 64%, 52% and 61% for herds A, B, and C. Conception risks for TAI and AHD were 32% and 32% in herd A, 40% and 44% in herd B and 26% and 29% in herd C. The mean annual 21-d pregnancy rates across the 3 herds were analyzed utilizing least squares means controlling for herd effect. There was no difference ($P = 0.25$) in the overall mean pregnancy rates between TAI program (15.9%) and AHD system (14.6%). Under the conditions in which a substantial minority of AI in both groups was based on visually detected estrus, herd pregnancy rate was not different between a TAI program and an AHD system. Further investigation of variables that may influence herd performance and of cow-level performance is required.

Key words: reproduction management, estrus detection, pregnancy rate

237 Effects of time and storage conditions on Johne's disease milk ELISA test results. C. M. Innes*, D. F. Kelton, D. L. Pearl, and T. F. Duffield, *University of Guelph, Guelph, Ontario, Canada.*

The Ontario Johne's Education and Management Assistance Program (OJEMAP) utilizes an individual cow milk ELISA test for antibody to *Mycobacterium avium* subspecies *paratuberculosis* (MAP) to determine the Johne's disease status of participating herds. Concerns were raised about the age of the samples at the time of testing and the temperature extremes that milk samples could be subjected to while being transported to the Dairy Herd Improvement (DHI) laboratory, and the impact on integrity of test results. This objective of this study was to investigate the impact of storage time and conditions (room temperature, frozen, refrigerated) on Johne's disease milk ELISA test results. Milk ELISA tests were completed using a commercially available kit following standard manufacturer instructions on days one, 4, 7 and 10 post collection. The time between collection and storage of the samples and the differences between storage conditions were compared graphically and statistically using the paired *t*-test, with a level of significance of $P < 0.05$. There were no significant differences in test results for any of the storage conditions for up to 7 d post collection. Based on these results, samples could be stored under various conditions for up to a week with no significant changes in test results.

Key words: Johne's, storage, ELISA

238 The evaluation of bulk tank tests for the surveillance of Johne's disease. C. M. Innes*, D. F. Kelton, D. L. Pearl, and T. F. Duffield, *University of Guelph, Guelph, Ontario, Canada.*

The objective of this study was to evaluate the utility of bulk tank tests to detect the presence of *Mycobacterium avium* subspecies *paratuberculosis* (MAP) antibody in dairy herds for the purpose of Johne's disease surveillance. Individual cow milk samples were collected by CanWest Dairy Herd Improvement customer service representatives in herds across Ontario, Canada. These samples along with bronopol preserved bulk tank samples collected by milk transporters from herds participating in the Ontario Johne's Education and Management Assistance Program (OJEMAP), a producer funded Johne's control scheme. The bulk tank ELISA results were expressed as percentage S/P (sample to positive). A S/P ratio of ≥ 30% was considered positive for MAP and a ratio of 20–30% was considered to be suspect for MAP.

The individual cow ELISA results were expressed as an optical density value, with a positive result having an optical density of 0.1 or higher. There were 309 farms tested, with herd size from 15 to 986 milking cows. The relative sensitivity and specificity of the bulk tank ELISA test when a positive herd was defined as 1 or more positive cows was 54.7% and 90.6%, respectively. When 2 or more positive cows defined a positive herd, the relative sensitivity increased to 63.3% while the specificity decreased to 84.2%.

Key words: Johne's, bulk milk, ELISA

Graduate Student Symposium: Becoming Your Own Best Advocate: How to Expand and Communicate Your Skills and Qualifications

239 Preparing an effective CV for an academic position. M. T. See*, *North Carolina State University, Raleigh.*

Your application for an academic job should be completed with the position description in mind. Position descriptions indicate what skills and experiences are valued and you want to present your information with that in mind. When applying for an academic position you will be asked to submit a cover letter that may include a statement of interest in teaching, research or extension, curriculum vitae (CV) and a list of professional references. Most institutions also have an online job application system. Thoughtful preparation of the cover letter should not be underestimated. An effective cover letter clearly and concisely answers 3 questions; 1) Why am I writing? 2) What do I have to offer in this position? 3) What are my significant achievements? A good cover letter summarizes the CV while highlighting your unique qualifications for the position you are applying to. Effective CVs are well organized and packed with relevant information that match and support your academic objective. The CV is a comprehensive record of what you have done. There is no set format for a CV and this allows you the opportunity to be creative. Also consider preparing the CV specifically for the job for which you are applying. The information that is most relevant for the position should be first. Don't make the search committee search through your CV to find out why you should be considered. State the reasons up front. Contact information goes first followed by education and work experience. You may include clear concise interest statements describing research or teaching goals. Categories to include in the CV are professional activities, teaching experience, memberships, honors and awards, grants, presentations and research publications. Within categories list each entry in reverse chronological order. Place references at the end, include phone numbers and e-mail addresses. It is good to show a breadth of connections with other people but stay within academia unless there is an excellent reason to list someone outside. Always have a variety of people proofread your CV before submitting. Remember there is no required length for a CV and this is an important first step to an interview and the position you seek.

Key words: student, CV, job

240 Grantsmanship—How to write a successful grant proposal. T. Davis*, *Baylor College of Medicine, Children's Nutrition Research Center, Houston, TX.*

Writing a successful grant application for submission to any funding agency requires considerable planning and action. This talk will provide tips on how to get started writing a grant proposal. Each section of the application will be discussed, focusing on the importance of the various sections and the specific information considered necessary in the abstract, specific aims, background, preliminary studies, and research design and methods sections. The grant review process and the criteria used by reviewers to evaluate applications will be described. Common problems and how to avoid these will be presented. Options for what to do if the submission of an application is not successful also will be discussed.

Key words: grant, writing, academia

241 Maximizing your graduate experience. N. C. Whitley*, *North Carolina A&T State University, Greensboro.*

The description of individual graduate experiences can be as varied and colorful as those queried; however, most would likely agree that the expected product of a successful graduate experience would be a satisfying job or career. If you agree with Henley that we are the master of our fates, the captain of our souls, then you may also believe that we, as individuals, have a great part to play in maximizing our experiences to achieve the success we seek. The objective of this presentation will be to discuss the kind of things that can be done to play that role to its fullest. Making informed, educated choices about the University you attend, your program or focus area and your advisor or mentor(s) within that program or focus area is a major first step. If that step has already been taken, you should look for opportunities within or even outside of the program to allow you to excel. It is important to never underestimate the value of networking, collaborating or even professional socializing on your part, or on the part of your advisor and/or mentors in finding or developing opportunities (and future jobs). There are many types of people who might become part of your network, so being able to communicate on a broad level and show people you value them for their unique skill set is important. Keeping well informed about current research topics in your focus area will assist you in networking and also demonstrate your enthusiasm for your field of study. Future mentors and employers are always looking for bright, educated and independent thinkers; therefore you need to do your best to set yourself apart from the competition. There are many ways to maximize your graduate experience so that it leads you down the path to success; with knowledge of some of these, you can more easily navigate that path.

Key words: graduate program, success, job

242 Becoming your own personal brand: How to market your talents and experiences for maximum results. C. Johnson*[1] and C. Luhman[2], *[1]Director Talent Acquisition & Diversity, Land O' Lakes, Inc, Arden Hills, MN, [2]Land O' Lakes Purina Feed, LLC, Gray Summit, MO.*

To stand out as a competitive potential employee, you must be able to portray your experiences and enthusiasm in a transparent and convincing manner. This seminar will address how to portray your own personal brand to potential employers for maximum results. We will specifically address the 3 main components of marketing your brand: 1. standing out on paper, 2. allowing your references and reputation to set you apart, and 3. impressing in person. With online, email, and mail application processes, your CV is often your first impression, and therefore, content and layout are critically important. Ways to convey your precise experiences, talents, and abilities in a concise, well laid out CV will be addressed. Potential employers will also become familiar with you through your references and your reputation, often before meeting you. Careful selection of references along with providing them with adequate and current information regarding your experiences and how you would meet the company's needs will help distinguish you from other candidates. How to protect your reputation as a professional will be addressed. Finally, when you get the oppor-

tunity to interview, be prepared to impress the potential employer. Think about potential interview questions and be prepared to answer with concise and accurate experiences and insightful answers. Also, become informed about the company and have thoughtful questions to ask the interviewer. By marketing yourself you improve your chances of successfully obtaining your perfect position.

243 Plane of dietary protein during late gestation in beef cows alters longissimus lumborum adipogenic gene expression in the offspring. S. Moisa*, D. Shike, D. B. Faulkner, and J. J. Loor, *University of Illinois, Urbana.*

The aim of this study was to evaluate potential carryover effects of the maternal diet on offspring performance, intramuscular adipogenic gene expression, and carcass characteristics. Two groups of pregnant Angus cows were fed a control diet (%DM = TDN 63.2, CP 9.48) or a higher-protein diet containing wet distiller's grain with solubles (WDGS; % DM = TDN 67.0, CP 13.0) during the last 96 d of gestation. Data were analyzed as a factorial design (maternal nutrition and stage of growth) with repeated measures using PROC MIXED in SAS. Seven early-weaned offspring (116 ± 6 d of age at weaning) from each group of cows were fed the same high-starch diet during a ~100-d growing phase. Subsequently, both groups of steers received the same diet during the finishing phase. Biopsies of the longissimus lumborum (LL) were collected at 0 (before start of growing phase), 100, 200 (mid-way through finishing), and 1 wk before harvest. Expression of the adipogenic transcription regulator peroxisome proliferator-activated receptor γ (PPARG), the lipogenic transcription regulators sterol responsive element binding factor 1 (SREBF1) and MLX interacting protein-like (MLXIPL), and the lipogenic enzymes fatty acid synthase (FASN) and stearoyl-CoA desaturase (SCD) was evaluated via quantitative PCR. Results showed no significant differences ($P > 0.05$) of maternal nutrition on offspring BW or ADG (1.4 and 1.6 kg/d during growing and finishing phases). At 100 d, steers from dams fed more dietary protein during pregnancy had greater (maternal diet × time $P < 0.05$) expression of PPARG, SREBF1, FASN, and SCD. In contrast, steers from cows fed the control diet during pregnancy had an increase (maternal diet × time $P < 0.05$) in expression between 100 and 200 d on study. Results indicated a precocious pro-adipogenic response during the growing phase in LL of steers born from cows fed a higher level of protein in the diet.

Key words: lipogenesis, marbling, gene expression

244 Oleic acid enhances G protein-coupled receptor 43 (GPR43) in cultured bovine intramuscular adipocytes. K. Y. Chung*[1], S. B. Smith[2], and B. J. Johnson[1], *[1]Texas Tech University, Lubbock, [2]Texas A&M University, College Station.*

G protein-coupled receptor 43 (GPR43) is a 7-transmembrane domain receptor that can be activated by fatty acids and regulates cAMP signal pathways in bovine adipocytes. The GPR43 is highly expressed in isolated murine adipocytes but lowly expressed in stromal-vascular cells. Our previous results did not detect the GPR43 protein in bovine perirenal or subcutaneous (s.c.) adipose tissues but the protein was present in bovine intramuscular (i.m.) adipose tissue. We hypothesized that oleic acid (18:1n-9) may regulate adipogenesis of bovine i.m. adipose tissue. Primary cultures of i.m. and s.c. preadipocytes were isolated from adipose tissues dissected from bovine longissimus muscle. Data were analyzed as a completely randomized design using the MIXED model, each treatment performed in triplicate. Means were considered different at $P < 0.05$. Preadipocytes were treated with various levels of oleic acid (1μM, 10μM, 100μM, and 500μM) for C/EBPβ, PPARγ, stearoyl CoA desaturase (SCD), and GPR43 protein and mRNA analysis. Real-time quantitative PCR was used to measure mRNA contents. The mRNA concentrations of C/EBPβ, PPARγ, and GPR43 were increased ($P < 0.05$) in the i.m. adipocyte by oleic acid, but no effects were observed in the s.c. adipocytes ($P > 0.05$). Western blot analysis revealed that treatment with oleic acid enhanced PPARγ protein in both i.m. and s.c. adipocytes in a dose-dependent manner. Relative GPR43 per GAPDH protein levels in i.m. adipocytes tended to be increased ($P = 0.10$) by treatment with oleic acid. Interestingly, mRNA concentrations of SCD were decreased with oleic acid treatment ($P < 0.05$). These data indicate that oleic acid alters mRNA and protein concentrations of C/EBPβ, PPARγ, and SCD in bovine i.m. adipocytes, and these effects may be mediated through the GPR43 receptor.

Key words: G protein-coupled receptor 43, adipocyte, oleic acid

245 Effect of stearoyl-CoA desaturase 1 inhibiters on lipid metabolism and cellular proliferation in primary bovine adipocytes. A. K. G. Kadegowda*, T. A. Burns, S. L. Pratt, and S. K. Duckett, *Clemson University, Clemson, SC.*

Objectives were to determine the effects of sterculic acid (SA) and trans-10, cis-12 conjugated linoleic acid (t10c12 CLA), known stearoyl-CoA desaturase 1 (SCD1) inhibitors, on lipid metabolism and cellular proliferation in primary bovine adipocytes. Bovine primary preadipocyte cultures were isolated from intermuscular fat of 18 mo-old Angus crossbred heifers (n = 3) and differentiated (D0) in differentiation media [DMEM containing 10% fetal calf serum, 2.5 μg/mL insulin, 0.25 μM dexamethasone (DEX), 20 μM troglitasone, 0.5 mM isobutylmethylxanthine (IBMX), and 10 mM acetate] for 2 d. Cells were further differentiated from D2 to D6 in media without DEX and IBMX. From D0 to D6, cells were treated with 1 of 4 levels (0, 50, 100, or 200 μM) of SA or t10c12 CLA. In Expt. 1, trans-11 18:1 was added at 0 or 100 μM to the media on D4 and the cells harvested for fatty acid (FA) analysis after 48h. In Expt. 2, stearic acid-^{13}C18 was added at 100 μM on D4 and cells harvested at 0, 6, 12, 24, and 48h for FA analysis by GC-MS. The effect of SA and t10c12 CLA on cell proliferation of undifferentiated pre-confluent cells was assayed using Cell Counting Kit-8 at 24, 48, and 72h post incubation. The experimental design was 2 × 4 factorial and data were analyzed by PROC MIXED (SAS). The total cellular FA yield (minus supplemented FA) did not change due to SA or t10c12 CLA (except 200 μM). The desaturation of trans-11 18:1 to c9t11 CLA was decreased ($P < 0.05$) up to 95% by both SA and t10c12 CLA compared with Control (0 μM). Stearic acid-^{13}C18 was enriched up to 75% by 6h of incubation. The enrichment of labeled oleate increased ($P < 0.05$) from 4.1% at 6 h to 28.4% at 48h in the control (0 μM SA). The SA inhibited the conversion of labeled stearate to oleate at all the supplemented levels and time points ($P < 0.05$). The SA and t10c12 CLA treatments did not affect the cell viability at the tested concentrations. Results showed both SA and t10c12 CLA inhibit SCD1 activity/expression at 50 μM concentration without affecting adipose lipid content. Also, SCD1 inhibition does not affect bovine preadipocyte viability.

Key words: stearoyl-CoA desaturase 1, adipocyte, inhibition

246 Palmitoleic acid (C16:1), not an elongation product, decreases lipogenesis and desaturation in bovine adipocyte cultures. T. A. Burns*, C. M. Klein, S. K. Duckett, S. L. Pratt, and T. C. Jenkins, *Clemson University, Clemson, SC.*

Our objective was to confirm the identity of fatty acids elongated from C16:1 and to determine if C16:1 or an elongated fatty acid is

responsible for decreased desaturation and lipogenesis rates previously seen in cultured bovine adipocytes supplemented with C16:1. Bovine stromal vascular cultures were isolated, propagated, and tested for their capacity to differentiate into adipocytes. Cells were passaged 4 times, allowed to reach confluence, and held for 2 d. On D0, primary differentiation media [Dulbecco's Modified Eagle's Medium (DMEM) containing 10% fetal calf serum (FCS), and 2X antibiotic/antimycotic (AB/AM), insulin at 2.5 μg/mL, 0.25 μM dexamethasone, 20 μM troglitasone (TRO), 0.5 mM isobutylmethylxanthine, and 10 mM acetate] was applied for 2 d and replaced with secondary media {DMEM, 10% FCS, 2X AB/AM, insulin at 2.5 μg/mL, 5 μM TRO, 10 mM acetate, containing 1 of 4 levels of fatty acid [0 μM (CON), 150 μM C16:0, 150 μM C16:1, or 150 μM C18:1cis11]} for 4 d. On D6, cells were harvested for fatty acid analysis. In addition, cells were incubated with ^{13}C2, ^{13}C18:0, or ^{13}C16:1 on D6 to estimate lipogenesis and desaturation rates and confirm elongation products of C16:1 using GLC-MS. Data were analyzed using Proc GLM of SAS 9.2. In C16:1-supplemented cells, C16:1, C18:1cis11, and C20:1 were elevated ($P < 0.05$) compared with CON cells. In C18:1cis11-supplemented cells, C18:1cis11 and C20:1 were elevated ($P < 0.05$) compared with CON, but C16:1 was not. The C18:1cis9/C18:0 ratio was decreased ($P < 0.05$) in C16:1 cells compared with all other treatments. Incorporation of ^{13}C16:1 into cells and presence of ^{13}C label in C18:1cis11 and C20:1 confirmed them as elongation products of C16:1 in bovine adipocytes. By 12 h of ^{13}C18:0 incubation, cells supplemented with C16:1 had reduced ($P < 0.05$) ^{13}C18:1cis9 compared with all other treatments. Similarly, ^{13}C16:0 was reduced ($P < 0.05$) in C16:1-treated cells compared with CON and C18:1cis11-treated cells following ^{13}C2 incubation. Therefore, inhibition of desaturation and lipogenesis can be attributed to C16:1 and not its elongation products; C18:1cis11 or C20:1.

Key words: bovine, adipocyte, palmitoleic acid

247 Palmitic and stearic acids induce adipogenic gene expression in single- or co-cultures of bovine intramuscular preadipocyte and satellite cells. S. H. Choi*[1], K. Y. Chung[2], B. J. Johnson[2], K. H. Kim[3], and S. B. Smith[1], *[1]Texas A&M University, College Station, [2]Texas Tech University, Lubbock, [3]National Institute of Animal Science, Suwon, Gyunggi, Korea.*

We hypothesized that saturated fatty acids would stimulate lipogenic gene expression in single- and cocultured intramuscular (i.m.) preadipocytes and myoblasts. Bovine satellite cells (BSC) and i.m. preadipocytes were isolated from 14-mo-old crossbred steers. Both cell types were cultured with 10% fetal bovine serum (FBS)/Dulbecco's modified eagle medium (DMEM), and 1% antibiotics during the 3-d proliferation period. After proliferation, BSC and i.m. preadipocytes were treated with 3% horse serum DMEM or 5% FBS/DMEM with antibiotics, respectively, for 4 d. Finally, single or combined BSC and i.m. preadipocytes were cultured with 40 μM palmitic, palmitoleic, stearic, oleic, or linoleic acids for 2 h. The endogenous 40S ribosomal protein S9 (RPS9) control was used to normalize the expression of AMP-activated protein kinase-α (AMPKα), C/EBPβ, carnitine palmitoyltransferase I - β (CPT1β), peroxisome proliferator activated receptor-γ (PPARγ), glucose transporter type 4 (GLUT4), and stearoyl-CoA desaturase (SCD). Data were analyzed as a 2 × 2 factorial ANOVA with chemical treatment and culture method as the main effects. Palmitic and stearic acids significantly stimulated C/EBPβ ($P < 0.0001$) and CPT1β ($P = 0.02$ and $P = 0.001$, respectively) gene expression in single- and co- cultured i.m. preadipocytes. Also, oleic and linoleic acids depressed SCD gene expression in single- and cocultured i.m. preadipocytes ($P < 0.0001$). In myoblasts, palmitic acid significantly enhanced C/EBPβ gene expression in both single- ($P = 0.036$) and cocultured ($P = 0.028$) myoblasts. Expression of GLUT4 in single- ($P = 0.006$) and co- ($P = 0.016$) cultured myoblasts was depressed by oleic and linoleic acids. Oleic acid and linoleic acid decreased SCD gene expression in both single- and cocultured myoblasts($P < 0.0001$). Saturated fatty acids stimulate genes associated with differentiation of i.m. preadipocytes, but have less effect in differentiating myoblasts. Funded in part by Beef Check-off dollars.

Key words: fatty acid, preadipocyte, satellite cell

248 The effect of chromium propionate on bovine intramuscular and subcutaneous preadipocytes and muscle satellite cells. R. J. Tokach*[1], W. Rounds[2], K. Y. Chung[1], and B. J. Johnson[1], *[1]Texas Tech University, Lubbock, [2]Kemin Industries Inc., Des Moines, IA.*

Chromium (Cr) propionate is a feed ingredient that has been used in the livestock industry to improve immune efficiency of livestock species, increase pork quality, and increase milk yield in dairy cattle. The aim of these in vitro experiments was to determine the effect of chromium propionate (Kemin Industries, Des Moines, IA) on changes in transcription factors and receptors important in adipose tissue differentiation and skeletal muscle growth. We hypothesized that Cr would increase mRNA expression of glucose transporter 4 (GLUT4) in intramuscular (IM) preadipocytes and protein expression in bovine muscle satellite cells (BSC). Intramuscular and subcutaneous (SC) preadipocytes and BSC were isolated from the semimembranosus to determine the effect of treatment on GLUT4 and peroxisome proliferator-activated receptor gamma (PPARγ) mRNA and GLUT4 protein abundance. Preadipocyte cultures were treated with differentiation media plus 0.1 μM, 1 μM, or 10 μM concentrations of Cr or 10 μM, of sodium propionate for 96, 120, and 144 h before harvest. Data were analyzed as a randomized complete block design using the MIXED model. Real-time quantitative PCR was used to measure the relative level of mRNA. For the IM and SC preadipocyte cultures, GLUT4 mRNA abundance tended to increase ($P = 0.10$) after 144 h of treatment with differentiation media plus either 1 μM or 10 μM of Cr. In the SC preadipocyte cultures, the GLUT4 mRNA abundance increased ($P \leq 0.05$) for the average of the 3 levels of Cr as compared with the differentiation media alone and this increase tended ($P = 0.10$) to be linear. These results indicated that Cr altered glucose uptake mechanisms regardless of adipose tissue type. The mRNA abundance for PPARγ increased ($P \leq 0.01$) when differentiation media was added to the preadipocyte cultures at 144 h. The GLUT4/GAPDH protein abundance decreased ($P \leq 0.01$) in a dose-dependent manner when Cr was added to the BSC. The results indicated that Cr may have caused a feedback mechanism in skeletal muscle, due to increased efficiency of glucose transport caused by the Cr supplementation.

Key words: chromium propionate, glucose transporter 4, preadipocyte

249 Effect of rate of gain during grazing 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.*

The stocker cattle production phase could benefit by influencing adipose tissue development before finishing. Previous research indicates that nutritional management can affect fat deposition in growing cattle. Our objective was to evaluate rate of gain to a common initial finishing BW on gene expression of adipose tissue in growing cattle. Angus

steers (n = 72; 259 ± 28 kg BW) were blocked by BW and sire and allotted to 4 treatments: (1) grazing dormant native range (NR) plus a protein supplement (1.0 kg/d) followed by season-long grazing NR (CON), (2) grazing dormant NR plus a corn-based supplement (1% of BW) followed by short-season grazing NR (CORN), (3) grazing wheat pasture (WP) at a high stocking rate (3.0 steers/ha) for a moderate ADG (LGWP), and (4) grazing WP at a low stocking rate (1.0 steers/ha) for a high ADG (HGWP). Supplements were fed individually 5 d/wk. Four steers per treatment were harvested at an estimated HCW of 200 kg before finishing, and subcutaneous (SC), perirenal (PR), and intramuscular (IM) adipose tissue collected. Gene expression was determined using qRT-PCR. Performance and carcass data are presented in a companion abstract (Sharman et al., 2011). MANOVA revealed a treatment × adipose tissue interaction ($P < 0.05$) for genes involved in lipogenesis and adipogenesis. Canonical variate analysis indicated that treatment did not affect lipogenic or adipogenic gene expression in IM, but in general, lipogenic and adipogenic gene expression in SC and PR was greater in HGWP and LGWP than CON and CORN. The lipogenic genes fatty acid synthase and diacylglycerol acyltransferase 2 were highly correlated ($P < 0.01$) with the canonical variate (0.91 and 0.64, respectively). The adipogenic genes peroxisome proliferator activated receptor gamma, sterol regulatory element binding protein, and CAATT/ enhancer binding protein β were correlated ($P < 0.05$) with the canonical variate (0.65, 0.95, and 0.32, respectively). In summary, moderate to high rates of gain of cattle grazing wheat pasture significantly increased lipogenesis and adipogenesis in SC and PR, but development of IM was not affected.

Key words: adipose tissue, gene expression, stocker cattle

250 Effect of ewe body condition during mid to late gestation on mammary growth and composition of female progeny. K. E. Boesche*, A. L. Hunter, K. M. O'Diam, S. C. Loerch, and K. M. Daniels, *The Ohio State University, Ohio Agricultural Research and Development Center, Wooster.*

The foundation for functional mammary secretory tissue, parenchyma (PAR), is established early in life; amount of PAR directly relates to future milk production. Dam body condition score (BCS) during mid to late gestation may affect progeny postnatal mammary growth and composition via in utero metabolic programming events. Pregnant ewes (n = 96; ≈80 d of gestation) were allotted to treatment groups based on initial BCS of 2, 3, or 4 (on a 1 to 5 scoring system with 1 being extremely thin and 5 being extremely fat). Ewes were housed in 18 pens (6 pens per treatment) and fed a maintenance diet of limit-fed corn silage (1.1 kg DMI/d), to which whole shelled corn was supplemented at 0.12, 0.26, and 0.47 kg DMI/d for BCS groups 2, 3, and 4, respectively. Diets were adjusted every 2 wk to maintain desired BCS throughout pregnancy. Prior to weaning, lambs nursed their mothers and were fed a common starter. Lambs were weaned (≈56 d of age; 23.59 kg) and placed on a common finishing diet that met NRC requirements. Female progeny from the 3 BCS groups (n = 73) were slaughtered at similar BW (46.9 ± 0.5 kg; $P = 0.913$), and age (126.3 ± 2.8 d; $P = 0.159$). Udders were removed and mammary tissue subjected to biochemical analysis. Total mammary gland weights (179.2, 167.4, and 175.6 ± 8.8 g for BCS 2, 3, 4, respectively) did not differ by treatment ($P = 0.615$). However, PAR weight of progeny from BCS 2 ewes (25.3 g) was greater ($P = 0.074$) than that of BCS 3 (18.5 g) or BCS 4 (18.8 g) progeny. Protein mass within PAR (BCS 2 = 1.43, 3 = 1.02, and 4 = 1.07 ± 0.13 g) varied by treatment ($P = 0.053$), as did DNA mass within PAR (BCS 2 = 134.8, 3 = 93.1, and 4 = 103.0 ± 13.4 mg; $P = 0.072$). Lipid mass within PAR did not differ by treatment and averaged 7.10 ± 1.17 g ($P = 0.228$). Despite detectable differences in PAR due to treatment, no differences in weight or composition of the mammary fat pad were found. Factors that promote mammary PAR growth may have a positive impact on future milk production. Our observations suggest that BCS during gestation may have important lactation performance implications for female progeny.

Key words: body condition score, sheep, mammary

251 Defining maturity of Nellore cattle based on growth and body composition. M. Marcondes*[1,3], L. Tedeschi[2], S. V. Filho[1,3], M. Gionbelli[1], and L. F. Silva[1], *[1]Universidade Federal de Viçosa/INCT-CA, Viçosa, MG, Brazil, [2]Texas A&M University, College Station, [3]INCT - Ciência Animal, Viçosa, MG, Brazil.*

The aim of this study was to understand the growth development and chemical composition of empty BW (EBW), soft tissues, and bone, and to determine a system to define maturity of Nellore cattle. A database containing carcass and body compositions of 249 animals from 11 studies was used. There were 63 intact males, 105 steers, and 81 heifers of Nellore breed. Allometric regressions were used to predict body water, CP, and ash; except for ether extract (EE) in which an exponential equation was used to fit the data. The maturity was defined as the point of which no significant accretion of protein in the fat-free DM (FFDM) was observed. The water in the soft tissue (STW) was regressed on Logistic, Gompertz, and brake lines equations whereas the fitting for bone chemical composition was performed using an exponential equation. Sex effect was evident on empty body water ($P = 0.057$) and EE ($P < 0.001$), therefore, this effect was not included in the analysis of fat-free DM, evidencing that maturity is more correlated with breed than sex. The fitting of the exponential equation suggested that Nellore cattle reach maturity with 445 kg and the break line analysis indicated a plateau around 429 kg. At this point, the relationship between CP and ash in the FFDM is 79.62:20.38. A high relationship between STW and EE in the soft tissue (STEE) was observed (STEE = 0.920 – 1.147 × STW; $P < 0.001$), but the soft tissue was not a good predictor for maturity because it depends on the type of diet. The analysis of bone chemical composition showed that EE, water, and ash become constant between 400 and 500 kg of EBW whereas CP in the bone is always constant at 19.1%. Our data also suggested that bone composition could be a good predictor of maturity; however due to the great variability in the database, it was not possible to determine a BW at which these components become constant with a reliable precision. We concluded that Nellore cattle reach maturity between 429 and 445 kg of EBW and that CP in the FFDM and CP, water, and ash in the bone are good predictors of maturity; however soft tissue composition alone cannot be used to predict maturity.

Key words: prediction, development, composition

252 Population dynamics of leukocytes during immune activation of the chicken immune system by *E. coli*. V. Arias* and K. Klasing, *University of California, Davis.*

The innate and adaptive systems must have appropriate levels of nutrients to support changes in leukocyte numbers and function during an immune response. As a first step at understanding the dynamics of these changes, we examined a time course of peripheral leukocytes in blood of adult Hyline chickens injected IV with dead *E. coli* at 1 × 10^{10} cfu/ml. After primary injection, blood was collected and total white blood cells (WBC), T cell ($CD4^+$ and $CD8^+$), B cell (IgM^+ and IgG^+), macrophage/monocyte, and thrombocyte cell numbers were determined. Data were analyzed by one-way ANOVA, and differences among treatments were determined by means contrasts. An increase in total WBC numbers occurred at 5 d, 7 d, and 10 d post-injection compared with baseline ($P = 0.01$, $P < 0.01$, $P = 0.04$). $CD4^+$ numbers increased compared with baseline at 7 d, 10 d, and 14 d post-injection ($P < 0.01$, $P < 0.01$, $P = 0.01$). However, $CD8^+$ cell numbers showed no difference. IgM^+ cell numbers increased compared with baseline at 5 d, 7 d, and 10 d post-injection ($P < 0.01$ for each day). IgG^+ cell numbers increased at 5 d, 7 d, 10 d, and 14 d post-injection compared with baseline ($P < 0.01$ for each day). Macrophage/monocyte cell numbers increased 3 d, 5 d, 7 d, 10 d, and 14 d post-injection compared with baseline ($P = 0.02$, $P < 0.01$, $P < 0.01$, $P < 0.01$, $P < 0.01$). Thrombocyte cell numbers increased at 5 d and 7 d post-injection compared with baseline. ($P = 0.01$, $P < 0.01$). Maximal percent increase in cell numbers for WBC, $CD4^+$, IgM^+, IgG^+, macrophage/monocyte, and thrombocyte were 83%, 66%, 117%, 336%, 214%, and 102%, respectively. These data indicate an increase in most cellular components of the avian immune system during systemic activation compared with naïve birds (maintenance). Supported by USDA Regional Research project 1013.

Key words: chicken, leukocytes, *E. coli*

253 Effects of dietary seaweed extract supplementation in sows and post-weaned pigs on performance, intestinal morphology, intestinal microflora and immune status. S. G. Leonard, T. Sweeney, B. Bahar, and J. V. O'Doherty*, *University College Dublin, Dublin, Ireland.*

The present experiment investigated the effects of dietary supplementation of a seaweed extract (SWE) to sows and weaned pigs on post-weaning growth performance, intestinal morphology, intestinal microflora, volatile fatty acid (VFA) concentrations, and immune status of pigs at d 11 and 117 post-weaning. Gestating sows (n = 20) were supplemented with SWE (0 vs. 10.0 g/d) from d 107 of gestation until weaning (d 26). At weaning, pigs (4 pigs/sow) were divided into 2 groups based on sow diet during lactation and supplemented with SWE (0 vs. 2.8 g/kg diet), giving 4 treatment groups; 1) BB (basal sows-basal pigs); 2) BS (basal sows-treated pigs); 3) SC (treated sows-basal pigs); and 4) SS (treated sows-treated pigs). Pigs weaned from SWE-supplemented sows had a higher ADG between d 0–21 ($P < 0.05$) post-weaning compared with pigs weaned from non SWE-supplemented sows. Pigs offered post-weaning diets containing SWE had decreased colonic *E. coli* populations on d 11 ($P < 0.01$) and decreased colonic *Enterobacteriaceae* numbers on d 117 ($P < 0.05$). Pigs offered post-weaning diets containing SWE had a greater mRNA abundance of MUC2 in the colon at d 11 post-weaning ($P < 0.05$) compared with pigs offered un-supplemented diets. In conclusion, these results demonstrate that SWE supplementation post-weaning provides a dietary means to improve gut health and enhance growth performance in starter pigs. Dietary SWE supplementation increased ADG during the grower-finisher (GF) phases. However, there was no growth response to SWE inclusion in the GF diets when pigs were weaned from SWE-supplemented sows.

Key words: sow, fucoidan, laminarin

254 Effect of maternal seaweed extract supplementation on suckling piglet growth, humoral immunity, selected microflora, and immune response after an ex vivo lipopolysaccharide challenge. S. G. Leonard, T. Sweeney, B. Bahar, and J. V. O'Doherty*, *University College Dublin, Dublin, Ireland.*

The present study was conducted to investigate the effect of maternal dietary supplementation (n = 10 sows/treatment) with seaweed extract (SWE: 0 vs. 10.0 g/d) from d 107 of gestation until weaning (d 26) on neonatal piglet growth, humoral immunity, intestinal morphology, and selected intestinal microflora. Furthermore, this study examined the effect of dietary treatment on the immune response following an ex vivo *Escherichia coli* lipopolysaccharide (LPS) tissue challenge at weaning in a 2 × 2 factorial arrangement. The main factors consisted of sow dietary treatment (SWE or control) and immunological challenge (yes or no). The SWE supplement (10.0 g/d) contained laminarin (1.0 g), fucoidan (0.8 g), and ash (8.2 g). The SWE-supplemented sows had greater colostrum IgA ($P < 0.01$) and had a trend for greater IgG ($P = 0.062$) concentrations compared with non SWE-supplemented sows. Piglets suckling SWE-supplemented sows had greater serum IgG ($P < 0.05$) concentrations on d 14 of lactation compared with those suckling non-SWE supplemented sows. Dietary SWE supplementation decreased fecal *Enterobacteriaceae* populations in sows at parturition ($P < 0.05$) and piglets suckling SWE-supplemented sows had a lower colonic *E. coli* population at weaning ($P < 0.01$) compared with non SWE-supplemented sows. Lipopolysaccharide challenge increased the mRNA abundances of the pro-inflammatory cytokines IL-1α and IL-6 ($P < 0.01$) in ileal tissue and TNF-α in colonic ($P < 0.01$) tissue. Piglets suckling SWE-supplemented sows had greater TNF-α mRNA expression following ex vivo LPS challenge compared with non SWE-supplemented sows ($P < 0.05$). However, there was no effect of sow dietary treatment on TNF-α mRNA expression in the unchallenged ileum tissue. In summary, these results demonstrate an important immunomodulatory role of SWE supplementation characterized by enhanced colostral IgA and IgG concentrations, greater piglet circulatory IgG concentrations and enhanced TNF-α mRNA expression in the ileum following an ex vivo LPS challenge.

Key words: sow, immunity, laminarin

255 Plant extracts for weaned pigs experimentally infected with porcine reproductive and respiratory syndrome virus. 1: Effect on growth performance and immune responses. Y. Liu*[1], J. J. Lee[1], M. Song[1], T. M. Che[1], J. A. Soares[1], D. Bravo[2], W. G. Van Alstine[3], and J. E. Pettigrew[1], *[1]University of Illinois, Urbana, [2]Pancosma SA, Geneva, Switzerland, [3]Purdue University, West Lafayette, IN.*

A study evaluated the effects of 3 different plant extracts (PE) on growth performance and immune responses of weaned pigs experimentally infected with porcine reproductive and respiratory syndrome

virus (PRRSV). Weaned pigs (n = 64, 7.8 ± 0.3 kg BW, 21 d old) were used in a 2 × 4 factorial arrangement. The first factor was with or without PRRSV challenge (10^5 intranasal dose; 50% tissue culture infective dose). The second factor was 4 diets: a nursery basal diet (CON), 10 ppm capsicum oleoresin (CAP), garlic (GAR), or turmeric oleoresin (TUR). Pigs were housed in disease containment chambers for 28 d: 14 d before and 14 d after the inoculation (d 0). Rectal temperatures (RT) were measured every 3 or 4 d post-inoculation (PI). The ADG, ADFI, and G:F were measured on d −14 to 0, 0 to 7, and 7 to 14. Blood was collected on d 0, 7, and 14 to detect serum viral load (SVL) by qPCR and PRRSV antibody titer (AT) by ELISA. The PRRSV infection decreased ($P < 0.01$) ADG and ADFI from d 0 to 7, d 7 to 14, and d 0 to 14, and G:F from d 7 to 14 and d 0 to 14, and increased ($P < 0.05$) RT on d 7, 9, 11, and 14 PI, SVL on d 7 and 14 PI, and AT on d 14 compared with the unchallenged group. In the PRRSV challenged group, CAP reduced ($P < 0.05$) RT (39.67 vs. 40.18°C) on d 4 and SVL (Ct, 18.94 vs. 16.15) on d 7; GAR increased ($P < 0.05$) ADG (328 vs. 236 g/d) from d 0 to 7 and reduced ($P < 0.05$) RT (39.67 vs. 40.18°C) on d 4; TUR increased ($P < 0.05$) ADG (469 vs. 333 g/d) from d 7 to 14, G:F from d 7 to 14 (0.70 vs. 0.42) and from d 0 to 14 (0.58 vs. 0.42), PRRSV AT (2.09 vs. 1.69 S/P ratio), and decreased SVL on d 7 (Ct, 18.97 vs. 16.15) and d 14 (Ct, 23.84 vs. 21.54). In the unchallenged group, all piglets were PRRSV negative during the overall period PI. The CAP increased ($P < 0.05$) ADFI from d 0 to 7 and overall period PI, and final weight of piglets compared with the CON. In conclusion, the 3 PE tested showed different effects on growth efficiency and humoral immune responses, and TUR might strengthen immune responses and efficiency of pigs infected with PRRSV.

Key words: plant extracts, PRRSV, weaned pigs

256 Plant extracts for weaned pigs experimentally infected with porcine reproductive and respiratory syndrome virus. 2: Effect on peripheral blood immune cells and inflammatory mediators. Y. Liu*[1], J. J. Lee[1], M. Song[1], T. M. Che[1], J. A. Soares[1], D. Bravo[2], W. G. Van Alstine[3], and J. E. Pettigrew[1], *[1]University of Illinois, Urbana, [2]Pancosma SA, Geneva, Switzerland, [3]Purdue University, West Lafayette, IN.*

A study evaluated the effects of 3 different plant extracts (PE) on peripheral blood immune cells and inflammatory mediators of weaned pigs experimentally infected with porcine reproductive and respiratory syndrome virus (PRRSV). Weaned pigs (n = 64, 7.8 ± 0.3 kg BW, 21 d old) were used in a 2 × 4 factorial arrangement. The first factor was with or without PRRSV challenge (10^5 intranasal dose; 50% tissue culture infective dose). The second factor was 4 diets: a nursery basal diet (CON), 10 ppm capsicum oleoresin (CAP), garlic (GAR), or turmeric oleoresin (TUR). Pigs were housed in disease containment chambers for 28 d: 14 d before and 14 d after the inoculation (d 0). Blood was collected on d 0, 7, and 14 to measure the total and differential white blood cells (WBC), and serum tumor necrosis factor-α (TNF-α), C-reactive protein (CRP), and haptoglobin (HP). Compared with the unchallenged pigs, the PRRSV infection reduced ($P < 0.01$) WBC and lymphocytes (LYM) on d 7, monocytes (MONO) on d 7 and d 14, and the ratio of neutrophils to LYM (NEU/LYM) on d 14, but increased NEU/LYM on d 7, WBC and LYM on d 14, and the levels of serum TNF-α, CRP, and HP. In the PRRSV challenged group, CAP reduced ($P < 0.05$) TNF-α (146.2 vs. 179.5 pg/ml) and CRP (27.9 vs. 41.0 μg/ml) on d 7, and increased ($P < 0.05$) HP (1503 vs. 890 μg/ml) on d 14; GAR increased ($P < 0.05$) HP (1485 vs. 890 μg/ml) on d 14; TUR reduced ($P < 0.05$) TNF-α (139.4 vs. 179.5 pg/ml) on d 7 compared with the CON. The 3 PE tested did not influence the populations of peripheral immune cells. In the unchallenged group, CAP increased ($P < 0.05$) LYM on d 7; GAR increased ($P < 0.05$) MONO and CRP (27.6 vs. 16.8 μg/ml) on d 7 and NEU/LYM (1.86 vs. 0.92) on d 14, but reduced ($P < 0.05$) MONO on d 14 (1.01 vs. 1.66 x10^3/μl), compared with the CON. In conclusion, the 3 PE tested showed different effects on immune responses of piglets with or without PRRSV infection, and CAP and TUR modulate the inflammatory mediators of pigs infected with PRRSV.

Key words: plant extracts, PRRSV, weaned pigs

257 Effects of spray-dried plasma on pregnancy rate and growth performance of mated female mice after transport as a model for stressed sows. M. Song*[1], T. M. Che[1], Y. Liu[1], J. A. Soares[1], J. J. Lee[1], J. M. Campbell[2], J. Polo[2], J. C. O'Connor[3], and J. E. Pettigrew[1], *[1]University of Illinois, Urbana, [2]APC Inc., Ankeny, IA, [3]University of Texas Health Science Center, San Antonio.*

Transportation stress can reduce implantation, impair embryo development, and decrease pregnancy rate after breeding of animals. A study evaluated the effects of spray-dried plasma (SDP) on pregnancy rate and growth performance of mated female mice (C57BL/6 strain) after transport as a model for stressed sows. The mated female mice (n = 250; 16 ± 1.2 g BW; 4 replicated groups, 62 or 63 mice/group) were shipped from Bar Harbor, ME to Urbana, IL on the day the vaginal plug was found (gestation day (GD) 1), arriving at the laboratory on GD 3. They were housed in individual cages, randomly assigned to dietary treatments with or without 8% SDP (SDP or CON), and fed for 2 wk. The diets were formulated to similar ME, CP, and AA levels without antibiotics. Measurements were pregnancy rate and growth performance (GD 3 to 17). Pregnancy was determined on GD17 on the basis of BW and shape of abdomen, and was confirmed by inspection post-mortem. The SDP markedly improved ($P < 0.05$) pregnancy rate compared with the CON (Table). The SDP also improved ($P < 0.05$) ADG (non-pregnant mice: 0.142 vs. 0.106 ± 0.008 g/d; pregnant mice: 0.712 vs. 0.638 ± 0.018 g/d) and G:F (non-pregnant mice: no data; pregnant mice: 0.223 vs. 0.202 ± 0.006) compared with the CON, but did not affect ADFI. In conclusion, SDP improved pregnancy rate of the mated female mice after transportation stress and growth performance of pregnant mice.

Table 1. Effect of SDP on pregnancy rate of mated female mice after transportation stress*

	CON			SDP		
Group	Pregnant	Total	% Pregnancy	Pregnant	Total	% Pregnancy
1	8	31	26	15	32	47
2	2	31	7	19	31	61
3	5	50	10	5	13	39
4	2	48	4	5	14	36
Overall	17	160	11	44	90	49

*Data are number of mice and analyzed by chi-squared test.

Key words: mice, pregnancy rate, spray-dried plasma

258 Dietary phosphate supplementation to neonatal pigs affects satellite cell proliferation and progression through their myogenic lineage. L. S. Alexander*, B. S. Seabolt, and C. H. Stahl, *North Carolina State University, Raleigh.*

Severe neonatal dietary phosphate (PO_4) deficiency reduces the proliferation of satellite cells (Alexander, 2010). The objective of this study was to examine the impact of dietary PO_4 on the growth, sera parameters, and tissue-specific stem cell proliferation in the neonatal pig. Seventy-five 1-d old pigs were pair-fed either a 25% PO_4 deficient (PD), a PO_4 adequate (PA), or a 25% PO_4 excessive (PE) liquid diet over an 18d period. Circulating PO_4 was lower ($P < 0.05$) in PD fed animals throughout the trial when compared with PA and PE fed animals. Sera Ca concentrations were higher ($P < 0.05$) in PD fed animals at all time points when compared with their PE fed counterparts. Increased ($P < 0.05$) sera PTH was observed among pigs fed the PE diet when compared with both the PD and PA fed groups. PD fed animals had lower ADG ($P < 0.05$) and G:F ($P < 0.05$) than PA and PE fed animals. Dietary PO_4 restriction reduced the in vivo proliferation of satellite cells, but no differences were seen between the PA and PE treatment groups. Satellite cells were additionally cultured to evaluate the effect of dietary PO_4 on their developmental programming. Altered gene and protein expression of muscle regulatory factors (Pax7, MyoD, and Myogenin) was observed among the satellite cells based on the PO_4 status of the pigs from which they were isolated. Our previous research demonstrated reduced satellite cell proliferation during severe PO_4 deficiency, and similar results were also seen in this study with a mild PO_4 deficiency. Although excess dietary PO_4 did not result in increased proliferation in vivo, differences in both proliferation and markers of the progression of these cells through their myogenic lineage was affected by excess dietary PO_4. Additional research is needed to further clarify how PO_4 status affects satellite cell activity and the subsequent impact on growth.

Key words: pig, phosphate, satellite cell

259 Flavour preferences conditioned by the effects of porcine digestible peptides (PDP) and soybean concentrate in post-weaned piglets. J. Figueroa*[1], D. Solà-Oriol[1], S. L. Vinokurovas[1], E. Borda[2], and J. F. Pérez[1], *[1]Universitat Autònoma de Barcelona, Bellaterra, Barcelona, Spain, [2]Bioibérica, Barcelona, Spain.*

It has been shown in mammals that an initially arbitrary or aversive flavor can become strongly preferred after a learned association between the flavor and the positive consequences of its consumption (hedonic or post-ingestive). In this experiment, 480 non-deprived weaning piglets (10 piglets/pen) were trained during 6 d (alternate sessions) with one flavor in odd days as a positive conditioned stimulus (CS+) when mixed into a protein solution (2% Soybean Protein Concentrate (SPC) or 2% Porcine Digestible Peptides (PDP)) and another flavor on even days (CS-) mixed into a neutral solution (water). Flavor products used (anis or garlic, 0.075%) were paired with each solution and counterbalanced across subjects to act as the CS+ or CS- flavor. Double choice test between the CS+ and CS- flavors were performed at d15 and d22 after weaning (in water) and at d29 after weaning (in feed). Solution and feed intakes were measured after 30 min. Data were analyzed using the GLM procedure of SAS. Preference was calculated as the percentage contribution of the CS+ solution to the total solution intake. Piglets preferred protein-paired flavors at all 3 d; they showed higher preference for the CS+ flavor in the SPC group (55%, 57% and 57%) and PDP group (60%, 62% and 55%) on d 15, 22 and 29, respectively ($P < 0.05$). No differences were observed between the conditioning power of PDP and SPC. The present results indicate that weanling piglets can acquire strong flavor preferences resistant to extinction through conditioning strategies by using protein products. Establishing a preference for a flavored solution by conditioning may enhance intake due to hedonic or post-ingestive effects driven by this association, and this could be a useful strategy to increase voluntary intake in critical periods, such as weaning.

Key words: flavors, conditioning, weaning

260 Influence of length of storage on parameters used to measure the quality of soybean meal. S. Sueiro[1], M. P. Serrano[2], M. González[1], M. Hermida[1], P. G. Rebollar[2], and G. G. Mateos*[2], *[1]Laboratorio de Mouriscade, Pontevedra, Spain, [2]Universidad Politécnica de Madrid, Madrid, Spain.*

Methods used by the Industry to estimate protein quality of soybean meal (SBM) include KOH solubility (KOHsol), protein dispersibility index (PDI), urease activity (UA), and trypsin inhibitor activity (TIA). In general, meals with KOHsol values between 78 and 85%, PDI values between 15% and 35%, and UA values between 0.00 and 0.10 mg/g are considered of acceptable quality. Similarly, TIA values of less than 2.5–4.0 mg/g are considered best. However, there is no agreement among the different Institutions and publications with respect to the more suitable values for these variables in commercial SBM. The reasons for the wide range of values for these variables are not well understood. It is known that protein solubility and TIA changes with the methodology used and explain in part the high variability existing among laboratories. Also, length and environmental conditions during storage might influence protein solubility and thus, KOHsol and PDI values. In a previous study, we observed that protein solubility of SBM samples from the USA or Latin America stored for 24, 48, and 80 wk under room conditions (12–15°C) had significantly lower PDI values than the original SBM. An experiment was conducted to determine the influence of length of storage on different parameters that define the protein quality of SBM. Eight samples (500 g) of SBM (55–56% CP on DM basis) were collected weekly during June–July 2010 directly from the crusher (USA). Samples were analyzed at arrival to the Spanish port and then, every 30 d of storage at 12 ± 2°C and 70 ± 3% humidity. Length of storage did not affect KOHsol, UA, or TIA values. However, PDI values decreased with time (21.8, 21.4, 20.1, 18.7, and 17.7% for 0, 30, 60, 90, and 120 d, respectively; $P \leq 0.001$). Therefore, care should be taken when comparing PDI values to evaluate the protein quality of SBM samples that have been stored for different lengths of time.

Key words: length of storage, soybean meal, protein quality traits

261 Effects of an abrupt change from mash to pellets and vice-versa on growth performance in finishing pigs. C. B. Paulk*[1], J. D. Hancock[1], J. C. Ebert[2], and J. J. Ohlde[2], *[1]Kansas State University, Manhattan, [2]Key Feeds, Clay Center, KS.*

A total of 200 finishing pigs (avg initial BW of 60 kg) were used in a 58-d growth assay to determine the effects of an abrupt change from mash to pellets and pellets to mash on growth performance and carcass measurements. The experiment was designed as a randomized complete block with 5 pigs/pen and 10 pens/treatment. Treatments were mash to mash, mash to pellets, pellets to mash, and pellets to pellets for phases 1 and 2 of the experiment. For phase 1 (d 0 to 36), pigs fed the pelleted diet had 4% greater ADG and 8% greater G:F ($P < 0.02$) compared with pigs fed mash. For phase 2 (d 36 to 58) and overall (d 0 to 58), pigs fed the mash diet had lower ($P < 0.02$) G:F than pigs fed the pelleted treatments. Indeed, pigs fed pellets the entire experiment had ADG and G:F that were 5 and 8% better, respectively, than that of pigs fed mash the entire experiment. Pigs fed mash during phase 1 then pellets during phase 2 had greater ($P < 0.01$) ADG and G:F for phase 2

compared with pigs fed pellets then mash. However, the overall effect was for pigs fed pellets for either phase 1 or 2, but not both, tended to have growth performance intermediate to those fed mash and pellets for the entire experiment. With hot carcass weight used as a covariate, no differences ($P > 0.15$) were observed in dressing percentage, fat thickness, or percentage fat free lean index (FFLI). In conclusion, pigs fed pellets tended to have the greatest growth performance, pigs fed mash the worst, and pigs fed pellets for only part of the grow-finish phase fell in between.

Table 1.

Item	Mash to mash	Mash to pellet	Pellet to mash	Pellet to pellet	SE
Phase 1 (d 0 to 36)					
ADG, g	1,124	N/A	N/A	1,167	23
G:F, g/kg	393	N/A	N/A	423	4
Phase 2 (d 36 to 58)					
ADG, g	1,163	1,230	1,117	1,240	25
G:F, g/kg	403	441	404	431	9
Overall (d 0 to 58)					
ADG, g	1,134	1,168	1,148	1,195	22
G:F, g/kg	393	414	416	426	6
Dress, %	74.6	74.3	74.2	74.4	0.3
Fat thickness, mm	18.9	19.7	19.6	19.7	0.9
FFLI, %	52.0	51.6	51.7	51.7	0.5

Key words: mash, pellets, pigs

262 The effect of weaning group-housed calves over a different length of time fed by automatic feeding machine. K. Shore* and A. Roy, *Grober Nutrition, Cambridge, Ontario, Canada.*

Pre-weaned dairy replacement calves were evaluated for growth and health differences when weaned off of milk replacer from an automatic calf feeding machine over a different number of days. Thirty 6 calves (BW 45.8 ± 3.1 kg; height 82.7 ± 5.3 cm) were used in a 1-way ANOVA model and randomly assigned at arrival to one of 2 treatments: 5 d short weaning (SW) (n = 18), and 10 d long weaning (LW) (n = 18). Calves were housed in 4 groups of 9; 2 groups had access to 1 feeding machine. All calves were offered 9 L of milk replacer (1.35 kg of dry matter) on a daily basis. Milk intakes were recorded; body weights and heights were measured weekly. Health was evaluated daily using an adapted version of the University of Wisconsin calf scoring sheet. Calves were on trial for 10 wk, 8 wk on milk replacer, grain and hay and 2 wk on grain and hay only. Water was offered free choice. Milk intake was not different between treatments before weaning (SW = 7.40 ± 0.71 L; LW = 7.43 ± 0.79 L). Body weight gain was not different between the groups over the entire 10 wk (SW = 51.5 ± 9.9 kg; LW = 55.1 ± 7.8 kg). However, BW gain was greater in the LW group ($P = 0.006$) over the weaning period (SW = 9.7 ± 5.6 kg; LW = 14.2 ± 3.0 kg). The LW group gained more while consuming less milk (SW = 4.45 ± 0.34 L/d; LW = 3.46 ± 0.17 L/d) and more grain (SW = 0.799 ± 0.484 kg/d; LW = 1.38 ± 0.313 kg/d). ADG was not different between treatments during weaning; it was higher in the LW group ($P = 0.04$) post weaning (SW = 0.747 ± 0.456 kg/d; LW = 1.01 ± 0.256 kg/d). There was no difference in height gain. Health was measured by the number of events, there was no difference between treatments during the weaning period; however, the LG group had fewer health events post weaning ($P = 0.04$). In summary, weaning calves over a longer period when fed by automatic feeding machine seemed to encourage higher body weight gains during weaning, improved average daily gains and less health events post weaning.

Key words: calf, group housing, weaning

Physiology and Endocrinology: Estrous Cycle Manipulation - Beef

263 Effect of 72 h temporary calf removal and/or equine chorionic gonadotropin (eCG) before timed AI on follicle development, concentrations of LH and estradiol, and ovulation rate in suckled beef cows. G. H. L. Marquezini*[1], V. R. G. Mercadante[1], J. S. Stevenson[2], G. A. Perry[3], and G. C. Lamb[1], *[1]North Florida Research and Education Center, University of Florida, Marianna, [2]Department of Animal Sciences and Industry, Kansas State University, Manhattan, [3]Department of Animal and Range Sciences, South Dakota State University, Brookings.*

We hypothesized that temporary calf removal (CR) and/or eCG at CIDR removal of an ovulation synchronization protocol may improve follicle development and alter patterns of LH, estradiol (E2), and progesterone (P4) secretion. Thirty-five multiparous crossbred cows in a 4.8 (range 4 to 7) BCS, and 29.2 (range 19 to 40) d postpartum, were assigned randomly to treatments: 1) 100 µg GnRH and a CIDR insert (d −7), 25 mg $PGF_{2\alpha}$ (PG) and CIDR removal (d 0), and 72 h later by GnRH and AI (d 3; Control; n = 9); 2) same as Control but calves were removed from their dams for 72 h between d 0 and 3 (CR; n = 9); 3) same as Control but cows received 300 IU eCG on d 0 (eCG; n = 9); 4) same as CR but cows received 300 IU eCG on d 0 (eCGCR; n = 8). Blood samples were collected every 4 h from d 0 to 3 and once on d 10 to determine concentrations of hormones. Transrectal ultrasonography was performed on d 0, 1, 2, 3, 4, and 10 to determine follicle diameters and to confirm ovulation. Control cows had decreased ($P < 0.05$) ovulation incidence compared with COCR, eCG, and eCGCR between d 0 and 4 (22, 78, 67, and 88%, respectively), and between d 0 and 10 (67, 100, 78, 100%, respectively). The COCR and eCGCR treatments had a shorter ($P < 0.05$) interval between PG and LH peak compared with Control, whereas eCG was intermediate (72.4 ± 2.3, 65.3 ± 2.3, 70.2 ± 2.3, and 66.5 ± 2.4 h, for Control, COCR, eCG, and eCGCR respectively). The COCR, eCG, and eCGCR treatments had greater ($P < 0.05$) follicle diameter on d 2 compared with Control (11.9 ± 0.7, 14.1 ± 0.7, 14.7 ± 0.6, and 15.6 ± 1.0 mm, for Control, COCR, eCG, and eCGCR, respectively) and concentrations of P4 on d 10 (1.4 ± 0.4, 2.7 ± 0.4, 2.7 ± 0.4, and 2.8 ± 0.4 ng/mL for Control, COCR, eCG, and eCGCR, respectively). We conclude that CR reduced the interval to the LH peak and both CR and eCG at CIDR removal enhanced follicle growth, ovulation incidence, and P4 concentrations in early postpartum suckled beef cows.

Key words: equine chorionic gonadotropin, calf removal, beef cows

264 Evidence that prostaglandin administration at the onset of a 5-day CO-Synch + CIDR synchronization protocol markedly improves fixed-time AI pregnancy rates in *Bos indicus*-influenced cattle. G. Williams*[1,2], R. Stanko[1,3], C. Allen[1,2], R. Cardoso[1,2], L. Prezotto[1,2], J. Thorson[1,2], and M. Amstalden[2], *[1]Texas AgriLife Research, Beeville, [2]Texas A&M University, College Station, [3]Texas A&M University-Kingsville, Kingsville.*

Protocols in the US for synchronization of ovulation and fixed-time AI (TAI) in beef cattle have emphasized recently the combined use of the controlled intravaginal drug-releasing insert (CIDR), GnRH and prostaglandin F-2α (PG) or its analogs. Together, these can be used effectively to control the corpus luteum (CL) and synchronize a new follicular wave in *Bos taurus* females. Using the 7-Day CO-Synch + CIDR (7-Day) or 5-Day CO-Synch + CIDR (5-Day) protocols, TAI pregnancy rates in *Bos taurus* beef cows often exceed 50% (7-Day), and frequently exceed 60% (5-Day). However, use of the 7-Day protocol in *Bos indicus*-influenced cattle has resulted consistently in TAI pregnancy rates of <40%. Initial objectives were to determine whether the 5-Day protocol in *Bos indicus*-influenced beef cows could improve TAI pregnancy rates compared with historical rates obtained with 7-Day. In Exp. 1, 79 postpartum (PP) Braford cows at least 45 d postpartum at TAI and BCS ≥ 5, and 21 nulliparous Braford and Brangus heifers (BCS ≥ 5), were administered the 5-Day protocol [5-Day CIDR; 2x PG (50 mg Lutalyse; Pfizer) at CIDR removal on Day 5; TAI + 100 Âµg GnRH 72 h later]. Pregnancy rate to TAI was not improved (cows, 30.3%; heifers, 42.9%) relative to 7-Day. In Exp. 2, we compared the standard 5-Day procedure to the 5-Day in which PGF was administered at CIDR insertion to regress mature CL (Bee Synch + CIDR; Bee Synch). *Bos indicus*-influenced beef cows (n = 150) as in Exp. 1 were stratified by days PP and assigned randomly to receive either the standard 5-Day or Bee Synch protocol. Pregnancy rate to TAI was greater ($P < 0.05$) in Bee Synch (52.4%) than in 5-Day (35.7%). In Exp. 3, 119 Braford and Brangus cows were treated with Bee Synch, with TAI at 66 h. Pregnancy rate to TAI was 52.1%. Eliminating data from a pasture containing cows (n = 37) having extreme temperaments increased pregnancy rate to 58% (n = 98). Results indicate a marked benefit of Bee Synch in *Bos indicus*-influenced cattle, with number of times through the chute remaining at 3.

Key words: 5-day CO-Synch + CIDR, prostaglandin, *Bos indicus*

265 Determination of appropriate delivery of $PGF_{2\alpha}$ in the 5-day Co-Synch + CIDR protocol in lactating beef cows. G. A. Bridges*[1], L. H. Cruppe[2], J. F. Currin[3], M. L. Day[2], P. J. Gunn[4], J. R. Jaeger[5], G. C. Lamb[6], A. E. Radunz[7], P. Repenning[8], J. S. Stevenson[5], J. C. Whittier[8], and W. D. Whittier[3], *[1]University of Minnesota, [2]The Ohio State University, [3]Virginia Tech, [4]Purdue University, [5]Kansas State University, [6]University of Florida, Marianna, [7]University of Wisconsin, Madison, [8]Colorado State University.*

The objective of this experiment was to determine if 2 doses of $PGF_{2\alpha}$ (PG) administered at CIDR removal was an efficacious method for delivery of PG in the 5-d CO-Synch + CIDR protocol. Postpartum beef cows (n = 2465; 67 ± 0.4 dpp) from 13 herds in 8 states were enrolled in the 5-d CO-Synch + CIDR protocol and assigned to receive either 2 doses of PG (25 mg/dose) 8 h apart with the initial injection given at CIDR removal (8hPG), 2 doses (25 mg/dose) of PG delivered in 2 injection sites with both administered at CIDR removal (CoPG), or a single 25-mg dose of PG at CIDR removal (1xPG). Cows were TAI 72 h after CIDR removal at second GnRH administration. Estrous cycling status (54% cyclic) was determined by evaluation of progesterone in 2 blood samples taken on d −10 and 0 relative to CIDR insertion. Determination of pregnancy was performed by transrectal ultrasonography 39 ± 0.1 d after TAI and after the conclusion of the breeding season. Data were analyzed with the Glimmix procedure of SAS, where herd was included as a random effect. Timed AI pregnancy rates were greater ($P < 0.05$) for the 8hPG (55%) than the 1xPG (48%) treatment, with the CoPG (51%) treatment intermediate and not different from the other treatments. Contrast analysis demonstrated that cows receiving 50 mg of PG (8hPG and CoPG) had greater ($P < 0.05$) TAI pregnancy rates than those receiving 25 mg (1xPG). Pregnancy rates to TAI were greater ($P < 0.05$) in cyclic (55%) than non-cyclic (47%) and greater ($P < 0.05$) in mature (≥3 y of age; 54%; n = 1940) than 2-y-old cows (40%; n = 525). Luteolysis following PGF treatment was assessed in a subset of cows (n = 277) and did not differ ($P = 0.13$)

among the 8hPG (96%), CoPG (93%), and 1xPG (88%) treatments. Breeding season pregnancy rates (88%) did not differ among treatments but was greater ($P < 0.01$) in mature (90.4%) than 2-y-old cows (77.7%). In summary, 50 mg of PG was required in the 5 d CO-Synch + CIDR protocol; however, TAI pregnancy rates did not differ when 50 mg of PG was administered simultaneously with CIDR removal or at 0 and 8 h following CIDR removal.

Key words: beef cow, estrus synchronization, prostaglandin

266 Comparison of long-term progestin-based protocols to synchronize estrus and ovulation prior to fixed-time AI in postpartum beef cows. J. M. Nash*, D. A. Mallory, C. C. Selby, T. M. Taxis, M. R. Ellersieck, S. E. Poock, M. F. Smith, and D. J. Patterson, *University of Missouri, Columbia.*

We compared follicular dynamics, ovulatory response to GnRH, steroid hormone concentration patterns, and synchrony of estrus and ovulation among estrous–cycling and anestrous postpartum beef cows after treatment with 2 long–term progestin–based protocols. Beef cows (n = 38) were assigned to treatments based on age, days postpartum (DPP), BCS and estrous cyclicity status. CIDR Select (T1, n = 19) treated cows received a controlled internal drug release insert (CIDR; 1.38 g of progesterone) from d 0 to 14 followed by GnRH (100 μg, i.m.) on d 23, and prostaglandin $F_{2\alpha}$ (PG; 25 mg, i.m.) on d 30. Cows assigned to the Show–Me–Synch (T2, n = 19) treatment received a CIDR insert from d 0 to 14 and PG on d 30. Blood samples were taken on d −8 and 0 of treatment to determine estrous cyclicity status (progesterone ≥ 0.5 ng/mL). HeatWatch estrus detection transmitters were fitted one day before CIDR removal for continuous estrus detection. 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 GnRH, PG and AI; and pregnancy diagnoses. AI was performed 72 h after PG for cows in each treatment and all cows were administered GnRH at AI. Follicle turnover on d 25 was higher among T1 than T2 treated cows ($P < 0.001$); however, progesterone at PG did not differ between treatments ($P = 0.64$). Mean dominant follicle diameter at GnRH and AI did not differ between treatments ($P > 0.05$), but T2 treated cows had larger follicles at PG than cows in T1 ($P = 0.06$). Estrous response after CIDR removal and PG did not differ between treatments; and variances for interval to estrus after CIDR removal and PG were similar for both treatments. T2 treated cows had higher pregnancy rates resulting from FTAI and final pregnancy rates than T1 treated cows ($P = 0.05$). In summary, future studies are needed to further evaluate long-term progestin based protocols in postpartum beef cows. This project was supported by National Research Initiative Competitive Grant no. 2005–55203–15750 from the USDA National Institute of Food and Agriculture.

Key words: fixed-time AI, beef cow, CIDR

267 Comparison of long- versus short-term progestin-based protocols to synchronize estrus and ovulation prior to fixed-time AI in postpartum beef cows. J. M. Nash*, D. A. Mallory, M. R. Ellersieck, S. E. Poock, M. F. Smith, and D. J. Patterson, *University of Missouri, Columbia.*

This experiment compared pregnancy rates in postpartum beef cows resulting from fixed–time AI (FTAI) after treatment with controlled internal drug release (CIDR)–based protocols to synchronize estrus and ovulation. Angus cows were assigned to one of 2 treatments by age, days postpartum (DPP) and BCS. Cows assigned to the 14-d CIDR-PG (Show-Me-Synch; T1, n = 167) treatment received CIDR inserts (1.38 g of progesterone) from d 0 through 14 followed by administration of prostaglandin $F_{2\alpha}$ (PG, 25 mg, i.m.) on d 30. Cows assigned to the 7-d CO-Synch + CIDR treatment (T2, n = 177) 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 −10 and 0 of treatment to determine pretreatment estrous cyclicity status of cows (progesterone ≥ 0.5 ng/mL estrous cycling; T1, 97/167 = 58%; T2, 96/177 = 54%). Continuous estrus detection was performed using HeatWatch beginning at PG and concluding at FTAI. AI was performed at predetermined fixed times (72 h, T1; 66 h, T2) and all cows were administered GnRH at AI. There were no differences between treatments for age, BCS, or DPP. Pregnancy rates resulting from FTAI did not differ ($P > 0.10$) between technicians; AI sires; or on the basis of pretreatment estrous cyclicity status. Pregnancy rates were greater ($P < 0.01$) among cows that exhibited estrus before FTAI than for those that did not (91/124 = 73% and 99/220 = 45%, respectively). However, anestrous cows in T1 were 2 times more likely to become pregnant to FTAI than to not become pregnant. Pregnancy rates resulting from FTAI did not differ between treatments ($P = 0.87$; T1 91/167 = 55%, T2 99/177 = 56%) and neither did final pregnancy rates ($P = 0.49$; T1 147/167 = 88%, T2 160/176 = 91%). In summary, pregnancy rates resulting from FTAI following treatment with T1 and T2 were similar among postpartum beef cows. This project was supported by National Research Initiative Competitive Grant no. 2005–55203–15750 from the USDA National Institute of Food and Agriculture.

Key words: fixed-time AI, beef cow, CIDR

897 Estrogenicity of sugar beet by-products used as animal feeds. N. W. Shappell*[1], E. M. Lenneman[1,2], and M. S. Mostrom[2], *[1]USDA-ARS, Fargo, ND, [2]North Dakota State University, Fargo.*

A veterinarian conducting embryo transfer observed reduction in transfer success rates on both a beef and dairy farm in Minnesota, which were both feeding sugar beet by-products. Beet tailings and pelletized post-extraction beet pulp purchased commercially were submitted for analysis of estrogenicity by E-Screen (proliferative assessment of non-transfected MCF-7 BOS cells). Samples were found to be estrogenic, with pelletized sample containing ~4 fold the estradiol equivalents of the unprocessed sample (3.8 and 1.2 E^2Eq μg/kg DM, respectively). Samples of whole beets, beet pellets and shreds were then obtained from several Midwest US locations, dried, extracted, and assessed for estrogenicity. All pellets examined were found to be estrogenic, with a wide range of concentrations (0.1 – 2.0 μg E^2Eq/kg dry matter) a mean of 0.46 μg, and median of 0.28 μg (n = 9). Relative E^2Eq for the other sample types ranked as follows: pellets > shreds (n = 3) > most unprocessed plant material (n = 7). These by-products are sold both within the United States and abroad, and are used as feed predominantly for cattle (both beef and dairy), but also for horses and elk. Using the recommended feeding regimen guidelines for these feedstuff cattle could consume 0.3 to 6.8 μg E^2Eq per day, however, these guidelines are often exceeded for financial reasons. Calculating possible blood concentrations from consumption of by-product containing 5 μg E^2Eq, a conservative estimate of 10% absorption, and 500 kg body weight, the resultant 12.5 pg/mL E^2Eq is similar to the 10 pg/mL estradiol typical of cows during estrus.

Key words: MCF-7, estrogenicity, fertility

268 Effect of length of the preovulatory period on estradiol, progesterone, ISG-15 and Mx2 in cows. L. H. Cruppe*[1], L. A. Souto[1], M. Maquivar[1], F. M. Abreu[1], M. L. Mussard[1], T. L. Ott[2], J. L. Pate[2], and M. L. Day[1], *[1]The Ohio State University, Columbus, [2]The Penn State University, State College.*

Postpartum primiparous beef cows (n = 23) were used to investigate the effect of preovulatory estradiol concentrations (Pre-E2) on ISG-15 and Mx2 mRNA expression in peripheral blood mononuclear cells (PBMC) from d 15 to 30 after ovulation. Estrus was synchronized, follicular aspiration was performed 5.5 ± 0.1 d later (d −7 of experiment) and cows received 25 mg PGF2α on either d −3 (high estradiol treatment; Hi-E), or on d −2 (low estradiol treatment; Lo-E). All cows received 100 μg of GnRH on d 0, creating a preovulatory period of either 3 or 2 d. Ultrasonography was performed on d −7, −3, 0, 2 and 6 to monitor follicular growth, ovulation and CL formation after GnRH. Blood samples collected at 12 h intervals from d −3 to d −0.5 and at d −0.25 and d 0 were used to determine Pre-E2. Blood samples collected every other day from d −3 to 13 were analyzed for progesterone (P4). Daily samples, collected from d 14 to 30, were processed for both P4 and mRNA analysis in PBMC. Embryos were implanted into cows in the Hi-E (Hi-E-ET, n = 6) and Lo-E (Lo-E-ET, n = 9). Cyclic control animals did not receive embryos (Hi-E-0, n = 4; Lo-E-0, n = 4). Gene expression was determined using RT-PCR for ISG-15 and Mx2. Diameter of the ovulatory follicle (13.4 ± 1.1 mm) did not differ between treatments. While Pre-E2 were greater ($P < 0.05$) in the Hi-E than Lo-E on d −2.5 and −2, they did not differ thereafter, and appeared to peak and then decline in most animals before GnRH. Furthermore, luteal P4 did not differ between Hi-E and Lo-E. Relative amount of mRNA did not differ between the Hi-E and Lo-E, but was greater in pregnant than cyclic cows for both ISG-15 and Mx2 after d 18 through d 30. A biphasic pattern of gene expression was observed for both ISG-15 and Mx2, where maximum amounts of gene expression in pregnant cows was detected by d 20 followed by a decrease, increase and finally a second decrease to d 30. In conclusion, decreasing the length of the preovulatory period appeared not to limit Pre-E2 in this study. Greater amounts of mRNA for ISG-15 and Mx2 were detected in pregnant cows after d 18 and followed a biphasic pattern thereafter to d 30

Key words: estradiol, ISG-15, Mx2

269 Effect of follicle age on conception rate in beef heifers. F. M. Abreu*[1,2], L. H. Cruppe[1], M. Maquivar[1], M. D. Utt[1], C. A. Roberts[2], M. L. Mussard[1], M. L. Day[1], and T. W. Geary[2], *[1]The Ohio State University, Columbus, [2]USDA-ARS Fort Keogh LARRL, Miles City, MT.*

The objective of this study was to determine the effect of age of the ovulatory follicle on fertility. Ovulation (d 0) was synchronized in post pubertal heifers in Montana (n = 153; MT) and Ohio (n = 152). All heifers received estradiol benzoate (EB; 1mg/500kg BW) on d 6 and were assigned to either receive PGF (25 mg, i.m.) 5 d (d 11 of the experiment; "young" follicle, YF, n = 154) or 9 d (d 15 of the experiment; "mature" follicle, MF, n = 151) after EB. Estrus was detected for 5 d after PGF with AI approximately 12 h after estrus. Ovarian ultrasonography (MT only) was performed on d 6, 11, 15 (MF only) and at AI. Heifers that failed to initiate a new follicular wave after EB (MT only) were excluded from further analyses (n = 11). Heifers from the MF treatment in MT that initiated a second follicular wave after EB, but before PGF on d 15 (n = 14, MF2) remained in the analyses. Estrous response and conception rate were analyzed using a model that included location, treatment, and their interaction, with the GLIMMIX procedure of SAS. Interval from PGF to estrus was analyzed with the MIXED procedure of SAS. In a second analysis, heifers with 2 follicular waves after EB (MF2) were compared with the MF heifers with one wave, and the YF treatment in MT. Interval from PGF to estrus was similar between treatments in MT (65.5 ± 1.6) but was greater ($P < 0.05$) in the YF (78.5 ± 1.4) than MF (53.6 ± 2.2) treatment in OH (trt x loc, $P < 0.01$). Estrous response (89%) and conception rate did not differ ($P > 0.10$) for MF (64.1%) and YF (67.2%) heifers. The MF2 heifers in MT had a greater ($P < 0.01$) interval to estrus and smaller ($P < 0.01$) ovulatory follicles at AI than MF heifers with a single follicular wave after EB. When MF2 heifers were removed from analyses, interval from PGF to estrus in MT was greater ($P < 0.01$) but follicle diameter was smaller ($P = 0.01$) in YF than MF heifers. Furthermore, this interval was similar for MF heifers between locations (54.6 ± 1.7), but was greater ($P < 0.01$) for YF heifers in OH (78.5 ± 1.4) than MT (67.4 ± 1.5). In conclusion, manipulation of age of the ovulatory follicle at spontaneous ovulation did not influence conception rate.

Key words: follicle age, heifers, conception rate

270 Effect of various doses of prostaglandin $F_{2\alpha}$ on estrous behavior and blood progesterone in beef cows. A. Ahmadzadeh*, K. Carnahan, T. Robison, and C. Autran, *University of Idaho, Moscow.*

Research indicates that 2 doses of prostaglandin $F_{2\alpha}$ (PGF), rather than one dose of PGF increased pregnancy rates when utilized with a 5-d CO-Synch + CIDR protocol. The objectives were to determine the effect of 3 PGF treatment protocols on estrual behavior and serum progesterone (P4) concentrations of suckled beef cows synchronized with a modified 5-d CO-Synch + CIDR protocol. The experiment was conducted over 2 consecutive breeding seasons. Ninety-seven Charolais cows received a CIDR (d 0) for 5 d. On d 5 CIDR's were removed, and cows were assigned randomly to receive one of 3 treatments; 1) Control; a single injection of 25 mg PGF (dinoprost tromethamine; n = 32), 2) Large; a single injection of 37.5 mg PGF (n = 32), or 3) Split; 2 injections of 12.5 mg PGF 7 h apart (n = 33). All cows were fitted with estrus detection aids, observed for behavioral estrus at least 3 times daily, and inseminated according to the am- pm rule after detected in estrus. Animals that were not detected in estrus received 100 μg GnRH and timed AI 96 h after PGF injection. Blood was collected on d 0 and d 7 (56 h after PGF treatment) to measure P4 concentrations. There was no effect of treatment by year interaction on any dependent variable. Mean P4 concentration on d 0 was not different between treatments. At 56 h post-PGF treatment, mean P4 concentrations were < 1 ng/mL for all groups and were not different between treatments. The mean interval from PGF treatment to detected estrus was different ($P < 0.05$) among treatments: Control = 60.5 ± 3.4 h, Large = 64.0 ± 2.8 h and Split = 52.8 ± 2.8 h. The proportion of cows detected in estrus was different between treatments ($P < 0.05$) and were 65.6, 84.4, and, 90.5%, for Control, Large, and Split groups, respectively. These results indicate that either 2 injections of 12.5 mg PGF 7 h apart or a single injection of 37.5 mg PGF effectively causes luteolysis 56 h post PGF treatment. However, the split dose of 2 injections of 12.5 mg PGF 7 h apart shortened the intervals from treatment to estrus, and increased proportion of cows detected in estrus.

Key words: beef cows, prostaglandin $F_{2\alpha}$, estrus

271 The use of ruminal temperature for the prediction of estrus in beef cows. B. H. Boehmer*, T. A. Pye, and R. P. Wettemann, *Oklahoma Agricultural Experiment Station, Stillwater.*

Ruminal temperature (RuT) is a measure of core body temperature and can be used for identification of physiological events in beef cows. The usefulness of RuT for predicting estrus, parturition, heat stress, and animal health may be influenced by elevated ambient temperature. Ruminal temperature increases when cows are exposed to an ambient temperature greater than 32°C. The objective of this experiment was to evaluate the use of RuT to predict estrus in beef cows in June and July. Angus cows (n = 58) were administered ruminal temperature boluses (SmartStock, LLC.) which were programed to transmit every hour. Cows were synchronized with $PGF_{2\alpha}$ at 60 to 90 d postpartum. Onset of estrus was determined as an increase of 0.7°C in RuT during 8 h compared with the preceding 72 h. Cows were artificially inseminated 8 to 16 h after estrus was determined by RuT. Progesterone was quantified daily in plasma samples and onset of estrus was recorded by HeatWatch (CowChips, LLC.). Ambient temperature was recorded hourly (www.mesonet.org). Ruminal temperature was evaluated using the MIXED procedure (SAS). Maximum daily ambient temperature was 27.5 ± 3.9°C (range 19 to 35°C). Mean RuT for all cows was 38.5 ± 0.8°C. Ruminal temperature was greater ($P < 0.05$) during the 8 h at the onset of estrus when determined by RuT or HeatWatch (39.2 ± 0.1°C, 38.8 ± 0.1°C, respectively) compared with the same daily hours the day before (38.5 ± 0.1°C, 38.4 ± 0.1°C) or after (38.7 ± 0.1°C, 38.4 ± 0.1°C) onset of estrus. Ruminal temperature correctly identified estrus in 33 of 58 cows as determined by HeatWatch. Ruminal temperature determined that the onset of estrus was within 24 h of the onset of estrus as determined by HeatWatch in 62% of the cows. Based on plasma concentrations of progesterone, RUT identified estrus in 57% of cows and 43% of non estrous cows were identified as estrus. Pregnancy rate was 40% when estrus was identified by RUT and cows were AI. Elevated ambient temperature may influence the usefulness of RuT to detect estrus in beef cows.

Key words: ruminal temperature, estrus, beef cow

272 Effect of acetylsalicylic acid on vasodilatation of uterine arteries, right external iliac arterial blood flow, and pregnancy in beef cows. H. L. Sanchez-Rodriguez*, R. C. Vann, E. Baravik-Munsell, S. T. Willard, and P. L. Ryan, *Mississippi State University, Mississippi State.*

B-mode and Duplex Doppler ultrasound were used to determine the effects of acetylsalicylic acid (ASA) on uterine arteries diameter, external iliac artery Resistance Index (RI), and subsequent pregnancy rate in open, cycling Angus crossbred cows [4.27 ± 1.22 yr old; 568.76 ± 46.56 kg BW (mean ± SD)]. Acetylsalicylic acid (2,500 mg, ASA; n = 19) was administered twice daily in the feed from d −9.5 to 45 (d 0 = AI date). Control cows (CN; n = 19) received 5 g/d of dry molasses in flakes (placebo) in the feed during the same period. Dimensions of both uterine arteries were recorded once daily during d −10.5, −2.5, 0, 3, 6, 10, 16, 20, 25, 32 in a subsample of 16 cows (8/treatment). Pregnancies were confirmed at d 45 post AI. Jugular vein blood samples were collected after each ultrasound sampling for serum progesterone, and plasma prostaglandin F2α and prostaglandin E2 analyses. No difference ($P = 0.31$) in the diameter was observed between right and left side uterine arteries within a cow. In general, cows receiving ASA had larger diameter of uterine arteries than cows receiving the placebo (4.67 ± 0.04 and 4.54 ± 0.04 mm, respectively; $P = 0.01$). Uterine arterial diameters were larger in the ASA than in CN cows during sampling d −2.5 (4.61 ± 0.12 vs. 4.23 ± 0.12 mm; $P = 0.03$) and d 0 (4.52 ± 0.12 vs. 4.10 ± 0.10 mm; $P = 0.04$). During sampling d 10, ASA cows tend to have larger uterine arterial diameter values than did CN cows (4.86 ± 0.18 and 4.41 ± 0.16 mm, respectively; $P = 0.06$). Acetylsalicylic acid-treated cows achieved a pregnancy rate ($P = 0.18$) of 73.7% (14/19) in comparison with 52.6% (10/19) for CN cows. In a subsample of 12 cows (6/treatment), the RI in the right external iliac artery was recorded. The RI values were higher ($P = 0.04$) in the ASA-treated compared with the CN cows (0.78 ± 0.02 and 0.72 ± 0.02, respectively).These preliminary findings demonstrate that treatment with acetylsalicylic acid improves uterine arterial blood perfusion in beef cows and thus, may be an economical means of enhancing reproductive efficiency in postpartum cows.

Key words: acetylsalicylic acid, beef cows, blood flow

273 Antimicrobial resistance and prevalence of virulence factor genes in fecal *Escherichia coli* of Holstein calves fed milk with and without antimicrobials. R. V. V. Pereira*, T. M. A. Santos, M. L. Bicalho, V. S. Machado, R. C. Bicalho, and L. S. Caixeta, *Department of Population Medicine and Diagnostic Science, College of Veterinary Medicine, Cornell University, Ithaca, NY.*

Diarrhea in calves has a significant impact on the dairy industry. A common management practice for preventing and reducing diarrhea in preweaned calves is by adding antimicrobials in the milk. In this study, *Escherichia coli* antimicrobial resistance in fecal samples collected from calves 2 to 8 d of age that had received or not received antimicrobials in the milk and that presented or did not present signs of diarrhea were investigated. Resistance of *E. coli* isolates to individual antimicrobials, multiresistance patterns, and presence of virulence factors were analyzed. *E. coli* isolates were tested for 12 antibiotics, by use of a Kirby-Bauer disk diffusion assay, and categorized as susceptible, intermediate or resistant according to interpretive breakpoints described previously. The study was conducted at 3 farms, one administering antimicrobials (GPA) in the milk (n = 154) and 2 not adding antimicrobials in the milk (NGPA) (n = 97). To analyze the effect of GPA on the inhibition zone diameter a general linear model was fitted to the data using the MIXED procedure of SAS (SAS Inst., Cary,NC). Ordinal logistic regression models, one for each antibiotic, were fitted to the data using the ologit procedure of STATA (STATA 9.2, Statacorp, TX).Chi-squared tests were performed in Jump® (SAS Inst., Cary,NC) to assess the difference in the presence of genes encoding virulence factors between isolates. For all statistical models and tests, variables were considered statistically significant when a $P < 0.05$ was observed. All isolates were susceptible to ciprofloxacin and cefepime. From the total isolates tested, 84% (n = 251) were resistant to at least 2 antimicrobials and 81% (n = 251) were resistant to 3 or more antimicrobials. When antimicrobial resistance was compared between GPA and NGPA, it was observed that the GPA group had higher odds of antimicrobial resistance for most of individual antimicrobial tested. No significant correlation of virulence factors in GPA or NGPA and diarrheic or non-diarrheic fecal samples was found.

Key words: antibiotic resistance, dairy calves, *E. coli*

274 Somatic cell count and management benchmarks in Minnesota dairy herds. R. F. Leuer* and J. K. Reneau, *University of Minnesota, St. Paul.*

Dairy Herd Improvement Association (DHIA) tests provide a large amount of information about herd milk production and milk quality. Many guidelines have been given about farm SCC performance and its relationship to mastitis and milk quality, however, statistics quantifying that association is lacking. The objective of this study was to investigate the relationship between herd SCC level and performance rank for mastitis and milk quality benchmarking on dairy farms. Minnesota DHIA monthly average herd records were collected from January 2007 to November 2010. Herd tests without SCC information were removed and only herds with an average of 10 tests per year were included. Herds were divided into 4 categories based on average herd SCC over the collection period. Low herds (L) with less than 200,000 SCC (n = 325), medium low (ML) herds between 200,000 and 300,000 SCC (n = 547), medium high herds (MH) herds between 300,000 and 400,000 SCC (n = 470), and high herds (H) above 400,000 SCC (n = 438). Monthly records (n = 66,296) were analyzed using PROC GLM with significant differences determined at $P < 0.05$ using Tukey's multiple comparisons test. The 4 categories were all significantly different in average SCC (L = 157,000, ML = 251,000, MH = 350,000, H = 513,000), average of total cows on test day (L = 116, ML = 141, MH = 110, H = 86), percent infected (L = 16.4, ML = 24.7, MH = 32.9, H = 43.4), percent of current cows with new infections (L = 8.1, ML = 10.5, MH = 12.5, H = 14.2), percent of fresh cows with chronic infections (L = 6, ML = 11.2, MH = 17.6, H = 27.4), percent of current cows with chronic infections (L = 8.3, ML = 14.2, MH = 20.4, H = 29.2), percent infected <30 d in milk (L = 1.7, ML = 2.3, MH = 2.8, H = 3.3), percent infected between 30 and 220 d in milk (L = 7.7, ML = 11.7, MH = 15.4, H = 20), percent infected >220 d in milk (L = 7, ML = 10.7, MH = 14.7, H = 20.1), percent of herd >220 d in milk (L = 35.4, ML = 36.7, MH = 38.5, H = 40.5), rolling herd average (RHA) milk production (L = 10,351, ML = 9,944, MH = 9,201, H = 8,440 kg), RHA protein production (L = 315, ML = 304, MH = 284, H = 263 kg), and RHA fat production (L = 386, ML = 371, MH = 348, H = 325 kg). The 4 categories demonstrated differences that contribute to herd SCC.

Key words: benchmarking, DHIA, SCC

275 Heritability of rectal temperature and genetic correlations with production and reproduction traits in dairy cattle. S. Dikmen*[1], J. B. Cole[2], D. J. Null[2], and P. J. Hansen[3], *[1]Department of Animal Science, Faculty of Veterinary Medicine, Uludag University, Bursa, Turkey, [2]Animal Improvement Programs Laboratory Agricultural Research Service, USDA, Beltsville, MD [3]Department of Animal Sciences, University of Florida, Gainesville.*

Heat stress affects production and reproduction in dairy cattle. Genetic selection for body temperature might help to decrease the effects of heat stress on those traits. Objectives of the current study were a) to estimate genetic parameters of rectal temperature in dairy cows under heat stress conditions, and b) to determine genetic and phenotypic correlations of rectal temperature with production and fitness traits. Rectal temperature was measured between 1500 and 1700 h in 1,695 lactating Holstein cows sired by 509 bulls during the summer in north central Florida. Genetic parameters were estimated with GIBBS1F90 and breeding values were estimated with MTDFREML. The heritability of rectal temperature was estimated as 0.21. Annual genetic trend for rectal temperature was positive and increased 0.000068 oC/year from birth year 2002 to 2008. Genetic correlations of rectal temperature with other traits were close to zero. However, 305-d actual somatic cell score (SCS) was positively correlated ($r = 0.056 \pm 0.024$, $P < 0.05$) with rectal temperature. On the other hand, productive life ($r = -0.058 \pm 0.024$, $P < 0.05$), daughter pregnancy rate ($r = -0.036 \pm 0.024$, $P < 0.05$) and net merit ($r = -0.030 \pm 0.024$, $P < 0.05$) were negatively correlated with rectal temperature. Phenotypic correlations among rectal temperature and production traits were positive and often significant. In conclusion, rectal temperature during heat stress is moderately heritable and generally does not have strong genetic correlations with economically important traits. Selection for rectal temperature would result an increase in health and fitness traits without adversely affecting production traits.

Key words: heritability, dairy cattle, rectal temperature

276 Analysis of twinning, abortion and calf mortality in Irish Holstein and Friesian populations. A. M. Doyle[1], R. D. Evans[2], and

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Twinning is associated with unfavorable effects such as lower calf survival, dystocia, increased incidence of retained placentas, occurrence of freemartins and longer calving intervals. However twinning in dairy animals is also associated with increased milk production and the potential for obtaining more progeny from genetically superior females. The objective of this study was to determine the factors associated with twin births, stillbirths, abortion, and calf death before 28 d of age in the Irish Holstein and Friesian populations. Data were obtained from the Irish Cattle Breeding Federation and consisted of calving and mortality records from Holstein (n = 1,388,840) and Friesian animals (n = 217,786) in Ireland from 2004 to 2009. Logistical regression was used to determine factors associated with twinning, stillbirths, abortions and calf death before 28 d of age. The twinning rate was 2.1% for Holsteins and 2.4% for Friesians. Twinning increased as the parity of the dam increased (odds ration (OR) = 2.13 for Holstein parity 5 vs. Parity 1; OR = 2.24 for Friesian parity 5 vs. Parity 1). Season affected twinning rate, with an increase in the rate of twins born in summer for both Holstein (OR = 1.45 summer vs. winter) and Friesian animals (OR = 1.32 summer vs. winter). Calf stillbirth was higher for twins births than for single births in Holstein (OR = 5.33 twin vs. single birth) and Friesian animals (OR = 4.63 twin vs. single birth). Calving difficulty greatly influenced the odds of stillbirth occurring, particularly in twins births, where Holstein (OR = 10.33 calving score 4 vs. calving score 1) and Friesian (OR = 12.44 calving score 4 vs. calving score 1). Abortion is also more likely for twin births than single births for in Holstein animals (OR = 2.72 twin vs. single birth). Season of birth, year or birth and dam parity also effected the odds of abortion occurring. The odds of calf death before 28 d was increased for twin births when compared with singles and were also affected by dam parity, season, sex of calf and year of calving. These results could be used in herd management to minimize the incidence of twins and calf mortality in the dairy herd.

Key words: twinning, mortality, abortion

277 Nation-wide evaluation of quality and composition of colostrum fed to dairy calves in the United States K. M. Morrill*[1], E. Conrad[1], A. Lago[2], J. D. Quigley[2], and H. D. Tyler[1], [1]*Iowa State University, Ames,* [2]*APC Inc., Ankeny, IA.*

The objective of this study was to characterize the quality (IgG and nutrient content) of maternal colostrum (MC) fed to newborn dairy calves in the United States. Samples of MC (n = 827) were collected immediately before feeding from 67 farms in 12 states between June and October, 2010. Samples were collected from Holsteins (n = 494), Jerseys (n = 87), crossbred (n = 7) and unidentified cattle (n = 239) from 1st (n = 49), 2nd (n = 174), 3rd and later (n = 128) and unknown (n = 476) lactations. Samples were identified as fresh (n = 196), refrigerated (n = 152) or frozen (n = 479) before feeding. Samples of MC were analyzed for IgG by radial immunodiffusion (Triple J Farm; Bellingham, WA), protein, fat, lactose, other solids, total solids and somatic cell count (Dairy Laboratory Service; Dubuque, IA). IgG in MC ranged from <1 to 200 mg/ml, with a mean IgG concentration of 68.8 mg/ml (SD = 32.8). Thirty percent of MC was < 50 mg of IgG/ml. IgG concentration increased ($P < 0.05$) with parity (42.4, 68.6, 95.9 mg/ml in 1st, 2nd, and 3rd and later lactations, respectively). No differences in IgG were observed across breeds or storage method. Fat content ranged from 1.0 to 21.7% with a mean content of 5.6% (SD = 3.2). Protein ranged from 2.6 to 20.5%, with a mean content of 12.7% (SD = 3.3). Lactose content ranged from 1.2 to 4.5%, with a mean content of 2.9% (SD = 0.5). No nutritional differences were observed across breed; however fat content was greater ($P < 0.05$) in MC from 1st lactation compared with other lactations (6.6, 4.2 and 5.1%, respectively). Lactose and total solids were greater ($P < 0.05$) in MC from 1st and 3rd+ lactation cows compared with 2nd lactation cows. Somatic cell count (SCC) ranged from 6,000 to 20,901,000 cells/ml with a mean of 2,531,655 cells/ml. Log SCC decreased ($P < 0.05$) from 1st to 2nd and 2nd to 3rd+ lactation MC (5.9, 5.6 and 5.3, respectively). These data suggest that a minimum of 30% of dairy calves are currently being fed colostrum classified below industry standards for IgG content (<50 mg/ml), and are at a greater risk of failure of passive transfer, mortality and morbidity.

Key words: colostrum, calves, passive transfer

278 Milk production and somatic cell counts: A cow level analysis. K. J. Hand*[1], A. Godkin[2], and D. F. Kelton[3], [1]*Strategic Solutions Group, Puslinch, ON, Canada,* [2]*Ontario Ministry of Agriculture, Food and Rural Affairs, Elora, ON, Canada,* [3]*University of Guelph, Guelph, ON, Canada.*

The objectives of this study were to determine milk loss at the lactation and 24 h level due to subclinical and clinical mastitis. Milk loss was determined by quantifying the relationship between 24 h milk yield (kg) and somatic cell count (SCC, 103 cells / ml) in a cow level analysis. Milk production as a risk factor was also examined. The study data consisted of test day records for the year 2009 from 2835 Holstein herds in Ontario, Canada. The average herd size was 73 animals. Data were model in 2 stages, beginning with a general linear model to estimate the change in 24 h milk (kg) per unit change in ln(SCC), (b1LSCC), accounting for the effects of 24 h fat production (kg), days in milk (DIM) and the quadratic effect of DIM for every animal in the study. In stage 2, the estimated b1LSCC's were analyzed in a mix model that included the covariates within herd milk production quartile (MQ), parity (P, for parities 1, 2 and 3 to 5) and a random effect of herd. The estimated slopes from the mixed model analysis were used to estimate milk loss (kg) by comparing to a referent animal with an SCC value of 100. Lactation milk loss (kg) for all completed lactations was calculated using the estimates of 24 h milk loss (kg) and by accounting for the intervals between test days. As expected, 24 h milk loss increased with increased in SCC. In general first parity animals were found to exhibit less milk loss than multiparous animals. Furthermore, higher producing animals within the herd exhibited greater milk loss. Lactation milk loss (kg) increased as lactation average SCC increased. Lactation milk loss (kg) is approximately 50% more in older animals than compared with first parity animals.

Key words: SCC, production, dairy

279 Daily Markov-chain simulation model for selection of reproductive management programs in dairy herds. J. O. Giordano*, P. M. Fricke, M. C. Wiltbank, and V. E. Cabrera, *Department of Dairy Science, University of Wisconsin-Madison, Madison.*

Our objectives were to: (1) present a daily Markov-chain model that simulated dairy herd dynamics and economic performance, and (2) compare the economic value of 2 reproductive programs. A dairy herd was represented by Markov-chains simulation of events with every cow following daily probabilistic events of aging, culling, mortality, pregnancy, abortion, calving, and starting a new lactation. Daily milk yield was determined based on parity (1 to 9), DIM (1 to 1020 d), and reproductive status (open vs. 1 to 282 d pregnant). Cows culled and

dying were replaced to maintain herd size constant. The probability of pregnancy depended on the combination of insemination risk (IR) and conception risk (CR) for each program. All open cows had a probability of pregnancy between the end of the VWP and a cut-off for breeding at 330 DIM. After the cut-off, cows were labeled as "do not breed" until their milk production was below 27 kg/d when they were culled. A large algorithm containing > 2.5 million equations was iterated until the number of cows in each specific state remained unchanged (steady state). The value of a program was calculated daily for each cow as the sum of 5 factors: milk income over feed cost (IOFC), culling and mortality cost, income from newborns, and AI costs. The model compared the economic value of a program performing AI after estrus detection (ED; A) vs. another combining timed AI (TAI) with ED (B). Program A had a 21 d IR of 50% and CR of 30% for 1st postpartum AI and 28% for subsequent AI. Program B combined AI after ED for all AI (60% of cows bred on ED with 28% CR) with Presynch-Ovsynch for 1st AI postpartum (42% CR) and Ovsynch initiated 32 d after a previous AI for subsequent AI (30%). Economically Program B outperformed A by 14.5 $/cow/y. Program B had slightly lower IOFC (-$3.9), and higher AI costs ($3.5), but lower culling cost (-$7.9) and greater income from newborns ($13.9). Program B had more pregnant cows (3.7%) and fewer days open (13 d). Under the conditions of the case study the model indicated that the program combining ED with TAI (B) was economically and reproductively superior to the program with ED only.

Key words: economics, reproduction, dairy

280 Timing to reach the new level of pregnancy and milk yield after an improvement in reproductive management in dairy herds. G. M. Schuenemann*[1], P. Federico[2], A. De Vries[3], and K. N. Galvão[3], *[1]The Ohio State University, Columbus, [2]Capital University, Columbus, [3]University of Florida, Gainesville.*

The objective of this study was to assess the impact of improving 10% in both compliance (COM) and the accuracy of estrous detection (ED) on the timing to reach the new level of pregnancy and milk yield using an individual cow-based stochastic model for a dairy herd. Programs evaluated were: 1) ED: ED only; 2) Pre-Ov: Ovsynch preceded by Presynch with 2 injections of PGF 14 d apart, and Ovsynch for resynchronization of open cows at 32 d after AI; 3) Pre-Ov-ED: same as Pre-Ov for first AI, but cows undergo ED and AI after first AI, and cows diagnosed open 32 d after AI are resynchronized using Ovsynch. Cows were not inseminated after 365 DIM and open cows were culled after 450 DIM. Culled cows were immediately replaced with a primiparous cow. Herd was maintained at 1,000 cows. Mortality was set at 6% and abortion at 11.3%. The dry period and VWP was 60 d. Conception rate to first service was set to 30% (decreased by 2.5% for every subsequent service), and ED was set to 60%. Accuracy of ED (85% or 95%), and COM with each injection (85% or 95%) were evaluated. Simulations were performed at 85% (for COM and accuracy of ED) for 3,000 d, then the model was set at 95% for the subsequent 2,000 d to calculate the new values for pregnancy and milk yield. The first day the new mean was reached was taken as the time since the change was made. Average values from 10 runs were used. At 95% COM and 95% accuracy of ED, the time length to reach the new level of pregnancy for ED, Pre-Ov, and Pre-Ov-ED was 3.4 mo, 6.7 mo, and 4.1 mo, respectively. The time length to reach the new level of milk yield for ED, Pre-Ov, and Pre-Ov-ED took an additional 5.4 mo, 8.8 mo, and 7.5 mo from pregnancy, respectively. According to the model, the new level of pregnancy should be evident around 3 to 6 mo post-change with an additional 5 to 8 mo for milk yield. Assuming that the herd size remains constant, the timing to event (new level of pregnancy and milk yield) provides a timeline to monitor the expected true benefits when an improvement in reproductive management is made (to improve COM and accuracy of ED) at the farm level.

Key words: compliance, dairy cow, estrous detection

281 Economic comparison of reproductive programs for dairy herds using estrus detection (ED), Ovsynch, or a combination of both. K. N. Galvao*[1], P. Federico[3], A. De Vries[1], and G. M. Schuenemann[2], *[1]University of Florida, Gainesville, [2]The Ohio State University, Columbus, [3]Capital University, Columbus, OH.*

Objective was to compare the economic outcome of reproductive programs using ED, Ovsynch, or a combination of both using a stochastic dynamic model. Programs evaluated: 1) ED: ED only; 2) Pre-Ov: Presynch-Ovsynch for first AI, and Ovsynch for resynchronization of open cows at 32 d after AI; 3) Pre-Ov-ED: same as Pre-Ov for first AI, but cows undergo ED and AI after first AI, and cows diagnosed open 32 d after AI are resynchronized using Ovsynch. Cows were not AI after 365 DIM and open cows were culled after 450 DIM. Culled cows were immediately replaced. Herd was maintained at 1000 cows. Death losses were set at 6% and abortion at 11.3%. Dry period of 60 d. Net daily value was calculated by subtracting the costs with replacement heifers ($1,800/heifer), feeding costs ($0.25/Kg of lactating cow diet; $0.25/Kg of dry cow diet), breeding costs ($0.1/cow/d for ED; $2.5/dose PGF; $3.0/dose GnRH; $0.17/injection administration), and other costs ($3.5/d) from the daily income with milk sales ($0.31/Kg milk), cow sales ($0.75/Kg live weight), and calf sales ($200/calf). Simulation was performed until steady-state was reached (3000 d), then average daily values for the subsequent 2000 d was used to calculate profit/cow/yr. first AI CR was set to 30% (decreased by 2.5% for every subsequent AI), and ED was set to 60%. Accuracy of ED (95 or 85%), and compliance with each injection (95 or 85%) were evaluated. Inaccurate ED resulted in 0% CR. Missing a Presynch injection resulted in loss of 50% of the benefit (40% increase to first AI), and missing an Ovsynch injection resulted in decrease in CR by 70%. At 95% accuracy of ED and 95% compliance, the profits for ED, Pre-Ov, and Pre-Ov-ED were $410, $379, and $485, respectively. At 85% accuracy of ED and 85% compliance, the profits were $347, $260, and $421, respectively. ED only is better than Ovsynch, but Ovsynch with good compliance is better than ED with poor accuracy. Combination of Ovsynch with ED resulted in the greatest profit even with low accuracy and low compliance. Dairies should consider their accuracy of ED and compliance before implementing a program.

Key words: economics, reproductive programs, dairy cows

Ruminant Nutrition: Beef: Additives and Supplements

282 The effect of Bovamine on feedlot performance of finishing cattle: A meta-analysis. K. J. Hanford*[1], W. M. Kreikemeier[2], and D. R. Ware[2], *[1]Department of Statistics - UNL, Lincoln, NE, [2]Nutrition Physiology Co. LLC, Overland Park, KS.*

A meta-analysis of the effect of Bovamine (Nutrition Physiology Co., LLC) on performance of finishing cattle was conducted. Bovamine contains a patented combination of a lactic acid-producing bacterium (Lactobacillus acidophilus NP51) and a lactic acid-utilizing bacterium (Propionibacterium freudenreichii NP 24). Summary data from 18 feeding trials comparing control vs Bovamine were included. PROC GLIMMIX (SAS Institute) was used with a model including the fixed effect of treatment (Control vs Bovamine), a covariate of initial body weight, a treatment by covariate interaction and a random study effect. Any non-significant ($\alpha > 0.05$) interaction or covariate terms were dropped from the final model. Meta-analytical methods that weight responses by size of the study and precision of result were used. A subset analysis of those studies that included a corn processing by-product was also performed (7 trials). Initial body weight was significantly linearly associated with hot carcass weight (HCW) in the full analysis (b = 0.3457). DMI was not different between Bovamine and Control (95% CI = −0.010 to 0.116, $P = 0.0949$). Cattle fed Bovamine had higher ADG by 0.041 kg (95% CI = 0.027 to 0.054, $P < 0.0001$) and HCW by 3.51 kg (95% CI = 2.38 to 4.65, $P = 0.0001$) and lower feed to gain ratio (F:G) by −0.09 (95% CI = −0.132 to −0.049, $P = 0.0002$). Similar results were found for the analysis of studies that included feeding a corn processing by-product. DMI was not different between Bovamine and Control (95% CI = −0.023 to 0.177, $P = 0.1087$). Cattle fed Bovamine had higher ADG by 0.031 kg (95% CI = 0.010 to 0.051, $P = 0.0104$) and HCW by 4.32 kg (95% CI = 2.35 to 6.29, $P = 0.0025$) and lower F:G by −0.07 (95% CI = −0.130 to −0.013, $P = 0.0239$). These results quantify the effects of Bovamine on performance of feedlot cattle.

Key words: meta-analysis, feedlot cattle, direct fed microbial

283 Effects of Min-Ad on growth performance and carcass characteristics of finishing steers. J. O. Wallace*[1], M. S. Brown[1], D. D. Simms[2], C. W. Coufal[1], C. L. Maxwell[1], J. C. Simroth-Rodriguez[1], K. J. Kraich[1], and S. L. Thomas[1], *[1]West Texas A&M University, Canyon, [2]Min-Ad Inc., Amarillo, TX.*

Crossbred steers (n = 280; initial BW = 368 ± 10.7 kg) were used to evaluate the effects of feeding wet corn distillers grains (WCDG) and a commercial source of calcium–magnesium carbonate (MA, Min-Ad Inc., Amarillo, TX) on growth performance and carcass characteristics. Cattle were adapted to a common finishing diet, blocked by BW, implanted with Revalor-IS, and assigned to treatments of MA supplementation (0 or 1% of diet DM) and WCDG concentration (0 or 15% of diet DM). Cattle were housed in 28 soil–surfaced pens. Diets were fed twice/d for 169 d and cattle were reimplanted with Revalor–200 on d 48. Interactions existed for both shrunk initial BW and LMA ($P = 0.02$ and 0.04 respectively); however, there were no effects of either MA or WCDG on either variable ($P \geq 0.26$). Cattle fed MA consumed less feed and had lower ADG on a live basis (1.47 vs. 1.52 kg/d); SE = 0.061) and carcass-adjusted (CA) ADG resulting in a lower final BW and CA final BW ($P \leq 0.02$) than cattle not fed MA. Cattle fed MA had lighter HCW ($P = 0.03$); however, their marbling scores were higher ($P = 0.04$) than cattle not fed MA. Cattle fed WCDG consumed more feed and had higher ADG and CA ADG ($P \leq 0.06$) than cattle not receiving WCDG, resulting in heavier final BW and CA final BW, and improved F:G ($P \leq 0.07$) for cattle fed WCDG. Feeding WCDG also increased HCW, although dressing percent was decreased by feeding WCDG ($P = 0.07$ and 0.05, respectively). An interaction for USDA average yield grade (YG) ($P = 0.13$) was evident; however, there were no effects of either MA or WCDG ($P \geq 0.11$) on USDA average YG and these data followed the same numeric trend as BF thickness. No interactions existed for YG or quality grade distributions. Feeding MA increased the percentage of premium carcasses ($P = 0.07$) and feeding WCDG decreased the percentage of YG 2 carcasses ($P = 0.03$). There were no differences in water consumption by treatment. Results suggest that there are no performance benefits from including MA in the diet at 1% of DM under the conditions of this study; however, supplementing an SFC-based diet with 15% WCDG on a DM basis may improve carcass-adjusted performance.

Key words: feedlot cattle, wet corn distillers grains, Min-Ad

284 Ractopamine hydrochloride reduces urinary nitrogen excretion of both implanted and non-implanted finishing beef cattle. M. M. Kappen*, J. Ham, H. Han, and S. L. Archibeque, *Colorado State University, Ft. Collins.*

The effects of ractopamine hydrochloride (RAC) and a steroidal implant (IMP), on whole body N metabolism were evaluated in 24 Hereford × Angus steers (BW 554.4 ± 26.8 kg). The experimental design was a completely randomized block design with a 2 × 2 factorial arrangement of treatments. Factors included: 1) RAC (0.0 or 400 mg × hd-1 × d-1) and 2) IMP (0.0 or 200 mg trenbolone acetate and 28 mg of estradiol benzoate). Steers were housed in individual pens and allowed ad libitum access to feed and water throughout the experiment. Steers were acclimated to the metabolism barn by bringing in, tying and currying for 12 d before the initiation of the experiment. Once cattle had been implanted for 48 d and had received RAC for 21 d a nutrient balance study was conducted for 6 d. An IMP × RAC interaction tended ($P < 0.09$) to exist for DMI. Implanted steers receiving RAC tended to have lower DMI compared with non-IMP steers receiving RAC as well as IMP steers not receiving RAC. N intake ($P > 0.11$) and fecal N ($P > 0.18$) were not different due to treatment, yet numerically reflected the trend noted for DMI. Urinary N excretion was decreased by feeding RAC ($P < 0.01$). There tended ($P < 0.08$) to be an IMP × RAC interaction for urinary N excretion. Implanted steers receiving RAC tended to have less urinary N than steers receiving an implant only. Similarly, urine urea N excretion was decreased by RAC treatment ($P < 0.02$) and excretion was greater in steers that had also received IMP (IMP × RAC interaction; $P < 0.08$). Overall N retention was not affected by treatment ($P > 0.14$). These results indicate that urinary N excretion may be reduced by incorporating RAC according to labeled usage during the final phase of the finishing period. However, further studies will be required to elucidate the potential interactions of RAC with implant status and various types of implants.

Key words: ractopamine hydrochloride, trenbolone acetate, urinary nitrogen

285 Impact of sorting prior to feeding zilpaterol hydrochloride on feedlot performance and carcass characteristics of yearling steers. E. M. Hussey*[1], G. E. Erickson[1], W. A. Griffin[1], B. L. Nuttleman[1], T. J. Klopfenstein[1], and K. J. Vander Pol[2], *[1]University of*

Nebraska-Lincoln, Lincoln, [2]Intervet/Schering-Plough Animal Health, De Soto, KS.

Crossbred yearling steers (342 ± 10 kg initial BW) were assigned randomly to pens with 3 arrival blocks (25 steers/pen, 40 pens) to evaluate sorting and feeding zilpaterol on feedlot performance and carcass characteristics. Five treatments included an unsorted negative control (-CON), unsorted zilpaterol fed positive control (+CON); and 3 treatments where the heaviest 20% within the pen were sorted and marketed 28 d early and the remaining 80% were fed zilpaterol. The 20% were identified at the beginning (EARLY), 100 d from slaughter (MIDDLE), or 50 d from slaughter (LATE) by weighing individuals. Because of sorting, remaining steers in sorted treatments were fed 14 d longer than -CON and +CON. Steers fed zilpaterol were fed Zilmax at 8.3 mg/kg DM for 20 d followed by a 3 d withdrawal. Data were analyzed using Proc Mixed using a protected F-test and 3 preplanned contrasts. Steers fed +CON were 12 kg heavier ($P < 0.01$) than steers fed -CON. Steers sorted EARLY, MIDDLE, and LATE were 33, 25, and 32 kg heavier ($P < 0.01$) than -CON, respectively. Gain and G:F were greater ($P \leq 0.03$) for +CON than -CON, but not different between +CON and sorted treatments. Steers fed +CON had 15 kg greater HCW than -CON. Steers sorted EARLY, MIDDLE, and LATE had 28, 24, and 24 kg heavier ($P < 0.01$) HCW than -CON, respectively. Carcass weight SD was greater ($P = 0.01$) for +CON than -CON, but not different ($P = 0.16$) between -CON and zilpaterol sorted treatments. Percentage of overweight carcasses was greater ($P \leq 0.05$) in sorted treatments than -CON. Fat depth was lower ($P = 0.02$) in +CON than -CON, but not different between -CON and zilpaterol sorted treatments. LM area was greater ($P < 0.01$) in +CON and zilpaterol sorted treatments than -CON, and similar ($P = 0.57$) for all treatments fed zilpaterol. Marbling score was lower ($P < 0.01$) for +CON than -CON, but not different ($P = 0.60$) between -CON and zilpaterol sorted treatments. Feeding Zilpaterol in combination with sorting to identify heavy carcasses increased HCW without increasing variation and equalized marbling score compared with a negative control.

Key words: feedlot cattle, sorting, zilpaterol

286 Effect of feeding Micro-Aid in diets containing wet distillers grains plus solubles to finishing cattle on performance and nutrient mass balance fed during the summer. A. J. Doerr*[1], B. L. Nuttelman[1], G. E. Erickson[1], T. J. Klopfenstein[1], W. A. Griffin[1], and M. J. Rincker[2], *[1]University of Nebraska-Lincoln, [2]DPI Global, Porterville, CA.*

Ninety-six calves (321 ± 8.5 kg) were stratified by BW, and assigned randomly to 12 pens to evaluate the impact of feeding Micro-Aid in diets containing wet distillers grains plus solubles (WDGS) to finishing cattle on performance and N mass balance. Micro-Aid is manufactured from an all-natural plant extract, which contains saponins that have natural detergent and surfactant properties. Steers were fed for 160 d from May to November. Dietary treatments consisted of 35% WDGS, 55% corn, 5% straw, and 5% supplement (CON), with Micro-Aid being added in the treatment supplement at an inclusion of 1g per steer daily (TRT). Nitrogen excretion was determined by the difference between N intake and individual steer N retention. Total N lost was calculated by subtracting manure and runoff N from excreted N. Intake, ADG, and G:F were similar among treatments ($P \geq 0.67$), as well as carcass characteristics. Nitrogen intake, retention, and excretion were also similar ($P \geq 0.73$). There was no difference ($P \geq 0.95$) in the amount of DM and N removed during pen cleaning. N runoff was not different ($P = 0.20$) between treatments at 3.68% of N excretion. The amount of N lost via volatilization was similar among treatments (24.0 kg and 24.5 kg for the CON and Micro-Aid, respectively). Therefore, the percent N loss expressed as a percentage of N excretion was 71.9% for the CON group and 73.8% for the Micro-Aid group. ($P = 0.60$) Treatment did not affect amount of OM removed ($P = 0.64$), with 125 kg for the CON group and 104 kg for cattle fed Micro-Aid. Performance and carcass characteristics were similar between the CON and TRT cattle. Additionally, inclusion of Micro-Aid in the diet fed during the summer has no effect on N and OM removed. However, this contradicts the previous winter experiment in which feeding Micro-Aid led to less N volatilization.

Key words: nitrogen, mass balance, saponins

287 Rumen-protected arginine supplementation alters vascular hemodynamics in forage-fed steers. A. M. Meyer*[1], C. B. Saevre[1], D. V. Dhuyvetter[2], R. E. Musser[3], and J. S. Caton[1], *[1]Center for Nutrition and Pregnancy, Department of Animal Science, North Dakota State University, Fargo, [2]Ridley Block Operations, Mankato, MN, [3]SODA Feed Ingredients LLC, Mankato, MN.*

We hypothesized that Arg supplementation would alter vascular hemodynamics and increase systemic blood flow through its role in nitric oxide synthesis. To test this, 4 steers were used in a 4 × 4 Latin square with the following twice daily treatments: ad libitum grass hay (7.2% CP and 67.6% NDF; CON), hay and 27 mg Arg/kg BW injected intravenously (Arg-INJ), hay with 90 mg rumen-protected Arg/kg BW (Arg-180), and hay with 180 mg rumen-protected Arg/kg BW (Arg-360). Arginine in Arg-180 was estimated to be equal to Arg-INJ. Each period consisted of a 7-d adaptation then 14 d of Arg treatments. Blood flow and hemodynamics of the carotid and caudal arteries were determined using color Doppler ultrasonography on d −1 (baseline), 5, 9, and 14 of Arg treatment. Data were analyzed as repeated measures with treatment, day, and their interaction as fixed effects and steer and period as random effects. As expected, daily serum Arg was greater ($P < 0.001$) in Arg-INJ than all other treatments. Additionally, serum Arg was greater ($P = 0.005$) in Arg-360 than CON, with Arg-180 intermediate. Pulsatility index (PI) and resistance index (RI) percent changes from baseline were affected ($P \leq 0.08$) by treatment in the carotid and caudal arteries. Steers fed Arg-180 had decreased ($P \leq 0.02$) carotid RI and caudal PI compared with CON and Arg-360, indicating reduced vascular resistance and increased tissue blood perfusion. Carotid PI also decreased ($P \leq 0.06$) in Arg-180 compared with CON and Arg-INJ. Furthermore, caudal RI decreased ($P \leq 0.01$) and caudal end diastolic velocity increased ($P \leq 0.06$) in Arg-180 compared with all other treatments. Steers receiving Arg-INJ had decreased ($P < 0.10$) carotid RI compared with CON and decreased ($P = 0.04$) caudal RI compared with Arg-360. There was no effect ($P > 0.19$) of treatment on carotid or caudal flow volume, peak systolic velocity, mean velocity, or cross sectional area. Heart rate, stroke volume, and cardiac output were also unaffected ($P > 0.15$) by treatment. These data suggest that 180 mg rumen-protected Arg/kg BW improved vascular hemodynamics and tissue perfusion without altering serum Arg concentration.

Key words: arginine, blood flow, vascular hemodynamics

288 Effect of supplemental vitamin C on performance and antioxidant capacity of cattle fed varying concentrations of dietary sulfur. D. J. Pogge* and S. L. Hansen, *Iowa State University, Ames, IA, USA.*

Increased dietary sulfur (S) may create oxidative stress which negatively affects performance of feedlot cattle and may contribute to S toxicosis. Therefore, the effect of supplemental rumen-protected vitamin C (Vit C) on antioxidant capacity of cattle consuming high S diets was evaluated in a finishing trial utilizing 120 Angus crossbred steers. Steers were stratified by initial BW (354.9 ± 22.6 kg), and assigned to treatments (4 steers per pen, 5 pens per treatment). Treatments included: 1) low S, corn-based diet, 2) low S + Vit C, 3) medium S, 40% DDGS diet, 4) medium S + Vit C, 5) high S, medium S + 0.3% S from sodium sulfate and 6) high S + Vit C. Diets were formulated to average 0.2, 0.4 and 0.6% S, for low, medium and high S, respectively, and Vit C supplementation was targeted at 10 $g \cdot h^{-1} \cdot d^{-1}$. Rumen hydrogen sulfide concentrations and blood sulfhemoglobin concentrations (n = 5 per treatment) were measured on d 14, 28 and 90. Data were analyzed as repeated measures, and both hydrogen sulfide and sulfhemoglobin concentrations were greater ($P < 0.05$) in steers receiving medium and high S diets compared with steers receiving low S diets. Initial antioxidant status was not different due to treatment (n = 5 per treatment); however, plasma antioxidant capacity measured on d 90 was decreased ($P < 0.01$) in steers receiving medium or high S diets versus low S steers. Increasing dietary S concentrations resulted in a linear decrease ($P < 0.05$) in 12th rib back fat and percent intramuscular fat as determined by ultrasound on d 90. Dry matter intake and ADG for the 112 d period were not affected by Vit C supplementation; however, ADG was negatively affected ($P < 0.05$) by the linear increase of dietary S. In conclusion, medium or high dietary S decreased total antioxidant capacity of steers compared with those fed low S diets, which may contribute to increased susceptibility to S toxicosis when cattle are fed high S diets.

Key words: antioxidant, sulfur, vitamin C

289 Use of MTB-100, provided through a mineral mix, to reduce toxicity when lactating beef cows graze endophyte-infected tall fescue. M. E. Hoar*, D. K. Aaron, D. G. Ely, M. M. Simpson, and A. K. Lunsford, *University of Kentucky, Lexington.*

Sixty, 3 to 5 yr-old, Angus and Angus × Beefmaster cows and their calves were used in a 3-yr study to evaluate response to gradient levels of a nutritional supplement produced from a carbohydrate-based toxin adsorbent (MTB-100 Alltech, Inc., Nicholasville, KY). The supplement was carried in a mineral mix and was available to cows ad libitum. The MTB-100 was mixed with a complete mineral, diluted with white salt, so daily intake was projected to be either 0, 20 or 40 g/cow. The grazing season began on May 8 each yr. From this date until July 10 (Period 1), cows and calves were managed in 9, endophyte-infected (>90%) KY 31 tall fescue pastures (3 pastures/supplement level, re-randomized each yr) stocked with 10 to 16 cow/calf pairs each. On July 10 each yr, 21 pre-designated cow/calf pairs were allotted to individual, 1.6-ha plots of equivalent pasture (7 plots/supplement, re-randomized each yr). Cows continued their respective supplement regimens from this date until calves were weaned on September 13 (Period 2). Cow weight changes in Period 1 were −11.7, −1.9 and −3.2 kg/hd ($P = 0.19$) for 0, 20 and 40 g supplement levels. Although corresponding weight changes in Period 2 showed no significant trend, total cow weight changes from May 8 to September 13 were −7.4, −0.5 and 0.5 kg/hd for 0, 20 and 40 g supplement levels. Cow BCS did not change from May 8 to July 10 (Period 1). Cow BCS on July 10 (5.5, 5.6 and 5.0) decreased to 5.1, 5.4 and 5.0 ($P = 0.03$) for 0, 20 and 40 g treatments (Period 2). Rectal temperatures were not affected by MTB-100^{TM} consumption. Calf weights for Period 1 were 53, 56 and 56 kg/hd (NS) for the 0, 20 and 40 g levels. Calf gains in Period 2 were not different. Overall calf gains from May 8 to September 13 were 109, 112 and 111 kg/hd for 0, 20 and 40 g MTB-100. These results show MTB-100^{TM} consumption, through a mineral mix available ad-libitum, did not increase performance of cows and calves grazing endophyte-infected tall fescue forage.

Key words: adsorbent, cows, fescue

290 In vitro mitigation of rumen hydrogen sulfide. M. Ruiz-Moreno*, E. Seitz, and M. D. Stern, *University of Minnesota, St. Paul.*

Excessive release of rumen hydrogen sulfide (H_2S) has been associated with sulfur-induced polioencephalomalacia. Bismuth subsalicylate (BSS) has been used to decrease H_2S production in humans but its effect on rumen H_2S production is unknown. An in vitro rumen incubation was conducted to assess the effect of 5 levels of BSS on H_2S release and rumen metabolism during 2 consecutive 24-h periods. A diet consisting of 50% corn, 40% dried distillers grains, 9.75% hay and 0.25% mineral premix provided substrate for microbial metabolism. Chemical grade BSS was added to a final concentration of 0 (Control), 0.5, 1, 2 and 4% of DM. Rumen fluid was obtained from a cannulated dairy cow and mixed with McDougall's saliva to a 1:2 ratio. Treatments were assigned in 5 replicates to 120-mL serum bottles containing 50 mL of the inoculum mix and 0.5 g of dietary DM. Bottles were flushed with N_2, crimp sealed and incubated during 24 h at 39.1°C. At the end of incubation, gas volume and H_2S in the headspace of bottles were quantified. Final pH was recorded and incubation fluid was analyzed for NH_3-N and VFA. Data were analyzed as a randomized complete block design using ANOVA with Bonferroni correction. Final pH increased ($P < 0.05$) with 2 and 4% BSS by 0.06 and 0.22 pH units, respectively. No effect ($P > 0.05$) of BSS on NH_3-N concentration was observed. At 4% of DM, BSS decreased ($P < 0.05$) total VFA concentration by 15% and molar proportion of propionic acid by 5.7% while increasing acetic acid by 1.5% and the A:P ratio from 2.4 to 2.6, compared with the control. With 2% BSS, molar proportion of butyric acid was 9% lower than the control ($P < 0.05$). Concentration of branched-chain VFA was 19% higher ($P < 0.05$) with the addition of 0.5% BSS, compared with the control. All levels of BSS increased ($P < 0.05$) valeric acid molar proportion compared with 0% BSS. Compared with the control, gas production decreased ($P < 0.05$) with the addition of 2 and 4% BSS by 12 and 25%, respectively. All concentrations of BSS reduced ($P < 0.05$) H_2S production by 18, 24, 82 and 99% for 0.5, 1, 2 and 4% BSS, respectively. Results indicate that BSS can markedly decrease H_2S production.

Key words: rumen, hydrogen sulfide, bismuth subsalicylate

291 Utilizing crop residues in winter feeding systems for beef cows. A. D. Krause*[1] and H. A. Lardner[1,2], [1]*University of Saskatchewan, Saskatoon, Saskatchewan, Canada,* [2]*Western Beef Development Centre, Humbolt, Saskatchewan, Canada.*

An experiment was conducted to evaluate the effects of winter feeding system on beef cow performance, reproductive efficiency and economics. Winter feeding systems were grazing pea (*Pisum sativum* cv. Performance 40–10) crop residue (PEA) (TDN = 47.7%; CP = 7.3%), grazing oat (Avena sativa cv. Baler) crop residue (OAT) (TDN = 44.9%; CP = 2.3%), and grass-legume hay fed in drylot pens (DL) (TDN = 52.8%; CP = 9.1%). Ninety dry, pregnant Angus cows (629 kg ± 74 kg) stratified by body weight (BW) and days pregnant were allocated to 1 of 3 replicated (n = 3) treatments. Statistical analysis was conducted as a one way ANOVA using the Proc Mixed Model

procedure of SAS. Experimental design for feeding was a completely randomized design. Cows were allocated crop residue in field on a 3-d basis and supplemented oat grain daily at 0.4-0.6% of BW depending on environmental conditions. Dry matter intake (DMI) was measured for each treatment using the herbage weight disappearance method. Cow BW, body condition score (BCS), and rib and rump fat were measured at start and end of trial. Cow BW was corrected for conceptus gain based on calving data. Reproductive performance data collected included calf birth weight, calf birth date, calving span and calving rate. Cow BW was different ($P = 0.0001$) between all grazing systems. Drylot system cows had the greatest positive BW change (66 kg), and cows in the PEA system had the lowest positive BW change (10 kg). Rib and rump fat were also different ($P = 0.002$) between systems. Rib and rump fat changes were greater for the DL cows compared to cows in the PEA wintering system. Estimated DMI averaged over the winter feeding period was 13.1, 7.1 and 6.9 kg for DL, OAT and PEA cows, respectively. Mean calf birth weights for DL, OAT and PEA cows were 40.9, 36.8 and 40.3 kg, respectively. Winter feeding system costs per cow per day were $1.34, $1.07 and $2.78 for PEA, OAT and DL treatments, respectively. Results of this study indicate that it is possible to maintain cow BW during winter months in western Canada while grazing crop residues, which have the potential to reduce winter feeding costs associated with winter cow management.

Key words: pea crop residue, oat crop residue, beef cows

292 Effect of supplementing dried distillers grains to cattle consuming low-quality South Texas forage. M. C. Briggs*[1], K. C. McCuistion[1], R. O. Dittmar III[2], J. E. Zradicka[1], D. Kinkel[1], and T. A. Wickersham[2], *[1]Texas A&M University, Kingsville, Kingsville, [2]Texas A&M University, College Station.*

Protein supplementation is often used in South Texas to improve cow performance on dormant forage. However, little data are available evaluating the use of dried distillers grains (DDG) as a source of supplemental protein. Therefore, we used 13 ruminally fistulated steers in a 13 × 4 incomplete Latin square with 13 treatments and 4 periods. Steers were provided ad libitum access to low-quality (3.6% CP, 72.7% NDF) mixed grass hay. Treatments were arranged in a 3 × 4 factorial plus a positive control, alfalfa. The first factor compared 3 supplemental protein sources: cotton seed meal (CSM; 42.2% CP, 30.0% NDF), DDG (25.2% CP, 32.4% NDF) and DDG plus urea (DDGU; 35.6% CP, 32.4% NDF). The second factor consisted of 4 levels of the 3 supplemental protein sources provided at 0, 52, 104, and 156 mg N/kg of initial BW. Experimental periods were 16 d long with 10 d for adaptation. Forage OM intake (FOMI) increased linearly with DDGU ($P \leq 0.02$; 44.9, 52.4, 52.2, and 56.1 g/kg $BW^{0.75}$, for 0, 52, 104, and 156 mg N/kg BW, respectively) and CSM ($P < 0.01$; 46.9, 49.3, 53.3, and 57.1 g/kg $BW^{0.75}$, for 0, 52, 104, and 156 mg N/kg BW, respectively). However, increasing provision of DDG did not significantly affect FOMI ($P \geq 0.32$). In contrast, there was a linear ($P < 0.01$) increase in total OM intake (TOMI) when DDG was supplemented, with intakes increasing from 45.2 to 51.7, 60.2, and 63.0 g/kg $BW^{0.75}$, for 0, 52, 104, and 156 mg N/kg BW, respectively. Similar linear increases in TOMI were observed for CSM ($P < 0.01$) and DDGU ($P < 0.01$). Ruminal ammonia concentrations increased linearly with CSM ($P < 0.01$) and DDGU ($P < 0.01$) but were not affected by DDG ($P \geq 0.44$) supplementation. Both CSM and DDGU were effective at stimulating TOMI, with a portion of this response attributable to increased FOMI. In contrast, DDG was effective at increasing TOMI, but this was largely driven by the intake of supplement. Supplementation with DDG alone may be most effective when forage quantity is limited and substitution is desirable.

Key words: cattle, dried distillers grains, forage

293 A mechanistic model of enteric methane emissions from ruminants. R. A. Kohn* and S.-W. Kim, *University of Maryland, College Park.*

Most models of microbial metabolism assume kinetic control wherein rates of reactions depend on substrate or enzyme activity, and enzyme activity may in turn be controlled by gene expression. However, such models are frequently unstable and inaccurate. Thermodynamic control occurs when concentrations of metabolites build up relative to concentrations of reactants, such as when there is a high degree of competition for substrate and limited opportunity for removal of products. The second law of thermodynamics explains why certain profiles of volatile fatty acids (VFA) and gases (e.g., CH_4, CO_2 and H_2) occur in the rumen. According to current dogma, methane is produced from CO_2 and $4H_2$ in the rumen, but from degradation of acetate to CO_2 and CH_4 in anaerobic digesters. It was thought that rapid dilution rates wash out the slow-growing acetate-degrading (acetoclastic) organisms from the rumen. However, calculations of ΔG show that the reactions: acetic acid $\longleftrightarrow 2CO_2 + 4H_2$ and $CH_4 + 2H_2O \longleftrightarrow CO_2 + 4H_2$ are near equilibrium on forage-based diets. Thus, rate of acetic acid degradation is limited by thermodynamics and not kinetics. The gases in the rumen under 1 atm pressure ultimately limit degradation of acetic acid. Rumen microbes degraded acetic acid when incubated under partial vacuum or N_2. We are developing an integrated thermodynamic and kinetic model to predict methane emissions from VFA concentrations, which are in turn predicted from VFA production rates and VFA absorption and passage. These rates are in turn predicted from organic matter digestion in the rumen. An explanation for the decrease in ratio of concentration of acetate to propionate follows: [acetic acid] / $\{[CO_2]^2[H_2]^4\} = K_{eq}$ so as acid concentration builds up with high grain diets, H_2 pressure builds up (as observed) to maintain equilibrium. The greater H_2 concentration increases the equilibrium concentrations of VFA, particularly of propionate, thereby decreasing production of CO_2 and H_2 as precursors for methane. The model explains mechanisms of some factors that change methane emissions and suggests ways to decrease enteric methane emissions.

Key words: methane emissions, mathematical model, thermodynamics

294 Impact of free-choice or restricted water intake during the pre-weaning and early post-weaning period on calf performance and health. A. Manthey*[1], D. Ziegler[2], H. Chester-Jones[2], M. Raeth-Knight[3], G. Golombeski[3], and J. Linn[3], *[1]University of Wisconsin-River Falls, River Falls, [2]University of Minnesota, Southern Research and Outreach Center, Waseca, [3]University of Minnesota, St. Paul.*

Two studies were conducted to compare the impact of free choice versus restricted water intake during the milk replacer (MR) feeding period and 2 wk following weaning on calf performance. Study 1 was conducted spring of 2009 and study 2, summer of 2010. A total of 114 (study 1 = 44; study 2 = 70) 2 to 4 d old Holstein calves were assigned to 1 of 2 treatments: 1) Free choice water intake for 56 d (CON) or 2) Restricted water intake (RW). The RW treatment was no water available the first 36 d of the study followed by limited amount offered (2.3 kg/d) d 36 to 42 and free choice d 42 to 56. All calves were fed 0.28 kg of a 20:20 MR powder in 2 kg water twice daily d 1 to 35 and once daily d 36 until weaning at 42 d. Medicated MR was utilized in study 1 and non-medicated MR in study 2. An 18% CP calf starter (CS) was offered free choice d 1 to 56. Water, MR and CS intakes along with fecal scores were recorded daily. Body weight (BW) was measured d 1, 14, 28, 42 and 56 and hip height d 1 and 56. Data were analyzed as repeated measures using the PROC MIXED procedures of SAS. Study was included in the model as a blocking factor and initial BW was used as a covariate. During the MR feeding period (d 1–42), CON calves in study 1 and 2 consumed more water ($P < 0.05$) per d than the RW calves (study 1 = 0.54 vs. 0.22 kg/d; study 2 = 1.9 vs. 0.34 kg/d). Due to differences in season between studies, CON calves in study 2 consumed 1.4 kg more water per d than CON calves in study 1 from d 1 to 42 ($P < 0.05$). Average daily water intake from d 1 to 56 was similar for calves on the CON and RW treatment in study 1 averaging 1.6 kg water/d, but in study 2, CON calves consumed 1.0 kg more water per d ($P < 0.05$) compared with RW calves (2.9 vs. 1.9 kg/d). In both studies, differences in water intake between CON and RW treatments did not affect daily gain, CS or total DM intake from d 1 to 42 or d 1 to 56. Across studies, overall CS intake, total DM intake and daily gain averaged 0.66, 0.91, and 0.55 kg/d, respectively. Under conditions of these studies restricting water intake in the first 42 d did not affect calf performance.

Key words: dairy calves, water intake

295 Effects of free-access feeding of acidified milk replacer on the performance and general health of veal calves. C. G. Todd*[1], T. J. DeVries[2], K. E. Leslie[1], J. M. Sargeant[1], N. G. Anderson[3], K. Shore[4], and S. T. Millman[5], *[1]Department of Population Medicine, University of Guelph, Guelph, ON, Canada, [2]Department of Animal Poultry Science, University of Guelph, Kemptville Campus, Kemptville, ON, Canada, [3]Ontario Ministry of Agriculture, Food and Rural Affairs, Elora, ON, Canada, [4]Grober Nutrition, Cambridge, ON, Canada, [5]Veterinary Diagnostic and Production Animal Medicine, Iowa State University, Ames.*

The aim of this research was to examine the effects of milk replacer acidification for free-access feeding on the performance, morbidity and mortality of veal calves. Holstein male calves were randomly assigned at birth to free-access feeding of A) milk replacer (22% CP, 17% fat; n = 32) or B) acidified milk replacer (n = 31). Acidified milk replacer was prepared using formic acid (target pH: 4.0 to 4.5). Calves were weaned off milk replacer at 42 d of age. Milk replacer, starter ration and water intakes were measured daily from birth until weaning. Preweaning BW gain was determined weekly. After weaning, calves were transitioned to a growing/finishing diet for grain-fed veal, weighed every 2 weeks and slaughtered at 6 mo of age. At slaughter, the lungs of each calf were collected and evaluated for gross pathological changes. Dressed carcass weights were obtained. Multivariable regression models were constructed to examine the effects of treatment on milk replacer intake, time to onset of starter consumption, BW gain and carcass weight. Differences between treatment groups for disease events and death were tested using Pearson's $\times^2$ or Fisher's exact. Calves assigned to the acidified treatment consumed less milk replacer (10.1 vs. 11.3 L/d, SE = 0.2, $P < 0.01$) and began consuming starter ration earlier (32.0 vs. 39.5 d, $P < 0.05$) than the control calves. Milk replacer acidification tended to be associated with reduced preweaning ADG (0.9 vs. 1.0 kg/d, SE = 0.1, $P < 0.1$), but did not affect BW at weaning (85.1 vs. 87.8 kg, SE = 2.0, $P > 0.05$), postweaning ADG (1.2 vs. 1.2 kg/d, SE = 0.01, $P > 0.05$) or carcass weight (150.2 vs. 149.2 kg, SE = 3.3, $P > 0.05$). Calves did not differ for diarrhea occurrence (A vs. B: 36.1 vs. 42.6%, $P > 0.05$) or death (A vs. B: 3.2 vs. 1.6%, $P > 0.05$). There was, however, a tendency for fewer acidified-fed calves to have lung tissue affected with lesions of pneumonia (6.9 vs. 19.0%, $P < 0.10$). These results indicate that under free-access feeding conditions, acidification limits the intake of milk replacer, but does not negatively affect long-term calf performance, and may support improved respiratory health.

Key words: acidified, calf, milk replacer

296 Effect of Celmanax SCP on calf performance when fed in the milk replacer and grower phase. R. J. Dennis[1] and S. Jalukar*[2], *[1]Kent Nutrition Group Product Development Center, Muscatine, IA, [2]Varied Industries Corporation, Mason City, IA.*

Effect of supplementing Celmanax SCP, an ultra-concentrated product consisting of yeast culture and hydrolyzed yeast cell wall, in milk replacer and starter feed on dairy calves was evaluated. Fifty, day-old calves were allotted based on body weight to following 2 treatment a) calf milk replacer (MR) (20%CP:20% fat; non-medicated fed 568g daily) for 6 wk and control starter and grower diet from wk 7–20 and b) MR + 1g/h/d of Celmanax SCP for 6 wk and starter and grower diet + 2 g/h/d Celmanax SCP from wk 7–20. Calves were housed individually through d42 and in super hutches with 5–6 calves/hutch and bunk fed starter (18%CP) till d56. In grower phase (d57–84) calves were penned in 2 groups (control and SCP) and fed a 14% grower diet via self feeders. Serum protein analysis and vaccination to BVD was done for each calf. Along with the MR, control calves were treated upon arrival with Sulfamethoxazole-trimethoprim antibiotic tablets for the first 3 d and Celmanax SCP calves were fed 3g/h/d SCP for the first 2 d. Thereafter, Celmanax SCP was fed at 1g/h/d to the treatment group. Weight gain, milk replacer and starter intake, and feed efficiency of the calves were recorded. Data were analyzed by ANOVA for a completely randomized design using Statistix 8 analytical software. MR intake was similar for both treatments but there was a trend for starter intake to be higher with Celmanax SCP treatment. Starter intake was 29.12 kg and 57.24 kg after 6 and 8 wk for Celmanax SCP verses 25.58 kg and 53.48 kg after 6 and 8 wk for the control calves ($P \geq 0.18$). Average weights at the start and end of the trial were 37.43 kg and 186 kg for the calves receiving Celmanax SCP verses 36.86 kg and 181.99 kg for control treatment respectively. Throughout the experiment, calves

on Celmanax SCP showed numerically higher weight gains and they were 2.4 kg and 4.0 kg heavier at the end of 8 wk and 20 wk ($P \geq 0.2$) compared with control. The feed efficiency (F/G) was also numerically lower compared with control ($P \geq 0.2$). In conclusion, calves supplemented with Celmanax SCP showed numerical improvement in starter intake, weight gain, and feed efficiency.

Key words: calves, yeast, milk replacer

297 Effect of different forage sources on performance and feeding behavior of Holstein calves. L. l. Castells*[1], A. Bach[1,2], G. Araujo[1], and M. Terré[1], *[1]Department of Ruminant Production, IRTA, Caldes de Montbui, Spain, [2]ICREA, Barcelona, Spain.*

One hundred and 70 9 Holstein male calves participated in a series of 3 studies to evaluate the effect of different forage sources on performance and feeding behavior. Each study was conducted involving 60 calves (initial BW 45.0 ± 5.33 kg and 14.1 ± 4.17 d of age). Animals were randomly assigned to one of 3 different dietary treatments: control (CTR) calves were fed concentrate without any forage provision (this treatment was repeated in each of the 3 studies), and the 2 other treatments consisted on the same concentrate plus a forage source depending on the study: chopped alfalfa (AH) or rye-grass hay (RH); chopped oats hay (OH) or chopped barley straw (BS); corn silage (CS) or triticale silage (TS). 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 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 and bedded with wood shavings. Performance data were analyzed with an ANOVA with repeated measures, and behavior data were analyzed with a Poisson regression analysis. Compared with CTR, animals receiving OH, TS and BS consumed more ($P < 0.01$) starter (880 vs. 1140, 1170, 1060 ± 28 g/d, respectively) and grew faster ($P < 0.01$; 722 vs. 926, 880, 876 ± 38.3 g/d, respectively). On average, animals in treatments RH, BS, CS, and TS consumed 51 g/d of DM of forage, that was less ($P < 0.01$) than that obtained with AH (120 ± 19.8 g/d) and OH (101 ± 19.8 g/d). Compared to CTR calves, animals in AH and RH treatments spent more ($P < 0.01$) time ruminating (odds ratio vs CTR: 5.24 and 5.40, respectively), calves AH, RH devoted less ($P < 0.01$) time to perform non-nutritive oral behavior (odds ratio vs CTR: 0.38, 0.34, respectively), and TS calves tended ($P = 0.06$) to devote less time to perform non-nutritive oral behavior (odds ratio vs CTR: 0.21). In conclusion, free-choice provision of a forage source to young calves improves feed intake, performance, and, depending on forage source, reduces non-nutritive oral behaviors and stimulates rumination.

Key words: forage, calves, performance

298 Effect of fatty acid intake by dairy calves on performance, health, and markers of immunity. T. M. Hill*[1], M. J. VandeHaar[2], L. M. Sordillo[2], H. G. Bateman II[1], and R. L. Schlotterbeck[1], *[1]Nurture Research Center, Provimi North America, Lewisburg, OH, [2]Department of Animal Science, Michigan State University, East Lansing, [3]Department of Large Animal Clinical Sciences, Michigan State University, East Lansing.*

The aim of the present study was to determine the effect of supplementing milk replacer (MR) with 1% NeoTec4, a commercially available blend of butyric, coconut, and flax oil, on calf growth, feed efficiency, and indices of immune function when the calves were fed 28% CP MR at a high rate of intake (powder fed at 2% of BW). In the Trial 1a, 48 calves were fed either a MR which contained only animal fat (control) or the same MR with NeoTec4 (treatment). In Trial 1b, weaned calves from Trial 1a, were fed dry feed for 28 d without NeoTec4, then half the calves fed NeoTec4 for 28 d. Data were analyzed as a completely randomized design with repeated measures using PROC MIXED and NPAR1WAY. In Trial 1a, NeoTec4 improved ADG, feed intake, feed efficiency, reduced the number days with scours, and tended ($P = 0.06$) to reduce treatments for Clostridium. In addition, NeoTec4 lessened the inflammatory response to vaccination with Pasteurella at 5-wk-old, as observed by reduced hyperthermia and hypophagia and alleviation of the TNF-α response. In addition, NeoTec4 tended ($P = 0.09$) to increase the post-Pasteurella challenge response in IL-4 in mononuclear cells, increased serum globulin protein. Post-booster vaccination titers for BVD and PI3 were increased in calves fed NeoTec4. In Trial 1b, there were no differences in performance during the first 28 d when no calves received NeoTec4, but calves receiving NeoTec4 in the second 28 d had greater ADG and feed efficiency. We conclude that supplementation of MR with NeoTec4, a blend of butyrate, coconut and flax oils, improves some immune responses, which may partly explain the reduction in scours and concurrent improvements in growth rate and feed efficiency.

Key words: dairy calves, immunity, fatty acids

299 Impact of feeding various fats and fatty acids on dairy calf performance, health, and markers of immunity. T. M. Hill*, H. G. Bateman II, J. M. Aldrich, and R. L. Schlotterbeck, *Nurture Research Center, Provimi North America, Lewisburg, OH.*

We evaluated the impact of feeding various fats and fatty acids on castrated Holstein calf performance in 3 56-d trials. PROC MIXED and NPAR1WAY were used and $P < 0.05$ was considered significant in all trials. In Trial 1, 48 3-d old calves were fed a milk replacer with 2 fat types (all animal or a blend of animal, coconut, and soy fats) and with or without 1.25% of a blend of butyrate, medium chain fatty acids, and linolenic acid (NeoTec4, Provimi North America, Lewisburg, OH) in a completely randomized design in a 2 × 2 factorial arrangement with repeated measures. Fat type did not affect performance. Calf ADG, starter intake, feed efficiency, hip width change, and post-booster serum titers to BVD and PI3 vaccines were greater in calves fed NeoTec4. The rectal temperature increase to a Pasteurella vaccine was greater in calves fed the fat blend vs. all animal fat. Post-vaccination rectal temperatures increase was less in calves fed MR with NeoTec4 vs. without NeoTec4. In Trial 2, 48 3-d old calves were fed starters with A) 0.5% NeoTec4, 0% soy oil, B) 0.5% NeoTec4, 2.0% soy oil, and C) 0% NeoTec4, 0% soy oil in a completely randomized design with repeated measures. Calves fed starter A had greater ADG than calves fed starter B or C. Calves fed starter A had greater hip width change than calves fed starter C. In Trial 3, 96 8-wk old calves were fed 4 growers: A) control, B) 0.25% Flaxtech (Virtus Nutrition, Corcoran, CA), C) 0.5% NeoTec4, and D) 1.5% soy oil as a randomized complete block design. There were 2 blocks based on 2 groups of calves starting the trial at different times. Calf ADG was greatest in calves fed NeoTec4 and least in calves fed soy oil. Hip width change was greater in calves fed NeoTec4 than in calves fed the control or soy oil diet. In summary, addition of soy oil to starter and grower feeds reduced ADG while adding NeoTec4 fatty acids to milk replacers, starter and grower feeds increased ADG and hip width change.

Key words: dairy calves, immunity, fatty acids

300 Impact of three times versus twice a day milk replacer feeding on calf performance, likelihood to reach lactation and future milk production in a commercial dairy herd. D. C. Sockett*[1], C. E. Sorenson[2], N. K. Betzold[3], J. T. Meronek[3], and T. J. Earleywine[4], *[1]Wisconsin Veterinary Diagnostic Laboratory, University of Wisconsin, Madison, [2]United Cooperative, Sauk City, WI, USA, [3]University of Wisconsin-Madison, College of Agricultural & Life Sciences, Madison, [4]Land O'Lakes Inc., Cottage Grove, WI.*

Seventy, Holstein heifer calves were enrolled in a trial designed to evaluate both the short and long-term effects of feeding a full potential milk replacer (MR) diet (28% protein, 20% fat) either 3 times or twice a day. Within 6 h of birth, calves were fed a commercial colostrum replacement product made from bovine colostrum that contained 150g of IgG. Calves were randomly assigned to either 3 times or twice a day feeding. A blood sample was collected from each calf 1–3 d after birth. Serum was tested for bovine IgG by single radial immunodiffusion. Calves were housed outdoors in individual calf hutches until they were weaned and moved to group pens at 50–55 d of age. All the calves were fed at 08:00 and 21:00 h. Calves fed 3 times a day received an additional meal at 14:30 h. Calves were fed 815g of MR/day from d 1–7, 1135g of MR/day from d 8–42 divided into either 3 or 2 feedings. Both groups of calves were fed 565g of MR once a day (pre-weaning process) from d 43–49. Calf starter (20% CP as fed) was offered to the calves beginning at 3–4 d of age. Calf starter intake was measured daily. Calves were weighed and had their hip height measured weekly. All the calves remained in the herd unless they died or were culled. Each animal's calving date was recorded and milk production assessed using mature-equivalent 305-d (ME305) milk yield estimated at ≥120 d in milk. Data (birth weight, serum IgG, hip height and weight gain, feed efficiency, calf starter intake, age at first calving and ME305) was evaluated using ANOVA and co-variance using a G.L.M. procedure (NCSS-2007, Kaysville, Utah). The likelihood of calves being weaned, entering lactation and calculation of relative risk was analyzed using 2-way contingency table analysis (JavaStat). Calves fed 3 times a day had improved growth (hip height and weight gain), better feed efficiency, consumed more calf starter during the pre-weaning process and were more likely to enter lactation (relative risk 1.21, 95% C.I. 1.02–1.45) than calves fed twice a day.

Table 1. Results

Item	2x Feeding	3x Feeding	*P*-value
Number calves	35	35	1.0000
Birth weight, kg	40.1	39.8	0.7385
Serum IgG mg/mL	11.2	12.2	0.3459
Calf starter intake, DM (1-42 days), kg	3.3	3.9	0.3448
Calf starter intake, DM (43-49 days), kg	3.8	4.8	0.0122
BW gain (1-42 days), kg	25.1	29.8	0.0001
Hip height gain (1-42 days), cm	8.6	10.3	0.0027
Feed efficiency (gain/DM intake, 1-42 days)	0.52	0.61	0.0001
Number weaned	32	34	0.3070
Number lactating	28	34	0.0250
Age first calving, days	734	718	0.2278
ME305, milk production, kg	13053	13568	0.2265

Key words: feeding, growth, lactation

301 Effects of a modified intensive milk replacer program fed two or four times daily on nursery calf performance. A. D. Kmicikewycz*, D. N. da Silva, and N. B. Litherland, *University of Minnesota, St. Paul.*

The objective of this study was to determine if milk replacer (MR) program and feeding frequency (2 vs. 4 meals/day) altered calf performance. Forty-eight Holstein and cross-bred heifer and bull calves were assigned according to body weight (BW), breed, sex, and total protein to 4 treatments (T) (n = 12): T1) 20% CP:20% fat MR fed at 1.5% BW 2 × daily (d); T2) 20:20 MR fed at 1.5% BW 4 × d; T3) 26:18 MR fed at 2.0% BW 2 × d; or T4) 26:18 MR fed at 2.0% BW 4 × d. All calves were fed at 0600 and 1700 h and T2 and T4 were fed additionally at 1100 and 1400 h. Treatments were fed from 1 to 42 d and all MR feeding rates were adjusted weekly to maintain 1.5% or 2.0% of BW reconstituted at 15% DM. Calves were weaned on d 42 by reducing the MR feeding frequency by 50% on d 36. Calves were housed in hutches bedded with straw and offered water and a texturized 18% CP starter ad libitum. Calf growth was measured weekly and starter intake and fecal scores recorded daily. Data were analyzed using Proc Mixed in SAS as a completely randomized design with repeated measures and the least significant difference test was used for mean separations when main effects were significant ($P < 0.05$). Birth BW averaged 41.8 kg. Average daily gain (ADG) d 1–42 was similar ($P = 0.39$) and averaged 0.59, 0.63, 0.69, and 0.71 kg/day for T1, T2, T3 and T4 (SEM = 0.05). ADG from d 1–56 was also similar among treatments ($P = 0.18$) and averaged 0.62, 0.72, 0.78 and 0.75 kg/d for T1, T2, T3, and T4 (SEM = 0.06). Starter intake averaged 0.88 for T1, 1.12 for T2, 0.81 for T3, and 0.75 for T4 (kg/day). T2 had the greatest starter intake on wk 6 and 7 ($P < 0.05$; T × wk). BW was greater for T3 vs. T1 on wk 8 ($P < 0.05$; T × wk). BW gain from d 1 to 42 were similar ($P = 0.4$) and averaged 24.9 and 26.4 kg for T1 and T2, while T3 and T4 calves gained 28.8 and 29.8 kg. BW gain from d 1 to 56 was not different ($P = 0.2$) and averaged 34.9, 40.1, 43.9, and 42.2 kg for T1, T2, T3 and T4. Fecal scores did not differ. Feeding a 20:20 MR 4 times daily resulted in greater starter intake yielding 5.2 kg additional gain through d 56.

Key words: calf, milk replacer, feeding frequency

302 Effect of different levels of alfalfa hay and sodium-propionate supplementation on performance and rumen development of dairy calves. H. Beiranvand, M. Khorvash, G. R. Ghorbani*, A. Riasi, S. Kargar, and M. Mirzaei, *Isfahan University of Technology, Isfahan, Iran.*

Forty 2 male Holstein calves (46 ± 3.0 kg) were used to evaluate the effect of alfalfa hay (as physical factor) inclusion at different levels and sodium-propionate (as chemical factor) supplementation on performance and rumen development. The experiment was conducted as complete randomized design with a 2 × 3 factorial arrangement. Treatments consisted of 1) concentrate only (Control); 2) concentrate plus 5% sodium-propionate (Control + Pro); 3) concentrate + 5% forage only (5% F); 4) 5% forage + 5% sodium-propionate (5%F+ Pro) = ; 5) concentrate + 10% forage only (10% F); and 6) 10% forage + 5% sodium-propionate (10% F+ Pro). All data were analyzed using the MIXED procedure of SAS (SAS, 2003). All dietary treatments were provided ad-libitum in addition to milk (4 kg/head/day). Concentrate was provided as meal form and alfalfa hay was chopped with geometric mean particle size of 2.6 mm. Nine calves from selected treatments (Control, 10% F, and 10% F + Pro; 3 calves per treatment) were euthanized at 70 d of age. Alfalfa hay supplementation increased dry matter intake and average daily gain but propionate effect or propionate ×

forage interaction were not influenced significantly. Adding alfalfa hay reduced feed efficiency ($P < 0.02$). Compared with calves on propionate those fed forage had lower weaning days (61 vs. 45 d). Rumen wall in calves fed forage showed thinner keratin layer and had stronger muscles layer compared with control. Results indicated that adding forage in the form of chopped alfalfa hay positively influenced growth performance and microscopic appearance of the rumen epithelium and rumen wall as well as decrease in weaning ages.

Key words: alfalfa hay, propionate, rumen development

303 Effect of pre-weaning feeding regimens on post-weaning growth performance of Sahiwal calves. S. A. Bhatti*[1], A. Ali[1], D. McGill[2], M. Sarwar[1], H. Nawaz[1], M. Afzal[3], M. S. Khan[1], M. A. Amer[4], R. D. Bush[5], P. C. Wynn[2], H. M. Warriach[2], and H. Nawaz[1], *[1]Institute of Animal Nutrition and Feed Technology, University of Agriculture, Faisalabad, Pakistan, [2]E H 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]Faculty of Veterinary Science, University of Sydney, Camden, Australia.*

The objective of the study was to establish the post-weaning growth potential of Sahiwal calves reared on 4 different pre-weaning diets. Sahiwal calves (n = 48; 24 of each sex 3 ± 2 d of age) were divided into 4 groups of 12 animals each (6 of each sex) and were offered one of the following dietary treatments from d 3 ± 2 postpartum: A: whole cow′s milk + starter ration (SR; CP = 20%, TDN = 72%) plus Berseem clover hay (H; *Trifolium alexandrinum*; CP = 21% TDN = 63%); B: Milk + H; C: Milk replacer (MR; reconstituted to specification; Sprayfo) + SR+H and D: MR + H. Milk or MR was offered at the rate of 10% of their body weight until d 56 and then withdrawn gradually until weaned completely by d 84. The SR and H were continued until d 84. During the post-weaning period the calves were fed a single total mixed ration containing 16% CP and 70% TDN, from the 13th to the 24th week of age. This ration was fed ad libitum, daily feed intake was measured and live-weights were recorded weekly. The data were analyzed by MIXED procedures of SAS. The initial live-weight, growth rate, total live-weight gain and final live-weight of calves at 24 weeks of age were 56 ± 1, 47 ± 1, 40 ± 1 and 30 ± 1 kg; 746 ± 33, 660 ± 34, 654 ± 33 and 527 ± 33 g/d; 63.2 ± 2.6, 55.2 ± 2.7, 54.9 ± 2.7 and 44.2 ± 2.6 kg; and 119 ± 4.2, 102 ± 4.3, 95 ± 4.3 and 75 ± 4.2 kg for the pre-weaning treatments A, B, C and D, respectively; these were influenced ($P < 0.05$) by the pre-weaning treatments. Offering whole milk from birth at the rate of at least 10% of bodyweight with concentrates leads to a higher weaning weight and post-weaning growth rate and hence a greater possibility of early maturity.

Key words: calf nutrition, post-weaning growth

Tuesday, July 12, 2011

POSTER PRESENTATIONS
Animal Health II

T1 Development of kit for bovine myeloperoxidase using enzyme-linked immunosorbent assay. J. Shi*, Y. Yang, Q. Li, and Y. Lv, *Key Laboratory of Dairy Science, Ministry of Education, Northeast Agricultural University, Harbin, China.*

Myeloperoxidase (MPO) is a heme glucoprotein found in the primary granules of mammalian neutrophils. At site of infection, MPO is released extracellularly or into phagocytic vacuoles. It had shown that MPO is abundant in milk taken from mammary glands of cows with mastitis and that the amount of MPO in milk is well correlated with the somatic cell count in mastitis milk. To evaluate the potential of using MPO in the diagnosis of mastitis in cows, this study developed a specific enzyme immunoassay for MPO in milk. Bovine MPO was isolated and purified from bovine whole blood by Sephadex G-200 chromatography and ConA-Sepharose 4B affinity chromatography. Antiserum against bovine MPO were produced using the purified MPO with ConA as a coated "antibody," and mouse anti-bovine antiserum against MPO as a second detection antibody, and chicken HRP-labeled polyclonal antibody as a anti-antibody, a special sandwich ELISA for MPO was established. ELISA kit was developed. Evaluating kit by methodology showed good specificity, reproducibility (variant coefficient: 1.09 to 7.2% in batch and 1.47 to 6.7% between batches), and the detection limit was 1.1ug/ml. The experiment certified that this kit could maintain over one year and the detection time of the kit was about 3.5h.

Key words: bovine myeloperoxidase, purification, ELISA kit

T2 Development of kit for bovine haptoglobin using enzyme-linked immunosorbent assay. Y. Yang*, J. Shi, Q. Li, and Y. Lv, *Key Laboratory of Dairy Science, Ministry of Education, Northeast Agricultural University, Harbin, China.*

Haptoglobin (Hp) is one of the important acute phase proteins of cows with mastitis, the concentration of Hp in milk and blood is closed to the mastitis condition. So the determination of Hp in milk could be an effective diagnostic tool for mastitis. Development of sandwich-ELISA: The haptoglobin in whey was captured with bovine-hemoglobin coated ELISA plates, and the sandwich ELISA using the anti-Hp-antibody and AP-conjugated-antibody was established, the reaction conditions of ELISA were optimized. The concentration of hemoglobin for coating 96-well microtiter plate was 10%, and incubated overnight at 4°C. The plates were subsequently blocked 1 h with 2% BSA-PBST, and then incubated for 1 h with diluted whey samples (1:10), after washing the plates, the diluted anti-Hp-antibody (1:1000) was added and incubated for 1 h at 37°C. The diluted AP-conjugated-antibody (1:500) was added and incubated for 1 h at 37°C, and then substrate of PNPP solution was added for incubation 15 min at 37°C to develop color. The ELISA test gave a cut-off value of 0.996 for detection of 100 Hp-negative whey samples. The threshold for ELISA was OD405nm ≥0.996 for positives, OD405nm <0.901 for negatives, and the other was suspectives. Correlation between analytical results of the ELISA test and the commercial kits test was similar ($R^2 = 0.996$) based on detection of 50 whey samples. The Hp detection limit of ELISA was 0.08 μg/mL. The ELISA test had no cross-reaction with other acute phase proteins of cows with mastitis. Packing and application of the ELISA test kit for Hp: Based on the sandwich-ELISA, the coating condition of the anti-Hp-antibody, AP-conjugated-antibody, the control positive/negative whey samples, the storage conditions of the plates and the kit were explored, and the ELISA test kit were packed. The variant coefficients of ELISA in a batch and between batches were from 3.27% to 4.98% and from 5.46% to 8.31%, respectively. The ELISA test kit provides an available technique for detection Hp of whey samples and a good foundation for the further development and commercialization of the kit.

Key words: haptoglobin, mastitis, sandwich ELISA

T3 Transcriptional factors SP1 and SP3 influence differentially the regulating sequence of the bovine osteopontin gene depending on promoter haplotype. N. Bissonnette* and C. Thibault, *Agriculture and Agri-Food Canada, Dairy Cattle and Swine Research and Development Center, Sherbrooke, Quebec, Canada.*

Osteopontin is a pro-inflammatory molecule which has been involved in numerous physiological aspects, from wound healing to metastasis. In cattle, osteopontin was associated to the paratuberculosis disease. In a previous study, we have identified DNA polymorphisms (SNP) in the osteopontin gene (*SPP1*) associated with the mammary health status of lactating cows. To better understand the factors that govern the expression of this gene, the activity of its regulating sequence (i.e., promoter) was study in vitro. The most prevalent haplotypes (H1–H3) of the *SPP1* promoter were cloned. Two SNP are located in the 5′ untranslated region and one in the first intron. The haplotype promoter sequences were analyzed in silico for identification of transcription regulating sites using the TRANFAC software. The two transcription factors SP1 and SP3 bindings might be affected by the presence of these SNP. The luciferase reporter constructs of the haplotype containing the 1736-bp regulating sequence were compared in cotransfection assays with, without, or in presence of both SP1 and SP3 using the BOMAC (bovine macrophage), MAC-T (bovine mammary epithelial) and the MCF7 (human mammary epithelial) cell lines. The basal activity of H2 was lower than H1 and H3 ($P = < 0.0001$) in BOMAC and MCF7 cells. In MAC-T, the H2 difference for H1 remained significant ($P = 0.031$) but with a tendency for the allele H3 ($P = 0.066$). In presence of the transfection factor SP1, the expression increased globally by ~2-fold in all cell types. The allele H2 was more responsive to SP1 in both BOMAC and MCF7 (H1, $P = 0.009$ and $P = 0.004$); H3, $P = < 0.001$ and $P = 0.021$, respectively), which was also observed in MAC-T ($P = < 0.0001$). In contrast, the transcription factor SP3 had a negative impact on the promoter activity. The co-expression of SP1/SP3 recovered partially the promoter activity. In this study, we demonstrated that the transcription factors SP1 and SP3 impact gene activity through the regulating sequence and that the presence of SNP within the *SPP1* promoter may interfere with osteopontin expression.

Key words: osteopontin, transcription factor SP1/SP3, haplotype

T4 Evaluation of interleukin 5 as a biomarker for parasite resistance in goats pasture exposed to *Haemonchus contortus*. M. M. Corley* and A. A. Saeed, *Virginia State University, Petersburg.*

In the meat goat industry, an animal that exhibits disease resistance characteristics can increase the price of goat from $250 to $800 per head. *Haemonchus contortus*, the blood sucking gastrointestinal nematode (GIN), costs the global livestock industry billions of dollars per year in lost production and anthelmintic drug costs. The annual expenditure on anthelmintics in the US is over $3 billion. Interleukin 5 is one of the cytokines secreted by Th2 immune cells implicated in the process of gut expulsion of GINs from humans, mice and sheep. However, studies on the mechanism of immunity to *Haemonchus contortus* infection and the ability to identify parasite resistance through IL-5 and other cytokine responses need to be assessed in goats. This study evaluated gene expression of IL-5 in selected pasture exposed parasite resistant Spanish and Myotonic goats. Whole blood, and intestinal tissues were harvested from goats exhibiting susceptibility and resistance to *Haemonchus contortus* based on (FAMACHA (FAM) eye color charts, packed cell volume (PCV), fecal egg counts (FEC) and quantitative real time PCR (qPCR) detection. Primers were designed from conserved regions of IL-5 bovine and ovine nucleotide sequence alignments. Total RNA was extracted from homogenized goat intestinal tissues and qPCR was performed to determine IL-5 expression. Results showed that parasite resistant goats expressed more ($P < 0.05$) IL-5 than susceptible goats. Gene expression of IL-5 was higher ($P < 0.05$) in infected Spanish vs. Myotonic goats. Infected does expressed higher ($P < 0.05$) IL-5 than bucks. Pearson correlation coefficients showed that there was a positive correlation between FEC, FAM, PCV ($P < 0.05$) and IL-5 expression. These data indicate that IL-5 expression can be used as a marker to screen for susceptibility or resistance to *Haemonchus contortus* infection in pasture exposed goats, allowing IL-5 based anthelmintic drug development and goat producers the ability to select parasite resistant animals.

Key words: parasite resistance, IL-5, *Haemonchus contortus*

T5 Influence of latency to collect blood samples from beef calves on ex vivo innate immune responses. L. E. Hulbert*[1,2], C. J. Cobb[1], M. D. Sellers[1], D. L. Hanson[1], M. L. Galyean[1], and M. A. Ballou[1], *[1]Department of Animal and Food Sciences, Texas Tech University, Lubbock, [2]Department of Animal Sciences, University of California-Davis, Davis.*

Objective was to evaluate the influence of latency to collect a blood sample from beef calves on the ex vivo innate immune responses. Innate immune responses evaluated included total leukocyte and differential counts, neutrophil L-selectin expression, whole blood (WB) killing of *E. coli* 0111:H8, tumor necrosis factor-α (TNF-α) secretion from lipopolysaccharide (LPS)-stimulated WB, and neutrophil phagocytosis and oxidative burst responses to E. Coli 0111:H8. Within each of 12 pens, whole blood was collected via jugular puncture from the first and last calf (n = 9 to 10 calves/pen; BW = 202 ± 18.7 kg) to enter the squeeze chute. The time from when research personnel entered the pen to move the cattle until the blood sample was collected averaged (±STD) 320 and 746 ± 44.2 s ($P < 0.001$) for the first and last calf in each pen, respectively. There were no treatment differences for secretion of TNF-α from LPS-stimulated WB or neutrophil phagocytosis. Total leukocyte counts tended ($P = 0.075$) to be less for calves sampled last in the pen vs. those sampled first. Although there were no differences between calf neutrophil:lymphocyte ratios ($P = 0.867$), neutrophil L-selectin expression tended ($P = 0.063$) to be less among calves that were sampled last in the pen. Whole blood from the calves sampled last also tended ($P = 0.060$) to kill less *E. coli* 0111:H8. Similarly, the calves sampled last had decreased ($P = 0.043$) neutrophil oxidative burst response to the *E. coli* 0111:H8. These data indicate that it is important to control for the latency until sample collection associated with handling and movement when designing ex vivo immunological studies with beef calves.

Key words: immunity, cattle, stress

T6 Characterization of bovine leukocyte differentiation molecules in Egyptian cattle using flow cytometry. G. S. Abdellrazeq*[1], M. M. El-Naggar[1], and W. C. Davis[2], *[1]Alexandria University, Edfina, Behara province, Egypt, [2]Washington State University, Pullman.*

Evaluation of the efficacy and cross-protectivity of any applied vaccine in Egypt requires preliminary studies to investigate the characteristics of the immune system in a chosen farm animal species including the proportions of subpopulations of leukocytes. In this report, we investigate the comparative changes of leukocytes, T cell subsets and MHC molecules. Twenty ml blood samples were collected from healthy Egyptian cattle from young (age ~6–8 mo, no 4) and adult cattle(age ~3–5 year, no 4). Blood was processed, stained with a panel of monoclonal antibodies (mAbs) and analyzed by flow cytometry (FC). FC analysis revealed that the whole leukocyte population in young animals was composed of granulocytes representing about 30%, monocytes representing about 11% and lymphocytes representing about 59% while in adult animals, the granulocytes represent about 22%, monocytes represent about 7% and lymphocytes represent about 71%. CD4+ T cells represent about 41% of T cells in young animals and the proportion of this cell subset represents about 44% of T cells in adult animals. The CD8+ T cell subset was found to represented about 22% of T cells in young animals while representing about 41% of T cells in adult animals. We conclude that the age-related changes of leukocytes and T cell subsets in Egyptian cattle are basically the same as those found in pure Holstein cattle. These results will serve as a reference value and need to be taken in consideration when attempting to analyze the immune response in Egyptian cattle to M. a. paratuberculosis and other pathogens and their derived vaccines.

Key words: leukocyte differentiation molecules, flow cytometry, Egyptian cattle

T7 Comparative evaluation of gene expression in bovine and caprine neutrophils. M. Worku*, N. Mikiashvili, and H. Ishamel, *North Carolina A&T State University, Greensboro.*

Recognition and destruction of bacteria by polymorphonuclear neutrophil leukocytes (PMN) is a major defense against infections by pathogens. Impaired innate immune defense to gram-negative *Escherichia coli* infections is associated with delayed influx of PMN into the mammary gland. An evaluation of gene expression in response to exposure to *Escherichia coli* O111-B4 lipopolysaccharide (LPS) was conducted in isolated bovine and caprine PMN. Blood samples were collected from 3 Holstein Friesian cows and 3 Spanish × Boer goats. Isolated blood PMN, were incubated with LPS (0, 10 or 100 ng/ml, at 37C for 15 or 30 min in the presence of 95% humidity and 5% CO2).Eight cytokines were measured in cell culture supernatants using Signosis Inflammation ELISA Strips for quantitatively profiling and measuring TNF-α, IFNr, G-CSF, GM-CSF, IL-1a, IL-8, IP-10, and Rantes. Quantitative reverse transcriptase-PCR was employed to test the synthesis of specific mRNAs. Both bovine and caprine neutrophils

expressed TLR4 (452 bp) and CD14 (600bp). Exposure to LPS significantly increased CD14, TLR4 ($P < 0.001$) and TNF α ($P < 0.05$), transcripts in cow PMN. In goat PMN exposure to 100ng LPS for 30 min increased transcripts for CD14 and TNF-α ($P < 0.05$). Changes were not observed with TLR4 transcript levels. Treatment affected secretion of TNF-α, IFNr, G-CSF, GM-CSF, IL-1a, IL-8, IP-10 and Rantes. Exposure to 100ng of *E. coli* LPS caused a strong induction of TNF-α, IFNr, G-CSF, GM-CSF cytokine synthesis, in cows. The concentrations of TNF-α and IL-8 increased 2 fold. Thus in both bovine and caprine neutrophils exposure to LPS results in transcription and translation involving TLR4 CD14, and TNFalpha. This response is affected by dose and exposure time to LPS and varied by species. The role played by neutrophils in immunity might be affected by species variations in gene expression.

Key words: neutrophil, TLR4, ruminant

T8 Detection and expression of the gene encoding low density lipoprotein receptor-related proteins 6 (LRP6) in goat peripheral blood. M. Worku*, H. Mukhtar, and N. Mikiashvilli, *North Carolina Agricultural and Technical State University, Greensboro.*

Previous studies in our lab have reported the identification and expression of Wingless (Wnt) 1 and Frizzled in the goat. Wnt ligands conduct their functions in canonical Wnt signaling by binding to 2 receptors, the single transmembrane low density lipoprotein receptor-related proteins 5 and 6 (LRP5/6) and 7 transmembrane Frizzled receptors. Polymorphisms of the LRP6 gene are associated with bone mineral density. The objectives of this study were to detect the LRP-6 gene and evaluate its expression in goat peripheral blood. Blood from goats (n = 9) was collected on FTA elute cards for DNA extraction and in PAXgene Blood tubes for RNA extraction. RNA samples were reverse-transcribed and the cDNA was obtained. Specific LRP6 primers were used for PCR amplification. The amplified product was run on a 1% agarose gel. GAPDH was used as loading control and primers in the absence of DNA were used as negative controls. Gels were stained with ethidium bromide and visualized. The amplicon was sequenced commercially and the BLAST tool was used to compare the sequence with the NCBI database. An ~400 bp fragment of LRP6 was present in genomic DNA and expressed at the RNA level the amplified sequences had 100% similarity to human LRP6. The results of this study show that LRP-6 is conserved between goats and humans. Human mutations in LRP6 cause early onset coronary disease, osteoporosis, late onset Alzheimer's and cancers. In goats osteoporosis has been reported to occur due to mineral deficiency and gastrointestinal parasitism. Further, the goat has been developed as a large osteoporotic animal model that resembles human osteoporotic changes. Thus, this gene could aid in studies in skeletal development and diseases of goats and humans.

Key words: goat, osteoperosis, Wnt LRP6

T9 Comparison of commercially available enzyme-linked immunosorbent assay with serum neutralization for measuring bovine viral diarrhea virus specific antibodies. M. Gonda*[1], X. Fang[1], G. Perry[1], and C. Maltecca[2], *[1]South Dakota State University, Brookings, [2]North Carolina State University, Raleigh.*

Our laboratory is focused primarily on mapping loci that affect bovine viral diarrhea virus (BVDV) vaccine response in beef cattle. Several methods for measuring humoral BVDV vaccine response are available: 1) a BVDV antibody enzyme linked immunosorbent assay (ELISA) which measures total BVDV antibodies, and 2) serum neutralization (SN) which measures only protective antibodies specific for BVDV-1 or BVDV-2. The SN tests are more biologically relevant, but the ELISA is cheaper and faster for measuring BVDV antibodies, and could be effectively used if the ELISA and SN tests were highly correlated. Our objective was to test if BVDV total antibody ELISA sample-to-positive (S/P) ratios were correlated with BVDV-1 and BVDV-2 SN antibody titers. A total of 406 blood samples were collected from 193 Angus and Angus cross calves raised in 2 South Dakota beef herds that vaccinate cows for BVDV-1 and BVDV-2. Serum or plasma were collected from blood and then BVDV-specific antibody concentration was measured on each sample by 1) IDEXX (Liebefeld-Bern, Switzerland) antibody ELISA, 2) BVDV-1 SN, and 3) BVDV-2 SN. Higher BVDV ELISA S/P ratios were positively correlated with higher BVDV-1 SN ($\rho = 0.809$) and BVDV-2 SN ($\rho = 0.638$) titers ($P < 0.0001$), although the relationship was weaker when SN titers were <1:64. Higher BVDV-1 SN titers were also correlated with higher BVDV-2 SN titers ($\rho = 0.708$; $P < 0.0001$). We conclude that IDEXX BVDV total antibody ELISA S/P ratios can be used as a surrogate for BVDV-1 and BVDV-2 SN antibody titers when mapping loci affecting BVDV vaccine response.

Key words: ELISA, serum neutralization, bovine viral diarrhea virus

T10 Effects of *Camellia* L. plant extract and mannan-oligosaccharide on growth performance, gut health, blood parameters, cecal microflora and immunity of broiler chicks. K. Hatami and M. Zaghari*, *Department of Animal Science, College of Agriculture and Natural Resource, University of Tehran, Karaj, Karaj, Alborz, Iran.*

An experiment was conducted with 128, 1-d-old, male broilers to investigate the effects of saccharicterpenin (composed of triterpenoid saponin and saccharide from the plant Camellia L.; CL) and Techno-Mos (rich in mannan-oligosaccharides and β-1,3-glucanes) on growth performance, gut health, blood parameters, cecal microflora and immune response of broiler chicks. Experiment was done as a completely randomized design with 4 treatments (control, 0.3 and 0.5 g/kg CL and 0.5 g/kg mannan-oligosaccharide), 8 replicates and 4 chicks in each battery cage. Two basal diets were formulated for starter (1 to 21) and grower (22 to 42) periods and levels of CL and MOS were added to basal diet. Body weight gain, feed intake and feed conversion ratio were measured at 21, 35 and 42 d of age. Plasma triglyceride, cholesterol, LDL, VLDL and HDL concentrations were measured at 42 d of age. Differential counting of monocytes, lymphocytes, eosinophils and neutrophils percent were done at 42 d of age. pH of gastrointestinal sections were measured at 42 d of age. Effects of diet on villi length and crypt depth were measured at 42 d of age. Immune response to PHA-P was measured at 35 and to SRBC at 28 and 42 d of age. Supplementation of diets with 0.5 g/kg CL decreased body weight gain, feed intake and feed conversion ratio significantly throughout the experiment ($P < 0.01$). Proventriculus, gizzard and ileum pH differed among the treatment but duodenum and jejunum pH were not affected ($P < 0.05$). Supplementation of diets by CL and MOS affected cholesterol level of plasma but had no effect on plasma levels of triglyceride, LDL, HDL ($P < 0.03$). Cecal microbial population did not differ among treatments. Supplementation of diets with CL and MOS significantly increased villi length and crypt depth ($P < 0.0001$). CL had no effect on immune response against PHA-P at 36 d of age, however an increase was observed with addition of CL and MOS, also CL and MOS decreased antibody titer against SRBC at 28 d of age($P < 0.01$).

Key words: *Camellia* extracts, performance, mannan-oligosaccharide

T11 Gastrointestinal nematode infection in Nelore and crossbred cattle. M. C. S. Oliveira*[1], M. C. D. Beraldo[2], E. Nakandakari[3], L. Boschini[1], M. M. Alencar[1], R. Giglioti[4], A. C. S. Chagas[1], B. Rubert[5], S. C. Bogni[2], and A. M. G. Ibelli[5], *[1]Embrapa Pecuaria Sudeste, São Carlos, SP, Brazil, [2]UNICEP, São Carlos, SP, Brazil, [3]Uniara, Araraquara, SP, Brazil, [4]UNESP, Jaboticabal, SP, Brazil, [5]UFSCAR, São Carlos, SP, Brasil.*

Cattle nematodes in Brazil are mainly controlled through application of anthelminthics. However, this causes concern about the presence of drug residues in meat and dairy products, prompting studies of alternative control methods. Among these, the use of animals that are genetically resistant is a very promising complementary strategy. Resistance to gastrointestinal nematodes was compared in males and females Nellore (NI, n = 28) and a 3 breed cross, 1/2 Angus 1/4 Canchim (5/8 Charolais + 3/8 *Bos indicus*) + 1/4 Nelore (TC, n = 17) that were born from October to December 2008. The animals were kept without treatment, in rotational paddocks of Tanzania grass. Monthly collections were conducted totaling 810 observations (August 2009 to January 2011). The feces samples were collected from each animal for fecal cultures and determination the number of eggs per gram of feces (EPG). Blood samples were collected monthly for packed cell volume determination (PCV) that was an indicator of animal health. The count data of EPG were submitted to log10 (n+1) transformation. The data were analyzed using the MIXED procedure of SAS (2002–2003), according to a model considering repeated measures on the animal, structured with a compound symmetry variance matrix, and also included the effects of genetic group, sex, month/year of collection and 2-way interactions involving these 3 factors. The means of PCV were significantly higher ($P < 0.01$) for NI animals (40.6%) compared with TC (38.6%). No significant effects of genetic groups or interaction between the genetic groups and month/year of collection on the EPG were found, but there was a significant influence of the month/year of collection ($P < 0.01$). The following nematode genera were found in the coprocultures: *Haemonchus*, *Cooperia*, *Esophagostomum* and *Trichostrongylus*, the latter in smallest proportion. There was no significant difference between the genetic groups for averages of all parasites identified, except *Cooperia*, which were present in higher numbers in the animals of the NI group ($P < 0.05$). These data confirm previous findings that showed greater susceptibility of purebred Nellore animals to *Cooperia*.

Key words: nematodes, resistance, cattle

T12 Concentrations of haptoglobin in bovine plasma determined by ELISA or a colorimetric method based on peroxidase activity. R. F. Cooke*[1], B. I. Cappellozza[1], F. N. T. Cooke[1], D. W. Bohnert[1], and J. D. Arthington[2], *[1]Oregon State University–Eastern Oregon Agricultural Research Center, Burns, [2]University of Florida–Range Cattle Research and Education Center, Ona.*

Our laboratory determines plasma concentrations of haptoglobin using a low-cost colorimetric procedure that measures haptoglobin-hemoglobin complexing by estimating differences in peroxidase activity (CPPA). Results are expressed as arbitrary units based on absorption readings, given that the CPPA method does not contain a standard curve. Conversely, commercially available ELISA methods generate results based on standards with known haptoglobin concentrations. Therefore, the objective of this study was to determine if the CPPA method generates results compatible with a commercial ELISA kit. Nine Angus steers were vaccinated against *Mannheimia haemolytica* (One Shot, 2 mL s.c) to stimulate an acute-phase response and blood samples were collected before vaccination (d 0), and on d 1, 3, 5, 7, and 10. Plasma samples were frozen in triplicates at −80°C. One set of the triplicates was analyzed for haptoglobin concentrations using the CPPA procedure. A day effect was detected ($P < 0.01$) given that haptoglobin peaked on d 1, 3, and 7 relative to vaccination. A second set of the triplicates was analyzed using a commercial ELISA kit. A similar day effect ($P < 0.01$) was detected. When Pearson coefficients were calculated among results obtained from CPPA and ELISA methods, a strong correlation was detected (r = 0.98; $P < 0.01$). Based on the ELISA results, the plasma sample with the greatest haptoglobin concentration was serially diluted with PBS (1:1 through 1:32 dilution) and used as known reference to generate a standard curve for samples from the third set of triplicates analyzed with the CPPA method. A linear standard curve was generated ($r^2 = 0.99$) and a day effect ($P < 0.01$) was again detected. However, the values generated by the CPPA procedure with standard curve differed ($P < 0.01$) when compared with those generated by ELISA. In conclusion, assessing concentrations of haptoglobin in bovine plasma using the CPPA method yields results highly correlated to ELISA. Therefore, the CPPA method can be adopted to evaluate plasma haptoglobin concentrations in cattle when absolute values are not required.

Key words: bovine, haptoglobin, assay

T13 Feed and water restriction elicits an acute-phase protein response in beef cattle. B. I. Cappellozza*, R. F. Cooke, C. Trevisanuto, V. D. Tabacow, F. N. T. Cooke, and D. W. Bohnert, *Oregon State University–Eastern Oregon Agricultural Research Center, Burns.*

The acute-phase protein response is an important component of the innate immune system, but can be highly detrimental to cattle productivity. A comprehensive understanding of the causes and mechanisms that stimulate the bovine acute-phase protein response is required for development of management strategies to modulate this immune reaction. Therefore, the objective of this study was to determine if feed and water restriction stimulates an acute-phase protein response in overtly healthy beef steers. Nine Angus × Hereford steers were ranked by initial BW (average 244 ± 8 kg) and assigned to 1 of 2 treatments: 1) CONT - ad libitum access to feed and water during the study (d 0 to d 10), and 2) RESTR - feed and water restriction for 24 h (d 0 to d 1 of the study) and subsequent ad libitum access to feed and water (d 1 to d 10). Blood samples were collected from all steers on d 0 (before restriction period), 1 (at the end of the restriction period), 3, 5, 7 and 10. Samples were harvested for plasma, and immediately stored at −80°C until analyzed for concentrations of haptoglobin and ceruloplasmin. Hay DMI was evaluated daily by measuring refusals. Results were analyzed with the MIXED procedure of SAS. Plasma haptoglobin concentrations tended to be greater ($P = 0.06$) for RESTR steers compared with CONT on d 3 of the study (6.35 vs. 4.62 absorbance at 450 nm × 100, respectively). Plasma ceruloplasmin concentrations tended to be greater ($P = 0.15$) for RESTR steers compared with CONT on d 3 (18.0 vs. 14.4 mg/dL, respectively) and d 7 of the study (19.3 vs. 15.8 mg/dL, respectively). A treatment × day interaction was detected ($P = 0.01$) for hay DMI because RESTR steers had greater ($P < 0.01$) hay DMI on d 1 (2.98 vs. 1.97% of BW, respectively) and tended to have greater ($P = 0.11$) hay DMI on d 2 (2.74 vs. 2.32% of BW, respectively) compared with CONT steers. Results from this study indicate that feed and water restriction elicits an acute-phase protein response in overtly healthy beef cattle, which may detriment subsequent health and productivity parameters.

Key words: acute-phase proteins, feed and water restriction, beef cattle

T14 Natural infestation by external parasites in beef cattle in southern Brazil. M. C. S. Oliveira*[1], E. Nakandakari[2], M. C. D. Beraldo[3], M. M. Alencar[1], A. C. S. Chagas[1], L. Boschini[1], R. Giglioti[4], and A. M. G. Ibelli[5], *[1]Embrapa Pecuaria Sudeste, São Carlos, SP, Brazil, [2]UNIARA, Araraquara, SP, Brazil, [3]UNICEP, São Carlos, SP, Brazil, [4]UNESP, Jaboticabal, SP, Brazil, [5]UFSCAR, São Carlos, SP, Brasil.*

The existence of genetic differences between groups regarding the degree of infestation by external parasites suggests the possibility of using crosses between breeds to increase the benefits of complementarity and heterosis for adaptive traits. In this experiment natural infestations were compared in males and females Nellore (NI, n = 28) and a 3 breed cross, 1/2 Angus 1/4 Canchim (5/8 Charolais + 3/8 *Bos indicus*) + 1/4 Nelore (TC, n = 17) that were born from October to December 2008., regarding the resistance to the tick *Rhipicephalusmicroplus*, to the horn fly (*Haematobia irritans*) and the botfly (*Dermatobia hominis* larvae). The animals were kept without chemical treatment, in rotational paddocks of Tanzania grass. Monthly collections were conducted totaling 810 observations (August 2009 to January 2011), being counted all engorged female ticks with more than 4.5 mm diameter located on the left and the botfly around the animal's body. Horn flies were counted with the aid of photographs of the lumbar region. Blood samples were also collected monthly for packed cell volume determination (PCV) that was an indicator of animal health. The count data of external parasites were submitted to log10 (n +1) transformation and analyzed using the MIXED procedure of SAS (2002–2003) according to a model considering repeated measures on the animal, structure with a compound symmetry variance matrix, and included the effect of genetic group, sex, month/year of collection and interactions involving these factors. The means of PCV were significantly higher for NI animals (40.6%) compared with TC (38.6%), and there was significant influence of collection month/year ($P < 0.01$). Animals of NI group had lower external parasites infestations than TC animals ($P < 0.01$). Means and standard errors for NI and TC animals were, respectively, 0.07 ± 0.01 and 0.36 ± 0.02 for *R. microplus*, 0.86 ± 0.05 and 1.25 ± 0.06 for *H. irritans* and 0.06 ± 0.03 and 0.47 ± 0.04 for *D. hominis* larvae. These results indicate that the control of external parasites should be done differently for each genetic group.

Key words: cattle, parasites, resistance

T15 Cinnamaldehyde enhances in vitro parameters of immunity and reduces severity of in vivo infection against avian coccidiosis. S.-H. Lee[1], H. Lillehoj*[1], S. Jang[1], K. Lee[1], and D. Bravo[2], *[1]Animal and Natural Resources Institute, ARS USDA, Beltsville, MD, [2]Pancosma S.A., Le Grand Saconnex, Geneva, Switzerland.*

We examined the effects of cinnamaldehyde (CINN) on in vitro parameters of immunity (splenocyte proliferation, macrophage activation, and killing of tumor cells and parasites), and in vivo protection against avian coccidiosis (body weight gain, oocysts production, antibody responses, and intestinal cytokine levels). In vitro stimulation of chicken spleen lymphocytes with CINN (25, 50, 100, and 400 ng/ml) induced greater cell proliferation compared with the media control ($P < 0.001$). CINN activated cultured macrophages to produce higher levels of nitric oxide at 1.2, 2.5, and 5.0 μg/ml ($P < 0.001$), inhibited the growth of chicken tumor cells at 0.6, 1.2, and 2.5 μg/ml ($P < 0.001$), and reduced the viability of *Eimeria tenella* parasites at 10 and 100 μg/ml ($P < 0.01$ and $P < 0.001$, respectively), compared with media controls. In in vivo experiments, chickens were fed a non-supplemented diet (control) or a diet supplemented with 14.4 or 125 mg/kg of CINN from hatch for 14 d. The levels of IL-1β, IL-6, IL-15, and IFN-γ transcripts produced by intestinal lymphocytes were 2- to 47-fold higher in CINN-fed chickens compared with controls ($P < 0.001$). To determine the effect of CINN-supplemented diets on body weight gain and excretal oocyst shedding following *E. tenella*, *E. acervulina*, *E. maxima* infection, chickens were fed a non-supplemented diet (control) or diets supplemented with 125 (*E. acervulina*-infected birds) or 14.4 mg/kg (*E. maxima*- or *E. tenella*-infected birds) of CINN from hatch for 24 d, and uninfected or orally infected with 2 × 10,000 sporulated oocysts of the homologous parasites at 14 d of age. CINN-fed chickens showed 16.5% and 41.6% increased body weight gains between 0 and 9 d post-infection (DPI) with *E. acervulina* or *E. maxima*, reduced *E. acervulina* oocyst shedding between 5 and 9 DPI, and increased *E. tenella*-stimulated EtMIC2 antibody responses at 9 DPI compared with controls. This study provides the first evidence that CINN enhances in vitro and in vivo parameters of immunity against experimental avian coccidiosis.

Key words: cinnamaldehyde, chicken, immunity

T16 Comparison of different levels of vitamin premix on chicken meat quality in floor and battery cage broiler raising. M. A. Shahrasb, H. Moravej, and M. Shivazad*, *Department of Animal Science, Faculty of Agriculture and Natural Resources, Tehran University.*

This experiment was conducted to comparison of different levels of vitamin premix (VP) on broiler finisher diets at 29 to 42 d of age on meat quality in floor and battery cage rearing systems. A total of 616 male broiler chicks (Ross 308) were allocated to 7 treatment groups (different levels and access time to VP), with 4 replicates per treatment group and all data were analyzed in a randomized complete block design. The oxidative stability, evaluated by thiobarbituric acid reactive substances (TBARS) on the thigh meat samples that storage 180 d in −20°C. The results of TBARS values in trial floor system showed there are not significant differences between TBARS values of thigh meat samples for birds slaughtered at 35 d of age, however, at 42 d of age TBARS values of treatments without VP were significantly higher than other treatments ($P < 0.05$). The results of TBARS values in trial battery cage system showed the highest TBARS values of treatments belong to the treatment without VP at 35 d of age ($P < 0.05$), although TBARS values of treatments without VP and 33% VP were significantly higher than other treatments of thigh meat samples for birds slaughtered at 42 d of age ($P < 0.05$). Finally, the results of this study demonstrated that (1) it is not possible withdrawal but it can be possible to reduce VP in finisher broiler diets without negative effects on performance and meat quality during the time of freezing in both methods of rearing; (2) it is possible to reduce the VP levels in diet of broilers rearing in floor system more than cage system.

Key words: broiler, vitamin premix, meat quality

T17 Effects of feeding OmniGen-AF to rats on gastrointestinal gene expression: Microarray analysis. B. R. Ou[2], Y. Q. Wang[1], and N. E. Forsberg*[1], *[1]OmniGen Research, Corvallis, OR, [2]Tunghai University, Taichung, Taiwan, ROC.*

OmniGen-AF is widely fed in the United States dairy industry and has been reported to reduce somatic cell counts and improve herd health. Yet, the fundamental mechanism(s) by which this product brings about these benefits remains unknown. Our hypothesis was that, because the product is fed, it alters gastrointestinal (GI) gene expression. To test

this hypothesis, 16 growing male CD rats (ca. 225 g) were assigned to 2 treatments: a control treatment (fed a Teklad 8604 powdered diet) and an OmniGen-AF treatment (Teklad supplemented with 0.5% w/w OmniGen-AF [Prince Agri Products, Quincy, IL]). Rats were maintained on diets for 28 d then euthanized. A 10 cm portion of small intestine was removed from each rat and RNA preserved via Trizol. Quality of RNA was assessed in an Agilent Bioanalyzer. RNA was hybridized to Agilent arrays containing 23000 genes. Normalization of the probe set was performed using the Robust Multiarray Analysis method. Gene expression intensities were compared using a moderated *t*-test and a Bayes smoothing approach. Analysis was performed using the affylmGUI Graphical Interface for the Limma microarray package. Differentially expressed genes and pathways were derived using DAVID functional analysis. Of the 23000 genes on the array, 288 were upregulated and 385 were downregulated ($P < 0.05$). DAVID pathway analysis identified 13 GI pathways which were specifically affected ($P < 0.05$) by the additive. Of these 13 pathways, 6 were related to "immune function." These included complement and coagulation, antigen processing and presentation, autoimmune thyroid disease, allograft rejection, graft versus host disease and viral myocarditis. Other regulated pathways included starch and sucrose metabolism and endocytosis. A limitation of these data are that we do not know which cell type, of the many GI cell types, was affected by feeding the product. Still, these data demonstrate that significant changes in GI metabolism apparently result from feeding the product. We propose that any nutrient or additive will similarly exert changes in GI gene expression. The specific pathways/patterns affected likely underlie efficacy.

Key words: OmniGen-AF, gene expression, intestine

T18 Inhibition of inflammatory processes in Caco-2 intestinal epithelial cells by an ethanolic extract of a polyphenol-rich grape seed meal. R. Ringseis[1], M. Siebers[1], J. Keller[1], A. Steinbeck[2], B. Eckel*[2], and K. Eder[1], *[1]Institute of Animal Nutrition and Nutrition Physiology, Justus-Liebig-University Giessen, Giessen, Germany, [2]Dr. Eckel GmbH, Niederzissen, Germany.*

Several pathologic stimuli, including bacteria and viruses, are known to stimulate inflammatory processes in the intestinal mucosa by cytokine-mediated activation of the proinflammatory transcription factor NF-κB. Through the subsequent release of inflammatory mediators which enter the circulation, the inflammatory process may also affect other tissues, and cause stimulation of protein catabolism in skeletal muscle and formation of acute phase proteins in the liver. Considering that such processes lead to an impairment of animal performance, the inhibition of inflammatory processes in the intestine is a reasonable approach to maintain performance characteristics of livestock animals. Therefore, the objective of the present study was to explore the anti-inflammatory potential of a polyphenol-rich grape seed meal (AntaOx E) using Caco-2 intestinal epithelial cells. Caco-2 cells were grown to confluence, and differentiated for 6 days. Subsequently, the differentiated Caco-2 cells were treated with the cytokine TNFα alone as a control or with TNFα and different dilutions of an ethanolic extract of AntaOx E for 24 h. Cell viability of Caco-2 cells treated with increasing dilutions of the ethanolic extract of AntaOx E was not impaired. Reporter gene assays using an NF-κB-driven reporter plasmid revealed that the lowest dilutions (1.00E-03, 1.00E-04) of the ethanolic extract of AntaOx E inhibited the TNFα-induced transactivation of NF-κB by 35% and 25% ($P < 0.05$), respectively, whereas higher dilutions (1.00E-05, 1.00E-06) had no effect. Moreover, the lowest dilution (1.00E-03) of the ethanolic extract of AntaOx E reduced the TNFα-induced mRNA levels of the NF-κB target genes IL-1β, IL-8, MCP-1 and CXCL10 by 20 to 35% ($P < 0.05$). It is shown that AntaOx E is capable of inhibiting the activation of the proinflammatory transcription factor NF-κB and, thereby, the expression of several inflammation-related genes in intestinal epithelial cells. Thus, polyphenol-rich grape seed meal may be useful in the inhibition of inflammatory processes in the intestinal mucosa of livestock animals.

Key words: inflammation, intestine, phytochemicals

T19 Association of slaughter and dressing traits with ultrasound and computed tomography data in cattle. G. Hollo*[1], J. Tõzsér[2], A. Szentléleki[2], F. Szabo[3], I. Anton[4], T. Somogyi[1], I. Repa[1], and I. Hollo[1], *[1]Kaposvár University, Kaposvár, Hungary, [2]St. István University, Gödöllö, Hungary, [3]Pannon University, Keszthely, Hungary, [4]Research Institute for Animal Breeding and Nutrition, Herceghalom, Hungary.*

The aim of this study was to establish the relationship among slaughter and dressing traits as well as cross sectional imaging data measured by ultrasound (UH) and x-ray CT method (CT) in cattle. Seventy growing-finishing bulls from 6 different genotypes were used. The animals were kept and fed under the same condition. Animals were ultrasound scanned (Falco 100, Pie Medical) for Longissimus muscle area between 12-13th rib (UHLMA), backfat thickness (P8) and rump fat (RF) determinations (average live weight of 398 kg). The target live weight was determined at 600 kg. At slaughter, slaughter weight (SW), hot carcass weight (HCW), kidney fat proportion (KF) and EU beef carcass classification data were recorded. After 24 hr chilling the right sides of carcasses were dissected. For the CT-analysis (Siemens Emotion 6) ribs joint was removed from right half carcasses between 11-13th ribs. Areas and proportions of muscle, fat and bone tissue were calculated and the area of Longissimus muscle (CTLMA) was measured. For estimation of linear association Pearson correlation analysis and multi- and bivariate regression were applied (SPSS 10.0). Slaughter data moderately correlated with UH and CT data. The KF positively related to P8 (r = 0.52) and RF (r = 0.53) as well as CT-fat area (r = 0.77) and CT-fat percentage (r = 0.78). A positive relationship was determined between EU conformation score and UHLMA (r = 0.59) and CTLMA (r = 0.66). The EU fatness score showed a higher relationship with RF (r = 0.42) than P8 (r = 0.57). The lean % and fat % in carcass correlated closer with CT-muscle and CT-fat % in rib joint (r = 0.85; r = 0.92) than UH data (r = 0.39; r = 0.65). Predictors derived from CT alone accounted for a high proportion of the variance in dissected fat proportion (R^2 = 0.85), but lower proportions for dissected lean meat yield (R^2 = 0.77). For predicting lean weight from combinations of HCW and UH measurements the R^2 value found 0.87. R^2 of 0.83 was measured for fat weight using UHLMA and CT fat area. In conclusion, the in vivo UH measurements and CT scanning of rib joint can provide opportunities to estimate the beef carcass value objectively.

Key words: cattle, carcass composition

T20 Effect of arrival health risk status of steer calves on feedlot performance and health during a 61-d preconditioning program. C. Flaig[1], L. Clark[1], O. C. Schunicht[1], M. L. May[1], R. E. Peterson[1], C. W. Booker[1], R. Krehbiel[2], G. K. Jim[1], B. P. Holland[3], and L. O. Burciaga-Robles*[1], *[1]Feedlot Health Management Services Ltd., Okotoks, Alberta, Canada, [2]Department of Animal Science, Oklahoma State University, Stillwater, [3]Department of Animal and Range Sciences, South Dakota State University, Brookings.*

Ranch-direct steer calves (n = 120; BW = 289 ± 6.84 kg; RANCH) and ultra-high risk steer calves (n = 120; BW = 250 ± 6.84 kg; UHR) were allocated to evaluate the effect of risk status at arrival on feedlot performance and health during a 61-d preconditioning program. Arrival processing included a metaphylactic treatment for control of BRD and proprietary health procedures based on animal health risk assessment (Feedlot Health Management Services, Ltd. Okotoks, Alberta, Canada) and individual numbered and electronic ear tags were also applied. Intact males were band castrated. After initial processing, cattle of the same risk group were randomly allocated to one of 6 pens (40 head/pen) equipped with individual feed intake data collection systems (GrowSafe Systems Ltd., Airdrie, Canada) and fed for 61 d. Cattle were observed by trained personnel for detection and treatment of disease during the trial. Cattle were re-weighed on d 30 and d 61. Animal performance was analyzed using PROC GLIMMIX (SAS Institute, NC). Animal was the experimental unit, and the model included the fixed effect of treatment and the random effect of replicate. Initial body weight was heavier for RANCH than UHR (289 vs. 250 ± 6.50 kg; $P < 0.001$) and it was included as a covariate in the model. Animal health parameters were analyzed using the chi-squared procedure of SAS. A total of 24 animals (15 RANCH and 9 UHR) were removed from the trial and not included in the analysis. In addition, 2 (1.67%) RANCH and 1 (0.80%) UHR died ($P = 0.56$) and were removed from the analysis. Treatments for BRD were higher for RANCH vs. UHR calves (22.5 vs. 10.0%; $P = 0.01$). No differences in ADG, DMI, or FG ($P > 0.05$) were observed from d 0 to 30 and d 0 to 61. Based on these data, health risk status at arrival has no effect on feedlot performance; however based on the differential arrival health protocol, RANCH were treated more often for BRD than UHR during a 61-d preconditioning program. Economic modeling is important when determining arrival health protocols and purchase price based on health risk assessments of specific populations of cattle.

Key words: feedlot performance, health risk status, BRD

T21 Effect of residual feed intake on blood urea nitrogen concentration in growing heifers from an Angus-Brahman multi-breed herd. R. O. Myer[1], M. A. Elzo[2], G. C. Lamb[1], and N. DiLorenzo*[1], *[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 assess the effect of residual feed intake (RFI) on blood plasma concentration of urea N (PUN) in 85 growing beef heifers ranging from 100% Angus to 100% Brahman born in 2008. Calves were assigned to pens in a GrowSafe feeding facility by sire group and fed ad libitum a total mixed ration (62% chopped grass hay, 30% whole corn, 3% cottonseed meal, and 5% molasses-mineral-vitamin supplement; 90% DM, 11% CP, and 68% TDN). The pre-trial adjustment period lasted 14 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 −10, 0, 56, and 70 for PUN. Residual feed intake (RFI) was computed as the difference between actual and expected intakes. Data (PUN) were analyzed using a mixed model. Fixed effects were pen, age, RFI of calf, Brahman fraction of calf, heterozygosity of calf, and daily feed intake. Random effects were sire and residual. Overall ADG was 0.91 ± 0.02 kg/d. Brahman had higher PUN concentrations at each sampling day compared with Angus ($P < 0.01$). Only d −10 PUN concentration was slightly related to RFI ($P = 0.07$), in that low RFI cattle also had low PUN beyond that expected due to the lowered feed intake; the other sampling days were not affected by the RFI of the calf ($P > 0.10$). Results indicate that PUN concentration appeared to be little affected by RFI beyond that accounted for by reduced feed intake.

Key words: beef cattle, blood urea, feed efficiency

T22 Post-weaning feed efficiency of tropically adapted purebred and crossbred calves when fed in either winter or spring. S. W. Coleman*[1], C. C. Chase[1], W. A. Phillips[2], and D. G. Riliey[1], *[1]USDA ARS Subtropical Agricultural Research Station, Brooksville, FL, [2]USDA, ARS, Grazinglands Research Laboratory, El Reno, OK.*

Earlier work has shown that young, tropically adapted (Brahman and Romosinuano) cattle do not gain as rapidly as temperately adapted (Angus) cattle during the winter in OK. The objective for this study was to compare efficiency of gains between tropically- and temperately-adapted cattle breeds. Over 3 yr, 239 purebred and crossbred steers (F1 and 3-way crosses) of Angus, Brahman or Romosinuano breeding were born in Brooksville, FL, transported to El Reno, OK in October each year, and fed in 2 phases to determine individual intake and performance. Phase 1 (W, ~127 d) began in November and phase 2 (S, 56 to 162 d) began in March. A grower diet (14% CP, 1.10 Mcal NEg/kg) was fed in W and a conventional feedlot diet (12.8% CP; 1.33 Mcal NEg/kg) in S. Body weights were recorded at approximately 14 d intervals, ADG was determined by regressing BW on days on feed (DOF) within phase. Daily DMI was then regressed by phase on median BW and ADG to determine residual feed intake (RFI). Gain to feed (GF) was also calculated as a measure of efficiency. The statistical model included fixed effects of yr, harvest group (3 per year), age on test, and a nested term DT(ST x XB) where DT = proportion tropical breeding of dam (0, 0.5, or 1), ST = proportion tropical breeding of sire (1, or 0), and XB whether the calf was straightbred or crossbred. Sire(ST x XB) and pen were random effects. In the W, 100% tropical steers ate less, gained less, and were less efficient (GF) than steers with some Angus breeding ($P < 0.01$), but not ($P > 0.10$) by RFI. Gain and efficiency in the S phase were not different ($P > 0.05$) due to tropical influence. Simple correlations between RFI of the same animal in W and S were 0.51 ($P < 0.01$) whereas that for GF was 0.20 ($P < 0.01$). Poor performance of tropically adapted steers as stockers in OK during the winter apparently resulted from a decrease in both feed intake and feed efficiency.

Key words: tropical adaptation, postweaning feed efficiency, seasonal performance

T23 Finishing steers and bulls with high-vitamin E diets: Effect on circulating immune cells and creatine kinase after a mild stress. C. Reyes, C. Fuentes, and R. E. Larraín*, *Pontificia Universidad Catolica de Chile, Santiago, Chile.*

Release of glucocorticoids to the blood stream after stress may change the number of immune cells circulating in blood within minutes. A stressful event may also increased creatine kinase (CK) in blood if muscle tissue is damaged or mobilized. Vitamin E reduced activation of the hypothalamic-hypophysial-adrenocortical axis in farm animals, so the objective of this study was to test if finishing bovines with a high vitamin E diet modulate changes in immune-cells counts and CK after a mild stress. Thirty-eight steers and bulls were blocked by sex, then grouped in 16 pens of 2 or 3 animals of similar weight, and randomly assign to one of 2 treatments: a control diet design to provide 60 IU vitamin E•animal^{-1}•d^{-1} and the control diet supplemented with 2,000 IU vitamin E•animal^{-1}•d^{-1}. Each pen was considered an experimental unit (n = 8). Feed was offered once daily to each pen to provide ad libitum access to feed. After 105 d of feeding the experimental diets, all animals were subjected to a mild stressor consisting of 45 min restraint in a single-file chute, with 3 brief shots (about 0.5 s each) of an electrical cattle prod at 0, 15, and 30 min. Blood samples were taken by jugular venipuncture at d 0 (to be used as baseline for CK) and after stress. Factors in the model were sex and treatment, and initial BW was included as covariate. Differences were considered significant when ANOVA had $P < 0.05$. We observed no changes in any of the variables analyzed, concluding that feeding 2,000 IU vitamin E•animal^{-1}•d^{-1} produced no changes in immune cells counts and CK after a mild stress.

Table 1. Immune cells (cells/μL) and creatine kinase (CK, U/L) after a mild stress in bovines fed vitamin E

Item	Control	Vitamin E	*P*-value
Leucocytes	9,448 ± 443	10,009 ± 439	0.35
Bacilliform	38.6 ± 23.6	66.1 ± 23.4	0.39
Neutrophils	2,858 ± 316	3,401 ± 313	0.21
Lymphocytes	5,870 ± 260	5,894 ± 258	0.94
Monocytes	99.5 ± 30.2	74.1 ± 30.0	0.53
Eosinophils	396 ± 52.3	345 ± 51.9	0.46
Basophiles	66.8 ± 16.3	32.4 ± 16.1	0.13
Change in CK from d0	−0.41 ± 29.2	−7.35 ± 29.0	0.86

Vitamin E: 2000 IU•animal^{-1}•d^{-1}.

Key words: vitamin E, immune cells, creatine kinase

T24 Quantitative genetics and differential performance and gene expression of half-sib families of hybrid striped bass in communal ponds. S. A. Fuller*, B. H. Beck, M. McEntire, and D. Freeman, *USDA ARS Stuttgart National Aquaculture Research Center, Stuttgart, AR.*

The US is one of the world's largest importers of seafood. A major constraint in producing hybrid striped bass is suboptimal production efficiency due to large performance variation of fish from undomesticated brooders. The objectives of this first-year study were to determine the genetic basis of production traits for selective improvement, and RNaseq superior and inferior performing representatives to identify global expression differences and develop predictive SNP markers as part of a multi-year improvement project. Domesticated F8 white bass and F4 striped bass were bred in a partial diallel breeding design and reared in replicate family tanks until large enough to tag with a PIT tag. Thirty-two fish from each of 44 half-sib families were tagged and initial length and weight was recorded before being randomly assigned to one of 4 0.04 ha communal ponds resulting in 5632 individually tagged fingerlings. Fish were allowed to grow for 115 d before harvest. At harvest tags were scanned to reveal family of origin, final length and weight were taken, fish were humanely sacrificed and a liver and muscle sample were flash frozen for qPCR and RNaseq analyses. Following pond production, hybrid striped bass averaged 235.3 ± 17.8 (SD)mm and 192.1 ± 48.7g across all families and ponds, with a range from 110 to 288mm and 47.3–371.7g. Analyses of covariance demonstrated highly significant differences in length and weight of fish among different paternal and maternal half-sib families with initial weight as the covariate ($P < 0.0001$). Estimates of heritability were high for both traits, with values for weight and length, respective, ranging from 0.74 to 0.97 for dams and 0.52 to 0.99 for sires. Liver RNaseq data are currently being analyzed from high and low performing families and individuals and SNP markers validated to identify markers for future marker assisted selection. Incorporating crossbred offspring performance into a genetic improvement program could be used to successfully produce more rapidly growing hybrid striped bass and improve the profitability of the industry.

Key words: hybrid striped bass, aquaculture, genetic improvement

T25 Effects of transgenic myostatin depression on reproductive parameters and placental superoxide dismutases in mice. S. Yarlagadda, C. N. Lee*, Y. S. Kim, J. Yang, and W. Y. Ho, *University of Hawaii-Manoa, Honolulu.*

Double muscled cattle carrying non-fuctional myostatin mutations have high incidences of dystocia, low calf viability and higher heat intolerance. Myostatin-null mice and transgenic mice with depressed myostatin function by its propeptide overexpression appeared normal in reproduction as no dystocia was observed in our colony. To gain insights into the effects of depressing myostatin on reproduction, we compared pelvic width, uterine length, hormonal profiles and the activities of placental superoxide dismutases (SOD) of transgenic mice overexpressing myostatin propeptide to those of their wild-type littermate controls. Ten pregnant transgenic females (TG, B6SJL strain) and 10 wild type females (WT) of greater than 2 mo old were used. Pelvic width of TG mice at 10 and 16 d of pregnancy was not different from wild type mice. Serum estrogen was not affected by genotypes while TG mice had higher concentrations of serum progesterone at 10 d of pregnancy than WT females (213 ± 38.9 pg/ml vs 101 ± 17.5 pg/ml, $P < 0.05$). However, by d16, WT females had higher serum progesterone vs TG females (447.4 + 37.3 pg/ml vs 318.4 + 37.1 pg/ml). Mn-SOD and Cu/Zn-SOD protein levels in placenta, 2 antioxidant defense proteins, decreased significantly from d 10 to 16 of pregnancy. However, their expression levels in placenta or ovarian tissue were not different between TG and WT mice. These results suggest that myostatin suppression has no effects on placental or ovarian tissue antioxidant proteins, serum estrogens and pelvic development.

Key words: myostatin suppression, superoxide dismutases, reproductive parameters

T26 Study of polymorphism at CSD gene in *Apis mellifera meda*. S. Karimi*[1], A. Nejati Javaremi[1], S. R. Miraei Ashtiani[1], and H. Alizadeh[2], *[1]University of Tehran, University College of Agriculture and Natural Resource, Department of Animal Science, Tehran, Karaj, Iran, [2]University of Tehran, University College of Agriculture and Natural Resource, Agronomy & Plant Breeding Department, Tehran, Karaj, Iran.*

About 20% of animal species have a haplodiploid system of sex determination. Males are haploid from unfertilized and females are diploid from fertilized eggs. It is known that a complementary sex determining (csd) gene is responsible for sex determination in honeybees. In this species, csd acts as the primary sex-determining signal with several alleles segregating in populations. Males are hemizygous and females are heterozygous at this locus; non-reproducing diploid males occur when the locus is homozygous. If inbreeding increases between bees, the possibility of cross between queen with drones with similar alleles at this locus will increase. Other studies indicated that this phenomenon leads to increase in the percentage of diploid drones in population which, in turn, leads to decrease of colony growth and, subsequently, economic losses. Genotypes of 17 queens from several apiaries were determined through genotyping of about 6 of their haploid drone progenies. A total of 108 samples from 16 colonies were made. RNA extraction was done with High pure RNA Isolation kit. Then sscDNA was produced by RevertAid MMulV RT enzyme. EF-1alpha was used as housekeeping gene and positive control. In the next stage with a pair of specific primers, the region between exons 5 and 9 of csd gene with 300 to 400 bp in length in different alleles was reproduced by using polymerase chain reaction. PCR product was run on 1.5% agarose gel and each of the 2 different alleles of each queen were sequenced. In cases where polymorphism could not be recognized by length differences of the PCR products, they were digested using SspI enzyme. Digested products were then run on the 6% polyacrylamide gel. Two different alleles of each queen were selected for sequencing. About 25 samples were sequenced. Seven functionally different alleles were found. Queens within the same apiary have more similar genotypes compared with the genotypes of queens form other apiary. Genotyping of queens of apiaries involved in production of commercial honeybee queens may help reduce the incidence of diploid drones.

Key words: haplodiploid, honeybee, drone

T27 Growth-related differential gene expression in the longissimus thoracis muscle of Iberian × Landrace back-crossed pigs. J. Casellas*[1,2], J. L. Noguera[2], R. N. Pena[2,3], J. M. Folch[1], M. Muñoz[4], and N. Ibáñez-Escriche[2], *[1]Departament de Ciència Animal i dels Aliments, Universitat Autònoma de Barcelona, Bellaterra, Spain, [2]Genètica i*

Millora Animal, IRTA-Lleida, Lleida, Spain, [3]Departament de Producció Animal, Universitat de Lleida, Lleida, Spain, [4]Departamento de Mejora Genética Animal, SGIT-INIA, Madrid, Spain.

The aim of this study was to identify growth-related differential gene expression in the longissimus thoracis muscle of finished pigs. A total of 102 Iberian (25%) × Landrace (75%) back-crossed pigs were reared under standard management conditions, weighted at 90 d (34.4 ± 0.6 kg), 105 d (43.6 ± 0.7 kg), 120 d (54.3 ± 0.8 kg), 135 d (65.0 ± 1.0 kg), 150 d (74.0 ± 1.1 kg), 165 d (86.8 ± 1.2 kg) and 175 d of age (96.1 ± 1.3 kg), and slaughtered at an average age of 179.9 ± 0.3 d. Samples of the longissimus thoracis muscle were collected at slaughter, snap frozen and stored until analysis. For each sample, total RNA was isolated and individually hybridized in the GeneChip Porcine Genome array (Affymetrix, Santa Clara, CA). After normalizing raw data with the RMA algorithm from the Bioconductor package, gene expression scores from 13,547 probes were analyzed with the GEAMM software under a multivariate mixed linear model accounting for the systematic effect of each array as well as 4 sources of variation modeled under normal priors: probe, sex (male or female), fattening batch (3 levels) and pig growth during fattening (continuous effect). Pig growth was calculated as the regression coefficient (i.e., slope) of pig weight against pig age across all weighting events during fattening (0.59 ± 0.1 kg/d). The Bayesian analysis launched a unique Monte Carlo Markov chain with 110,000 iterations, the first 10,000 of them being discarded as burn-in. Focusing on the link between pig growth and gene expression, 14 probes reached the significance threshold after correcting for multiple testing by false discovery rate ($\alpha = 0.05$; $P < 0.000052$), although 3 of them belonged to the same locus (GAPDH) and showed similar estimates. It is important to highlight that most of the significant loci could be grouped on the basis of their biological pathway, i.e., carbohydrate metabolism (ENO3, GAPDH, LDHA and PGM1), muscle contraction (MYL1 and TNNT3) and ribosomal structure (RPL36A).

Key words: gene expression, longissimus thoracis, pig growth

T28 Path analysis of candidate genes for intramuscular fat in pigs. N. V. L. Serão*[1,3], J. Braccini Neto[2], A. M. F. Ribeiro[3], P. V. Silva[3], S. L. Rodríguez-Zas[1], and S. E. F. Guimarães[3], *[1]University of Illinois at Urbana-Champaign, Urbana, [2]Universidade Federal do Rio Grande do Sul, Porto Alegre, RS, Brazil, [3]Universidade Federal de Viçosa, Viçosa, MG, Brazil.*

High levels of intramuscular fat (IMF) have generally a positive influence on the sensory experience associated with eating pork. This study aimed to identify gene expression profiles with direct and indirect association with IMF content in pigs. Longissimus dorsi samples from 72 male and female pigs representing 3 genetic groups slaughtered at different weights were used to quantify the IMF content and to measure the expression of 9 candidate genes: ATN1, EEF1A2, FABP3, LDLR, MGP, OBSCN, PDHB, RYR1 and TRDN. The IMF content was determined by ether extraction and expressed as percentage in fresh meat. Gene expression was measured using real-time PCR. To determine the basic causal model of the path analysis for IMF and associated genes, 10 path models were created. The first model included IMF as the outcome variable and the 9 genes as predictors. The other path models had one gene as outcome variable and the other 8 as predictors, until all 9 genes were used as the outcome variable. Predictor genes were selected in the model following a stepwise method ($P < 0.1$). Using these relations and path analysis, the associations between genes and IMF were inferred using the PATH statement of the TCALIS procedure (SAS version 9.2). The basic causal model was sequentially analyzed, removing the least significant relation at a time until all remaining genes were significant ($P < 0.05$). This model included 29 direct relations, where only FABP3, EEF1A2 and LDLR had direct effects on IMF. After a progressive selection, the final causal model included 13 direct relations ($P < 0.05$). The same direct predictors of IMF were kept, but ATN1 was dropped from the path model. The higher effect was observed from OBSCN to RYR1 (0.7219) and the smallest from MGP to RYR1 (−0.1785). All genes in the model acted as predictors and outcomes, with the exception of MGP (only as predictor). Genes FABP3 through LDLR and PDHB through FABP3 showed indirect effect of their expression on IMF. The results of this analysis provided an intuitive and comprehensive path diagram with estimates of direct associations among candidate genes, and direct and indirect associations between these genes and IMF.

Key words: gene expression, meat quality

T29 Evaluating statistical models to assess differential gene expression in PRRSV infected pigs using plasmode datasets. M. E. Arceo*[1], C. W. Ernst[1], M. Wysocki[2], J. K. Lunney[3], and J. P. Steibel[1], *[1]Department of Animal Science, Michigan State University, East Lansing, [2]Lehrstuhl für Tierzucht, Technische Universität München, Munich, Germany, [3]Animal Parasitic Diseases Laboratory, ARS, USDA, BARC, Beltsville, MD.*

Porcine reproductive and respiratory syndrome virus (PRRSV) causes substantial economic losses for US farms. The variability of pig response to PRRSV infection suggests a host genetic component involved in the pathogenesis of the disease. With data collected from Hampshire-Duroc cross and NE Index line pigs infected with PRRSV, Petry identified low (LR) vs. high (HR) PRRSV burden pigs (with low vs. high viremia, good vs. low/no weight gain, and few vs. many lung lesions). Microarray technology has been applied to identify differentially expressed genes using RNA from lung and bronchial lymph node (BLN) tissues of HR and LR pigs. The objective of this work was to use this data to assess different statistical models for analyzing microarray data using plasmode data sets. To build the plasmode data sets, we permuted array-treatment labels resulting in 34 independent data sets where no differential expression is expected, but the normal biological variation is conserved. Plasmode data were used to compare linear fixed models to linear mixed models. Test statistics that borrow information from data across all genes (moderated tests) to estimate variances and assess significance were also considered. Type I errors were evaluated at nominal 0.05, 0.01, 0.005, 0.001 and 0.0001 levels. To attain control of nominal type-one error rates, moderated tests required the use of permutations to compute p-values. We modified R/maanova software to obtain such permutations more efficiently (3-fold decrease in elapsed computational time) at the expense of reusing estimated variance components from the data. The most powerful results were obtained from a mixed effects model with moderated tests (Fs test) and unmodified permutation scheme (69 significant genes at FDR 10%). Using the modified permutation scheme resulted in less power than a fixed effects model with unmodified permutations (3 versus 21 significant differences at FDR 10%). In summary, powerful analysis of gene expression data remains a computationally challenging task. This work was supported by the PRRS CAP, USDA NIFA Award 2008–55620–19132.

Key words: PRRSV, microarray, linear models

T30 Structural changes at bovine IgE as related to variation at the DNA level. I. Rivera, M. Pagan*, E. Jimenez, and G. Ortiz, *Department of Animal Industry, University of Puerto Rico at Mayaguez, Mayaguez, PR.*

Bovine immunoglobulin E (IgE) was evaluated as a candidate gene to study potential variations in resistance to parasite infestation and anthelmintic efficiency. A DNA pooling and nucleotide sequence strategy was used to identify single nucleotide polymorphisms (SNPs) at the IgE heavy chain constant region gene (GenBank Accession no.: U63640). General (n = 319 bulls) and individual breed pools were constituted using DNA from Angus (n = 39), Senepol (n = 60), Charbray (n = 43), Charolais (n = 62), Bos Indicus (n = 39), and crossbred (n = 76) cattle. Polymerase chain reaction primers were designed to amplify regions of exons 1–3. At exon 1, a cytosine/guanine transversion and a cytosine/thymine transition resulting in silent mutations (threonine and serine, respectively) were identified. At exon 3, an adenine/guanine transition corresponding to an arginine to glycine amino acid change was recognized (only the Angus bulls were completely homozygous GG for such SNP). Meanwhile, exon 2 was highly polymorphic (n = 5 SNPs). Of the SNPs located in that part of the IgE gene, a cytosine/guanine transversion was silent (alanine). However, a cytosine/thymine substitution changed a polar amino acid (proline) by another (leucine). In this case, all the Charbray animals were classified as homozygous TT. The other 3 SNPs corresponded to a proline (non polar) to histidine (basic), proline to glutamine (polar), and an asparagine (polar) to aspartic acid change. In the last 2, homozygosity was observed within the Angus and Charolais breeds (AA and GG for Pro/Glu and Asp/Asn, respectively). Moreover, the SNP responsible of the Pro/His residue substitution was not segregating in Angus. Because polymorphism at IgE has been implicated in resistance to gastrointestinal nematodes infection in ovines, the structural changes reported herein in bovines needs further evaluation to elucidate potential association with immune response and overall health.

Key words: IgE, polymorphisms, bovine

T31 Association between SNPs in candidate genes and residual feed intake in Angus cattle. A. I. Trujillo*, A. Casal, P. Grignola, J. P. Marchelli, and P. Chilibroste, *Departamento de Produccion Animal y Pasturas, Facultad de Agronomia, Universidad de la Republica, Montevideo, Uruguay.*

Residual feed intake (RFI) is a measure of feed efficiency which is an economically important trait in livestock. Single nucleotide polymorphisms (SNPs) that show associations with RFI may be useful for marker-assisted selection. There is limited research examining the relationship between specific genes mutations and RFI. Neuropeptide Y (NPY), leptin (LEP) and insulin like growth factor-1 (IGF-1) are candidate genes due to their roles in the regulation of feed intake, energy balance, and growth. This study examined the relationship between SNPs previously identified in NPY (A/G, intron 2), LEP (C/T, exon 2) and IGF-1 (C/T, promoter region) genes with feed efficiency and performance in beef Angus calves. Thirty 8 female calves were selected from a total of 1700 genotyped calves born in spring 2009. Half of the calves were carrying 3 "favorable" alleles simultaneously (V, validation group) while the other half was carrying 3 "unfavorable" alleles (C, control group). Calves were allocated to individual pens in a completely randomized design (initial BW = 186.2 ± 32 kg). Individual feed intake (FI) and body weight (BW) were measured during 56 d. Calves were fed twice daily of a mixed diet (60:40 as fed) compound concentrate: chopped alfalfa hay. FI was estimated daily by difference between feed offered and refused. Phenotypic RFI was calculated as the residuals from a regression model regressing FI on ADG and mid test metabolic weight (MMW). Mean ADG, FI, feed conversion ratio (FCR), and RFI were 1.24 ± 0.19, 7.89 ± 1.19, 6.22 ± 0.73 and 0.00 ± 0.42 kg/d, respectively. Differences among groups in ADG and FCR were not significant ($P = 0.42$, $P = 0.86$, respectively). However, calves of V group tended to have lower FI ($P = 0.065$) and to be more efficient (RFI = −0.115; $P = 0.105$) than animals of C group. RFI was correlated with FI (r = 0.36) and FCR (r = 0.54), but not with ADG or MMW. Our preliminary results show a suggestive association between the SNPs studied and RFI in Angus cattle despite further research is warranted.

Key words: residual feed intake, beef cattle, SNPs

T32 Identification of a JY-1 gene variant in Nellore cattle. G. M. F. de Camargo*[1], A. C. de Freitas[1], A. C. Andrade[1], F. M. M. Gil[1], D. F. Cardoso[1], P. D. S. Fonseca[1], F. R. P. Souza[1], M. Cervini[1], F. Baldi[1], L. G. de Albuquerque[1], L. C. A. Regitano[2], and H. Tonhati[1], *[1]Sao Paulo State University, Jaboticabal, Sao Paulo, Brazil, [2]Brazilian Agricultural Research Corporation - Southeast Cattle Center, Sao Carlos, Sao Paulo, Brazil.*

The JY-1 protein is found in monoovulatory species and was first described in cattle. It is an oocyte specific protein and it plays a key role in the regulation of the granulose cells functions. It also influences the early embryo development. Other genes with similar functions were described in polyovulatory animal. The aim of this study was to analyze a region of the exon 3 of the JY-1 gene in Nellore cattle to investigate possible polymorphisms and their association with reproduction performance. DNA was extracted from tail hair of 298 Nellore heifers by the phenol-chloroform-isoamyl alcohol protocol. The heifers were divided in 2 groups: 149 heifers that conceived at 16 mo of age and 149 heifers that failed to conceive at 16 mo. The primers 5′ATCAAACTGAACAGGGCAGA3′ and 5′AAGTATGACAAGAGATACGGTCAGG3′ were designed to amplify a partial region of exon 3. The fragment amplified by the PCR has 373 bp. After, the RFLP analyses were done with the restriction enzyme SspI whose restriction site is 5′AATATT3′. It was possible to identify 2 genotypes (TT and TC) and characterize 2 variants: T and C (GenBank accession numbers: JF262042 and JF262043). The genotype TT has 2 bands with 208 bp and 165 bp and the genotype TC has 3 bands of 373 bp, 208 bp and 165 bp. The allelic frequencies were 0.97 and 0.03 for variant T and variant C, respectively. The genotypic frequencies were 0.94 and 0.06 for the genotypes TT and TC, respectively. The genotypic frequencies deviated ($P < 0.05$) from Hardy-Weinberg equilibrium, which could be due to the low frequency of variant C. The sequences available at GenBank for this region (NM_001110098.1, EF642497.1 and EF642496.1) characterize the variant C in *Bos taurus taurus*, which is the variant with the lowest frequency in *Bos taurus indicus*. The correlation between the genotypes and the pregnancy at 16 mo was not done because of the divergence between the frequencies and also because of the equal distribution of the patterns between the heifer groups. So, future studies must be done to identify other polymorphisms in JY-1 gene segregating in Nellore cattle and analyze their possible correlations with heifer pregnancy.

Key words: PCR-RFLP, polymorphism, SNP

T33 Novel associations between a SNP in the bovine *DDEF1* gene and production traits in Nellore breed. P. C. Tizioto*[1], S. L.

Meirelles[1], G. B. Veneroni[1], M. M. de Souza[1], F. Siqueira[2], A. do Nascimento Rosa[2], L. O. Campos da Silva[2], R. de Almeida Torres[2], S. R. Medeiros[2], R. R. Tullio[3], M. M. de Alencar[3], G. Feijó[2], and L. C. de Almeida Regitano[3], *[1]Federal Universidade of São Carlos, São Carlos, São Paulo, Brazil, [2]Embrapa Beef Cattle National Center, Campo Grande, Mato Grosso do Sul, Brazil, [3]Embrapa Southeast Cattle Research Center, São Carlos, São Paulo, Brazil.*

Concomitant with the traditional selection, which has produced interesting results, marker assisted selection (MAS) can help breeding programs and improve profiles for economically important traits. The identification of markers associated with interest production traits is a fundamental step for implementing MAS in breeding programs. This project aimed to study the association between a SNP (G/A) in intron 13 of bovine DDEF1 (development and differentiation enhancing factor 1) gene and the traits weaning weight adjusted to 240 d (WW), yearling weight adjusted to 450 d (YW), backfat thickness (BFT), ribeye area (RYA) and shear force at 24 h postmortem (SF), in reference families of Nellore breed. We used about 270 steers, descendants of 20 Nellore bulls selected to represent variability within the Nellore breed. SF measures were available from only 140 steers. At approximately 18 mo of age, animals were transferred from grazing systems to feedlots, where they were finished for about 100 d before slaughtering for meat quality data collection. The genotypes were determined by amplification refractory mutation system (ARMS-PCR). A mixed model with fixed effects of contemporary group and genotypes, and age of the animal at the time of measurement (linear effect) as a covariate and the random effect of bull was used to evaluate the marker effect. For SF data the model also included pH as a covariate. Analyses were done by the maximum restricted likelihood (REML) using PROC MIXED of the Statistical Analysis System (SAS). The SNP in DDEF1 gene showed significant association with WW ($P = 0.0021$), YW ($P = 0.0109$), RYA ($P = 0.0109$) and SF ($P = 0.0083$). It represented 2.18%, 4,61%, 4.28% and 1.13% of total additive variance and 6.16%, 4.32%, 4.74% and 17.51% of total phenotypic variance for WW, YW, RYA and SF, respectively. Therefore, this SNP is a good candidate for application in MAS of meat production and quality traits in Nellore breed.

Key words: beef, SNP, DDEF1

T34 CAPN4751 and UOGCAST effects on feed efficiency, carcass traits and feedlot performance in Nellore (*Bos indicus*) cattle.

R. C. Gomes*[1], M. E. Carvalho[2], M. H. A. Santana[1], S. L. Silva[1], P. R. Leme[1], P. Rossi[3], and J. B. S. Ferraz[1], *[1]Faculdade de Zootecnia e Engenharia de Alimentos, Universidade de São Paulo (FZEA/USP), Pirassununga, SP, Brazil, [2]Escola Superior de Agricultura Luiz de Queiroz, Universidade de São Paulo (Esalq/USP), Piracicaba, SP, Brazil, [3]Departamento de Zootecnia, Universidade Federal do Paraná (UFPR), Curitiba, PR, Brazil.*

The calpain system is related to protein turnover and may affect productive traits in livestock. Thus, the aim was to examine associations among SNP polymorphisms in the calpain and calpastatin genes and carcass traits, growth and feed efficiency in beef cattle. Nellore steers and bulls (n = 290; 378 ± 42 kg BW, 23-mo ± 42d old) were feedlot fed in tests conducted at FZEA/USP, Pirassununga, Brazil, from 2007 to 2010. Dry matter intake (DMI) and average daily gain (ADG) were recorded for 50 to 84 d and carcass traits were assessed by ultrasound. Feed conversion ratio (FCR), gross feed efficiency (GFE), partial efficiency of growth (PEG) and residual feed intake (RFI) were computed. Cattle were genotyped for CAPN4751 (C/T, 6545 bp of AF248054) and UOGCAST (C/G, 282 bp of AY008267) in the calpain and calpastatin genes, respectively. The genotyping was carried out using TaqMan Real Time PCR assays. Association analyses used a linear mixed model with contemporary group, sex and genotype as fixed effects, age as covariate and sire as a random effect. Frequencies for C and T alleles of CAP4751 and C and G alleles of UOGCAST were 0.13, 0.87, 0.55 and 0.45, respectively. Genotypic frequencies were 0.02, 0.22 and 0.76 for CC, CT and TT of CAP4751 and 0.29, 0.51 and 0.20 for CC, CG and GG genotypes of UOGCAST, respectively. Because the low CC frequency, CAP4751 effects were tested by CT vs. TT contrasts. No CAP4751 effects were observed for DMI ($P = 0.11$), GFE ($P = 0.25$), FCR ($P = 0.46$), PEG ($P = 0.67$), RFI ($P = 0.75$), backfat thickness (UBFT; $P = 0.74$) and ribeye area (UREA; $P = 0.76$). There were differences between CT and TT genotypes of CAP4751 on final BW (486 vs. 473 kg, $P = 0.03$), ADG (1.53 vs. 1.44 kg/d, $P = 0.04$) and rump fat thickness (URFT, 7.5 vs. 6.70 mm, $P = 0.04$). UOGCAST did not affect BW ($P = 0.59$), DMI ($P = 0.48$), GFE ($P = 0.12$), FCR ($P = 0.31$), PEG ($P = 0.40$), RFI ($P = 0.45$), UBFT ($P = 0.76$), URFT ($P = 0.90$) and UREA ($P = 0.61$). An additive effect was observed for UOGCAST on ADG (−0.0685 ± 0.026 kg/d, $P = 0.0093$). The UOGCAST and CALP4751 polymorphisms can affect growth and carcass traits in Nellore cattle but not feed efficiency.

Key words: *Bos indicus*, DNA marker, residual feed intake

T35 Bialellic expression studies of *CAST* gene in bovine muscle.

M. M. de Souza[1], S. C. M. Niciura[2], A. M. G. Ibelli[1], S. L. Meirelles[1], M. I. Rocha[1], P. C. Tizioto*[1], G. Gasparin[3], M. E. Carvalho[3], G. B. Veneroni[1], F. A. Bressani[2], P. S. N. de Oliveira[1], F. Siqueira[4], L. L. Coutinho[3], and L. C. de Almeida Regitano[2], *[1]Federal University of São Carlos, São Carlos, São Paulo, Brazil, [2]Embrapa Southeast Cattle Research Center, São Carlos, São Paulo, Brazil, [3]University of São Paulo, Piracicaba, São Paulo, Brazil, [4]Embrapa Beef Cattle National Center, Campo Grande, Mato Grosso do Sul, Brazil.*

Bovine meat tenderness is the main feature appreciated by consumers and is influenced by calpastatin protein activity. This protein is codified by CAST gene and is the main modulator of μ-calpain protease, which in turn, degrades the myofibrillar proteins of skeletal muscle in the post-mortem period. In general, models used for gene-phenotype associations consider equal expression of both alleles. Therefore, departures from biallelic expression patterns must be incorporated in models of quantitative genetic analysis because it may result in differences in males and females breeding values. This study aimed to analyze allelic expression pattern of CAST gene in muscle tissue of Nellore steers immediately after slaughter. A group of 270 animals were genotyped for the polymorphism A/G within the 3′ UTR of CAST gene by using TaqMan probes in real-time PCR. RNA was extracted from muscle of 14 heterozygotes to produce first strand cDNA. The allelic expression has been analyzed by using the same TaqMan probe used for genotyping. A standard curve was made to normalize the specific probe fluorescences for each allele in the TaqMan assay. This was made with dilutions of genomic DNA from 2 homozygous animals AA and BB; the dilutions were 8:1, 4:1, 2:1, 1:1, 1:2, 1:4 and 1:8. For each dilution the log2 (FAM intensity/VIC intensity) was calculated at the last cycle (40) of PCR, thus the allele fluorescence ratio of the 14 steers was extrapolated in the standard curve. Therefore it was possible to measure whether there were differences in allelic expression and whether it was inherited from mother or father. The non-parametric randomization test was used for statistical analysis. Parental origin was not found to affect allele expression ($P > 0.05$). Although the expression of the G allele was 1.4 times that of the A allele, that difference was not significant. Finally, considering that other published papers described

allelic specific gene expression using smaller sample size, it is possible to conclude that the CAST gene shows biallelic expression in skeletal muscle during the post-mortem period in Nellore cattle breed, compatible with general quantitative models for marker-assisted selection.

Key words: CAST, SNP, imprinting

T36 The polymorphism Msp I in intron 3 of the growth hormone gene in Nellore cattle (*Bos taurus indicus*). D. F. Cardoso[1], G. M. F. de Camargo*[1], P. D. S. Fonseca[1], F. M. M. Gil[1], M. G. Chiquitelli[1], F. R. P. de Souza[1], L. G. de Albuquerque[1], M. E. Z. Mercadante[2], and H. Tonhati[1], *[1]Department of Animal Sciences, Sao Paulo State University, Jaboticabal, Brazil, [2]Animal Science Experimental Station, Sertãozinho, SP, Brazil.*

The growth hormone gene is very studied in animals due to its key role in biological functions. In *Bos taurus taurus*, this gene is correlated to growth, body composition and even milk composition. The growth hormone in cattle (bGH) has a polymorphic structure that characterizes it as a potential molecular marker that may assist selection process. The aim of this work was to verify and analyze the polymorphism described in the intron 3 of *Bos taurus taurus* in Nellore cattle (*Bos taurus indicus*) to validate these associations in this breed. The DNA was extracted from blood samples of 238 Nellore cattle belonging to 3 lines selected for growth from the selection program of the Animal Science Experimental Station in Sertãozinho-SP, Brazil. A fragment of 329 bp from intron 3 was amplified by PCR with the primers 5′CCCACGGGCAAGAATGAGGC3′ and 5′TGAGGAACTGCAGGGGCCCA3′. The RFLP was done with the restriction enzyme MspI. It was possible to identify 3 migration patterns, the first one has one fragment of 329 bp and corresponds to the homozygote −/−, the second one has 2 fragments of 224 bp and 105 bp and corresponds to the homozygote +/+, the third one has these 3 fragments above and corresponds to the heterozygote +/−. The allelic frequency was 0.26 to the allele MspI(+) and 0.74 to the allele MspI(−). The genotypic frequencies were 0.06, 0.41 and 0.53 to the genotypes +/+, +/− and −/−, respectively. Although these animals belongs to a selection program, the frequencies are in Hardy-Weinberg equilibrium at 5%, indicating that this locus of the bGH is not affected by selection. It is important to emphasize that the polymorphism recognized by the endonuclease MspI has different frequencies in Zebu and European cattle. The MspI(+) allele that is correlated to milk production and composition has high frequencies in European breeds and low frequencies in *Bos taurus indicus*. The results indicate that the PCR-RFLP/MspI is efficient to detect the polymorphism in the intron 3 of the bGH in Nellore cattle and it may be associated with important economic traits. Financial Support: FAPESP

Key words: molecular marker, beef cattle, RFLP

T37 Polymorphisms of the *IGF1* and *MSTN* genes in Nellore beef cattle (*Bos indicus*) and in their crosses with *Bos taurus*. R. A. Curi[1], M. R. S. Fortes[2], D. M. Vankan[2], J. A. V. Silva*[1], H. N. Oliveira[3], M. D. S. Mota[1], and A. C. Silveira[1], *[1]Faculdade de Medicina Veterinária e Zootecnia, Unesp, Botucatu, São Paulo, Brasil, [2]School of Veterinary Science, University of Queensland, St. Lucia, Queensland, Australia, [3]Faculdade de Ciências Agrárias e Veterinárias, Unesp, Jaboticabal, São Paulo, Brasil.*

The aim of this study was to estimate the segregation of the single nucleotide polymorphism (SNP) AF_017143.1:g.198C > T of the IGF1 gene and AF_320998.1:g.433C > A of the MSTN gene in Nelore (*Bos indicus*) and Nelore × Bos taurus beef cattle, and to evaluate their effects on carcass and meat traits. A total of 300 animals (114 Nelore and 186 crosses) were genotyped and phenotyped for rib eye area (REA), backfat thickness (BT), intramuscular fat (IF), shear force (SF) and myofibrillar fragmentation index (MFI). The allele substitution effects for each of the polymorphisms on the traits of interest were estimated by regression of the phenotypes analyzed on the number of copies of a particular allele using the General Linear Model procedure. The polymorphism of the IGF1 was non-informative in Nelore animals with allele C was found to be fixed. Although association between allele C and greater REA has been verified in animals from crossing ($P < 0.05$), this is no longer significant after the Bonferroni correction of hypothesis tests for multiple comparisons. The allele A of the SNP of the MSTN was absent in Nelore and it is only found in 2 crossbred animals, impairing association studies. The present results suggest the lack of potential for application in marker-assisted selection of the analyzed SNPs in cattle with breed compositions similar to those described here. Furthermore, the absence of these SNPs in Nelore cattle, a situation that may extend to other *Bos indicus* breeds, indicates the need to use other identified polymorphisms or the search for new polymorphisms in the IGF1 and MSTN genes to carry out futures association studies involving this subspecies.

Key words: fat deposition, meat tenderness, molecular markers

T38 Characterization of polymorphism in the ORL1 gene in Nellore cattle (*Bos taurus indicus*) by PCR-RFLP. P. D. da Silva Fonseca[1], F. R. P. de Souza[1], G. M. F. de Camargo*[1], F. M. Gil[1], D. F. Cardoso[1], M. G. Chiquitelli[1], L. G. Albuquerque[1], M. E. Z. Mercadante[2], and H. Tonhati[1], *[1]São Paulo State University, São Paulo State University, Jaboticabal, Brazil, [2]Animal Science Experimental Station, Animal Science Experimental Station, Sertaozinho, Brazil.*

The ORL1 gene, under normal conditions, has low expression in adipocyte cells. In obese animals its expression is higher and it causes an increase in the cholesterol content and promotes the capture of fatty acids. Cholesterol and triglycerides concentration are highly correlated with fat deposition, so the ORL1 gene is a candidate gene to subcutaneous and intramuscular fat deposition in cattle. The aim of this study was to investigate the existence of the ORL1 polymorphism in Nellore cattle and characterize the allelic and genotypic frequencies. The DNA was extracted from blood of 240 animals from Animal Science Experimental Station, Sertaozinho, Brazil. The animals were genotyped by PCR-RFLP using the restriction enzyme *Pst*I. Three genotypes were obtained. The genotypes AA, AC and CC have the frequencies 0.22, 0.25 and 0.53, respectively. The allelic frequencies of A and C were 0.35 and 0.65, respectively. These results indicate that there is a good distribution of the alleles among the animals, therefore permitting verification of the association of the SNP with growth and carcass traits in Nellore cattle. Financial support: CNPq and Fapesp

Key words: PCR-RFLP, adiposity, SNP

T39 Analysis of MUC1 alleles in Nellore cattle using single-allele and multi-allele models. F. R. P. Souza[1], S. Sartore[2], S. Maione[2], D. Soglia[2], V. Spalenza[2], G. M. F. de Camargo*[1], P. Sacchi[2], R. Rasero[2], and M. E. Z. Mercadante[3], *[1]Sao Paulo State University, Jaboticabal, SP, Brazil, [2]University of Torino, Grugliasco, TO, Italy, [3]Instituto de Zootecnia, Sertãozinho, SP, Brazil.*

The aim of the present study was to analyze the association of the highly polymorphic mucin MUC1 with economic traits in Nellore

cattle. A total of 295 Nellore heifers, born between 2003 and 2005, from a selection experiment running at Instituto de Zootecnia, Sertãozinho - São Paulo/Brazil, were used. The animals were genotyped by PCR. The traits analyzed were birth weight (BW), weaning weight (W210), yearling weight (W550), yearling height (YH550), longissimus muscle area (LMA), subcutaneous backfat thickness (BF), and rump fat thickness (RF). Data were analyzed by a mixed model including absence or presence of the allele (coded as 0 and 1, respectively), contemporary group (selection line and year of birth, 1, ..., 9) and month of birth (September, October, November) as fixed effects, age of dam and age at recording (only for YH550 and the carcass traits LMA, BF and RF) as linear covariates, and the random effect of sire (1, ..., 41). Initially, "single-allele" models were used for each trait, subsequently "multi-allele" models, including all alleles, were applied. Five alleles were identified (1–5). Single-allele model results showed that the allele 3 was associated with W550 ($P = 0.03$). Considering the multi-allele model, significant effects of the alleles 1 and 4 were found on BW ($P = 0.02$ and 0.04, respectively), however, allele 3 did not affect W550 significantly. Despite these findings, application of this marker in marker-assisted selection will require more studies with a larger number of animals genotyped to increase the accuracy of the statistical analyses.

Key words: VNTR, molecular markers, QTL

T40 Association between a SNP in intron 1 of the ghrelin gene with milk production traits in Murrah buffaloes (*Bubalus bubalis*). F. M. M. Gil, F. R. P. Souza, G. M. F. de Camargo*, P. D. S. Fonseca, D. F. Cardoso, R. R. Aspilcueta-Borquis, G. Stefani, and H. Tonhati, *São Paulo State University, Jaboticabal, São Paulo, Brazil.*

Ghrelin is a gastrointestinal hormone and a potent release stimulator of growth hormone (GH) in the somatotropic cells of the hypophysis and hypothalamus. It also influences the general metabolism of the body. Studies demonstrated that ghrelin and GH have high plamastic concentration in dairy cows with high breeding value. Other studies consider GH the most important hormone related to milk yield in lactating cows. The characterization of the ghrelin gene (GHRL) in buffaloes is important because it is a candidate gene to identify molecular markers related to growth, carcass and milk production traits. The aim of this study was to associate the SNP A/G in intron 1 (GenBank accession number: GU071074 and GU071075) of the GHRL gene in Murrah buffaloes with milk production traits. The DNA was extracted from hair of 212 dairy buffaloes from one farm in the São Paulo state, Brazil. The animals were genotyped by PCR-RFLP using the restriction enzyme BstUI. Three genotypes were obtained. The genotypes AA, AG and GG have the frequencies 0.37, 0.47 and 0.16, respectively. The allelic frequencies of G and A were 0.4 and 0.6, respectively. In analyses, the GLM procedure of SAS was used, the model included as fixed effects birth season, birth year and genotype, and as a covariable the age of the buffalo. The possible association of the polymorphism with the phenotypic values of milk yield, protein yield, fat yield, protein percentage and fat percentage at a statistical significance of 5% was tested. The results indicate that there is no association of the SNP described with milk yield ($P = 0.3965$), fat yield ($P = 0.2320$), protein yield ($P = 0.5334$), fat percentage ($P = 0.6224$) and protein percentage ($P = 0.1305$) in dairy Murrah buffaloes.

Key words: restriction enzyme, PCR-RFLP, milk yield

T41 Identification of polymorphism in leptin gene in *Bubalus bubalis*. V. A. Ferreira Junior[1], G. M. F. de Camargo*[1], A. L. F. Lima[2], F. M. M. Gil[1], and H. Tonhati[1], *[1]Sao Paulo State University, Jaboticabal, SP, Brazil, [2]Santa Catarina Federal University, Florianopolis, SC, Brazil.*

The leptin is a hormone synthesized by the adipocyte tissue and regulates the feed intake in many species as well as in ruminants. It is highly correlated with body weight and adiposity. The gene of the leptin is a potential molecular marker because it is related to feed intake, a trait that is difficult to be measured especially in systems based on pastures. The trait also has high economic value and is correlated with production traits. The aim of this study was to investigate polymorphisms in partial region of intron 2 of the leptin gene in Murrah buffaloes. The DNA was extracted from hair of 150 dairy buffaloes from one farm in the Sao Paulo state, Brazil. The animals were genotyped by PCR-RFLP. In the PCR reaction the primers used were 5′GTCTGGAGGCAAAGGGCAGAGT3′ and 5′CCACCACCTCTGTGGAGTAG3′ and in the RFLP reaction, the restriction enzyme used was Bsa AI. Three genotypes were obtained. The first one has one fragment of 522 bp and corresponds to the homozygote AA, the second one has 2 fragments of 441 bp and 81 bp and corresponds to the homozygote GG, the third one has 3 fragments (522 bp, 441 bp and 81 bp) and corresponds to the heterozygote AG. The genotypes AA, AG and GG have the frequencies 0.3, 0.52 and 0.18, respectively. The allelic frequencies of A and G were 0.56 and 0.44, respectively. The technique was efficient to detect the SNP A/G in intron 2 in buffaloes. The same SNP is also present in cattle. The genotypic frequencies are in Hardy-Weinberg equilibrium at 5%. This SNP seems to be interesting to be studied because it is a SNP conserved between species and also because the frequencies are well distributed among the animals.

Key words: SNP, buffaloes, PCR-RFLP

T42 Relationship between kappa-casein genotype in inseminated bulls and the milk composition of their daughters. J. Bezdicek*[1] and J. Riha[2], *[1]Agriresearch Rapotin, Ltd., Rapotin, Czech Republic, [2]Research Institute for Cattle Breeding, Ltd., Rapotin, Czech Republic.*

Using genotypes that positively influence cattle milk production is an important breeding aim. The goal of this study was to evaluate the relationship between one milk protein kappa–casein genotype (CSN3) in inseminated Czech Fleckvieh and Holstein bulls, used between the years 1997–2007 and the milk composition of their daughters. We included only cows with a milk yield C100 (5000–7500 L) and H100 (7000–10 000 L). The statistical analysis was done using SPSS 15.0 program for Windows and PowerMarker (Liu, K., Muse, S. V., 2005). The average genotype frequency in the case of Czech Fleckvieh bulls (n = 136) was AA = 0.39; AB = 0.48; AE = 0.01; BB = 0.09; BE = 0.02; and EE = 0.01 and allele frequencies were A = 0.64; B = 0.34 and E = 0.02. Genotype frequencies found in Holstein bulls (n = 60) were AA = 0.55; AB = 0.28; AE = 0.12; BB = 0; BE = 0.03 and EE = 0.02 and allele frequencies were A = 0.75; B = 0.16 and E = 0.09. In the Holstein breed we found a higher frequency of the E allele and a higher frequency of genotypes with this allele. The genetic diversity and heterozygosity in Czech Fleckvieh Bulls were the following 0.47; 0.52. In Holstein Bulls 0.40; 0.43. These results show the higher genetic variability of bulls of the Czech Fleckvieh breed. At the same time we carried out an assessment of the milk fat and protein percentage of the daughters of the observed bulls. The measurement was made on cows in the 1st lactation separately for the Czech Fleckvieh (n =

607 cows) and Holstein (n = 702 cows). Significance of differences is marked as *($P \leq 0.05$), **($P \leq 0.01$). A found higher protein content in Czech Fleckvieh was associated with particular genotypes: BB (3.56%) > AB (3.55%) > *AA (3.48%) > AE (3.43%) > EE (3.41%) > * BE (3.37%). Protein in Holstein: AB (3.32%) > AA (3.31%) > AE (3.30%) > BE (3.28%) > * EE (3.26%). Fat in Czech Fleckvieh: AB (4.2%) > AA (4.14%) > BB (4.11%) > BE (4.09%) > EE (4.05%) > **AE (3.93%). Fat in Holstein: AB (3.86%) > AA (3.85%) > EE (3.83%) > AE (3.82%) > ** BE (3.72%). From the above it is clear that differences between CSN3 genotypes were not considerable and only in some cases significant.

Key words: kappa-casein, milk composition

T43 Effect of DGAT1, TG and leptin gene polymorphisms on milk production traits in Holstein-Friesian cows in Hungary. I. Anton*[1], K. Kovács[1], G. Holló[2], V. Farkas[3], F. Szabó[3], and A. Zsolnai[1], *[1]Research Institute for Animal Breeding and Nutrition, Herceghalom, Hungary, [2]University of Kaposvár, Faculty of Animal Science, Kaposvár, Hungary, [3]University of Pannonia, Georgikon Faculty of Agriculture, Keszthely, Hungary.*

The objective of this study was to estimate the effect of the acylCoA-diacylglycerol-acyltransferase 1 (DGAT1), thyroglobulin (TG) and leptin locus on milk fat, milk protein and milk yield in Hungarian Holstein-Friesian cows. A lysine/alanine (K232A) polymorphism in DGAT1 -a microsomal enzyme that catalyzes the final step of triglyceride synthesis- has been proved to affect milk yield, as well as milk fat and protein content in different dairy cattle breeds. The effect of a 5′-polymorphism of TG gene- which product is the precursor of hormones that influence lipid metabolism- has been shown to affect milk fat content in cattle. Polymorphisms in the leptin gene have been associated with milk protein yield and milk yield. A total of 417 blood samples have been collected from different Holstein-Friesian herds and genotypes were determined by PCR-RFLP (polymerase chain reaction-restriction fragment length polymorphism) assay. Milk production data were recorded throughout 3 consecutive lactations and statistical analyses have been carried out to find association between individual genotypes and milk production traits. The data set was analyzed with SPSS 15.0 for Windows software. Multivariate ANOVA (general linear model, GLM) was applied to determine differences in milk production traits, where DGAT1, TG and leptin genotypes, birth year, number of lactations and calving season were included as fixed effects and 305-d-milk yield, 305-d-milk fat percentage and yield and 305-d-milk protein percentage and yield were considered as dependent variables. In case of DGAT1 locus, AA homozygous animals produced the highest values of fat yield and protein yield ($P < 0.05$). Milk yield decreased consistently ($P < 0.05$) from genotype AA/AA through to GC/GC. Among TG genotypes, TT animals had the highest ($P < 0.05$) 305-d-milk fat percentage and yield values. Referring to leptin polymorphism, CC cows produced higher ($P < 0.05$) 305-d-milk protein values than TC animals. The project was supported by the Hungarian Scientific Research Fund (project 78174).

Key words: DGAT1, TG, leptin

T44 Correlation analysis of hepatic transcript abundance and lactational performance in postpubertal Holstein dairy heifers. J. Doelman, J. M. Kim*, H. Cao, N. G. Purdie, and J. P. Cant, *University of Guelph, Ontario, Canada.*

Dairy genomic research has recently grown in popularity, though investigation into the use of transcript abundance as a marker of future performance remains limited. The objectives of this study were to employ a statistical method to reduce variability within a microarray data set and subsequently identify correlations between gene expression signal intensity and performance measures during first lactation of 81 Holstein dairy heifers. Pearson correlation can be used to determine the underlying structure of a large data set through identification of a data subset that is well correlated to a particular variable. Partial Least Squares regression seeks to model dependent variables by means of a set of predictor variables but has yet to be applied in the field of dairy genomics. These 2 types of analysis were performed on microarray data from previous research that quantified gene expression signal from yearling Holstein heifers. To reduce the total number of genes used in the data set for regression analysis, the linear dependence of all genes in the entire normalized data set was measured against 18 DHI variables using Pearson correlation analysis. Results were pooled to generate 4 lists based on coefficient values and significance of $P < 0.05$. List 4 featured 1541 genes ($r^2 > 0.04$), list 3 contained 453 genes ($r^2 > 0.09$), list 2 was comprised of 140 genes ($r^2 > 0.12$) and list 1 consisted of 31 genes ($r^2 > 0.16$). Test set validation was used to fit the partial least squares model by creating a test and training set using the normalized expression data sets. The strongest correlation coefficients, $r^2 = 0.62$ (protein percentage) and $r^2 = 0.54$ (fat percentage) were obtained using list 1. Strong correlations were also found for 305 d protein yield ($r^2 = 0.40$, list 3) and protein percentage ($r^2 = 0.33$, list 4). Moderate correlation coefficients were also identified for breed class average milk ($r^2 = 0.21$, list 1) and protein ($r^2 = 0.24$, list 1). Identification of gene expression patterns in a predictive nature such as this offers a potential selection tool to be employed by producers.

Key words: heifer, correlation, gene expression

T45 Identification of a SNP in the gene *IL2* and its association with resistance against gastrointestinal infection by nematodes in goat. F. A. Bressani[1,5], P. C. Tizioto*[2], S. L. Meirelles[2], W Malagó Junior[1,2], R. Giglioti[3], A. M. G. Ibelli[2], J. G. G. Gromboni[4], E. Carrilho[5], L. G. Zaros[6], L. da Silva Vieira[7], and L. Correia de Almeida Regitano[1], *[1]Embrapa Southeast Embrapa Southeast Cattle Research Center, São Carlos, São Paulo, Brazil, [2]Federal University of São Carlos - UFSCar, São Carlos, São Paulo, Brazil, [3]State University of São Paulo - UNESP, Jaboticabal, São Paulo, Brazil, [4]UNICEP, São Carlos, São Paulo, Brazil, [5]University of Sao Paulo, São Carlos, São Paulo, Brazil, [6]Federal University of Rio Grande do Norte, Natal, Rio Grande do Norte, Brazil, [7]Embrapa Goats and Sheep, Sobral, Ceará, Brazil.*

The gene IL2 encodes an interleukin which plays a role in inducing the maturation of T and B cells, important factors in the immune response to parasites in several species. Two hundred twenty-nine individuals of a F2 goat population were studied aiming at finding genetic markers for resistance to gastrointestinal infection. To accomplish this, a SNP in the IL2 gene was identified and its association with resistance to gastrointestinal infection was tested. The population investigated was an F2 generated from F1 Saanen (susceptible to gastrointestinal endoparasites), Anglo-nubian (resistant) crosses. Phenotypes consisted of eggs per gram (EPG) and were obtained by parasitological examination of feces samples. The data were transformed as log 10(EPG+1) and analyzed using the mixed procedure of SAS. Fixed effects included in the model were sex, sampling order, and age at sampling; while animal was fitted as random effect. Based on this analysis, 44 individuals with extremes EPG were selected. The gDNA of these animals

was obtained from isolated leukocytes by the salting-out method. Specific oligonucleotides were designed to obtain PCR products from IL2 gDNA which were sequenced in the ABI Prism 3100 Avant Sequencer (Applied Biosystems). The sequences were further analyzed using the Phred, Phrap, and Consed programs. A SNP (G/A) identified within the intron 2 of IL2 gene was analyzed by Fisher test and showed association with resistance against gastrointestinal infection by nematodes ($P = 0.0489$). Further studies with the whole F2 population are in progress to confirm this association.

Key words: IL2, SNP, goat

T46 Effect of the DGAT1 gene polymorphism on the backfat thickness and fat-tailed weight in Iranian Lori-Bakhtiari sheep. H. Mohammadi*, M. Moradi Shahrebabak, and M. Sadeghi, *Department of Animal Science, University College of Agriculture and Natural Resources, University of Tehran, Karaj, Tehran, Iran.*

Backfat thickness refers to the amount of fat over the animals back and strongly associated with percentage of retail product, represents a valuable sheep quality trait, and fat-tail demands sheep industry attention for many reasons. To name a few, lean to fat-tail ratio improvement means better feed conversion efficiency. The DGAT1 catalyzes the final step of triglyceride synthesis and the gene is located on the centromic end of bovine chromosome 14. The DGAT1 gene has been mapped to ovine chromosome 9. Polymorphism in the DGAT1 gene has been associated with milk fat percentage and body fatness. The objective of this study was to evaluate the effect of the DGAT1 gene locus on ovine quality traits in the Lori-Bakhtiari sheep breed in Iran. A total of 152 blood samples were obtained from different sex Lori-Bakhtiari sheep. PCR primers were assumed from previously reported studies (Xu et al., 2008). A 309 bp fragment from exon 17 was amplified and digested by AluI with PCR-RFLP method. The association between genotypes and fat-tailed weight and backfat thickness was analyzed. DGAT1 CC animals showed the highest fat percentage values for fat-tail and backfat thickness, the difference between CC and TT genotypes was significant ($P < 0.05$). The results of this study identified novel associations; The C allele had a positive effect on fat-tail weight and backfat thickness in fat-tailed sheep. The results of this study suggest that the TT genotype of DGAT1 could be regarded as a molecular marker for breeding programs to improve carcass traits in fat-tailed sheep breed.

Key words: DGAT1, single nucleotide polymorphisms (SNP), fat deposition and carcass traits

T47 Identification and evaluation of an IGF-I gene polymorphism in a Zel sheep population using RFLP/HaeII. S. M. Kazemi*[1], C. Amirinia[2], S. Gharaveysi[1], H. Emrani[2], and A. Yilmaz[3], *[1]Department of animal Science, Islamic Azad University, Qaemshahr Branch, Qaemshahr, Mazandaran, Iran, [2]Department of Animal Biotechnology, Animal Science Research Institute of Iran, Karaj, Alborz, Iran, [3]Department of Animal Sciences, The Ohio State University, Columbus.*

The IGFs play an important role in regulating somatic growth, and they are affected by nutritional and other conditions during growth. Polymorphisms of IGF genes are reported to be significantly associated with many traits including growth and reproductive traits. In this study, 142 DNA samples from Zel sheep were used to detect a promoter region polymorphism in the insulin-like growth factor-1 (IGF-1) gene. To extract DNA from blood we used a Salting-out procedure. Primers were obtained for amplification of the specific segment. Polymerase Chain Reaction (PCR) was accomplished after finding the best reaction conditions and the specific segment amplified well. RFLP fragments were used to detect the polymorphism in the segment. RFLP analysis was performed by incubating the PCR products with HaeII restriction enzyme at 37°C for 4 h. Gels (3.5% agarose) were visualized by using ethidium bromide. The polymorphism was observed and the evaluation of the results relieved 2 alleles and 3 genotypes. The alleles were A and B with frequencies of 0.71 and 0.29, respectively. The genotypes AA, BB and AB had frequencies of 0.47, 0.06 and 0.47, respectively. The data were analyzed for genetic variation statistics using PopGene software (version32) and no deviation from Hardy-Weinberg equilibrium was observed in this study.

Key words: Zel sheep, IGF-1, polymorphisms

T48 Haplotype structure of telomerase reverse transcriptase (*turTERT*) gene in the turkey, *Meleagris gallopavo*. A. M. J. B. Adikari*, J. Xu, X. Guan, and E. Smith, *Virginia Polytechnic Institute and State University, Blacksburg.*

The recently released turkey genome sequence offers an opportunity to characterize and define the role of some genes that affect turkey performance and productivity. Our objective for this study was to screen the telomerase reverse transcriptase (*turTERT*) gene for structural variation based on single nucleotide polymorphisms (SNPs) and haplotypes using a diversity panel consisting of birds from heritage, commercial, and wild varieties. The rationale is that TERT influences some metabolic diseases including heart diseases, metabolic syndrome, and hypertension. Further, the levels of functional telomerase are critical for telomere maintenance whose shortening is associated with organismal aging and concomitant metabolic diseases. Primers used for long-range polymerase chain reaction (LR-PCR) were designed using the Primer 3 software. Each amplicon was gel purified, sequenced, and the SNPs detected using standard methods. Linkage disequilibrium (D') among SNPs was estimated using Visual Haplotype software. From 34 kb of *turTERT* gene screened, a total of 4 SNPs were detected in the introns. Allelic diversity ranged from 0.14 to 0.68. A total of 3 haplotypes were derived from the SNPs with frequencies that ranged from 0.09 to 0.59. While the diversity panel maximized detection of variation, both the SNPs and haplotypes appear to show that the Royal Palm's *TERT* alleles appear to be distinct. Visual haplotype analysis revealed that the first 3 SNPs, which were about 300 bp apart, were strongly associated ($r^2 = 0.87–1.00$) while the fourth, about 9 kb from the nearest SNP, was not strongly linked ($r^2 < 0.1$) to the others. The distribution of the SNPs and haplotypes, as well as the D', provide a foundation that will facilitate future association and linkage studies between *turTERT* and metabolic diseases in the turkey.

Key words: Turkey, single nucleotide polymorphisms, linkage disequilibrium

T49 Changes in the proteome and metabolic profiles of broiler chickens during adipose tissue accretion. G. Kelley*, X. Wang, F. Chen, and S. Nahashon, *Tennessee State University, Nashville.*

Fat accretion in poultry directly influences the efficiency of feed utilization and consumer acceptability of poultry and poultry products. Losses estimated at about US$250–300 million are incurred by consumers and processors annually in pollution control, extraction and disposal of excess carcass fat. Understanding underlying mechanisms of excessive fat deposition in poultry will aid in improving carcass

quality and minimize production cost. We hypothesized that chicken adipocity is highly influenced by factors beyond the genome. Therefore, the aim of this study was to employ a proteomics approach to identify proteins that may be associated with fat accretion in broiler chickens. Metabolic profiles of the experimental birds were also evaluated. One hundred and 20 1-d-old broiler chickens were randomly assigned to floor pens and fed standard broiler diet for 8 weeks. At 8 WOA, experimental birds were bled, sacrificed and adipose tissue from the abdominal and visceral areas was collected, weighed and frozen in liquid nitrogen before storage at −80 oC until used. Adipose proteome from the birds with the highest and lowest abdominal fat percentage (8 birds each) was assayed using 2-dimensional differential gel electrophoresis (2D-DIGE) followed by in-gel digestion and Matrix Assisted Laser Desorption/ionization Time-of-Flight (MALDI-TOF) mass spectrometry. A total of 132 spots were found to be differentially expressed between the extreme birds ($P < 0.05$). Several of the proteins are unique and some are involved in metabolic pathways that are associated with fat accretion including vimentin, apolipoprotein, and anexin. Obese birds exhibited high levels of potassium and serum glutamic oxaloacetic transaminase than their lean counterparts. The lean birds on the other hand exhibited higher levels of alkaline phosphatase than obese birds.

Key words: broiler chickens, adipose tissue proteome, metabolic profiles

T50 PCR-RFLP analysis of promoter region of Interferon gamma gene in high and low immunocompetent Aseel native chicken. S. Choudhary*[1], S. Kumar[2], and B. Nautiyal[1], *[1]MJP Rohilkhand University, Bareilly, U.P. India, [2]Central Avian Research Institute, Bareilly, U.P. India.*

Resistance to diseases is under the control of certain immune response genes. Interferon gamma (INFG), a cytokine is one such candidate gene that plays a critical role in immune system function. In this study, DNA polymorphism of INFG gene at promoter region was studied using polymerase chain reaction- restriction fragments length polymorphism (PCR-RFLP) technique in 48 random bred Aseel native chicken, 24 in high and 24 in low immunocompetence index group. Two sets of PCR primer, set I for full length promoter and set II for partial length promoter, amplified product with 670 bp and 495 bp in size, respectively. Agarose gel electrophoresis and DNA sequencing of PCR amplified product confirmed amplification of INFG gene promoter region. PCR-RFLP analysis of full length promoter with enzymes, *Eco*RI and *Taq*I and partial length promoter with enzymes Alu I, Hinf I, Dde I and *Taq*I was monomorphic, whereas, full length promoter with enzyme Tsp509 I was polymorphic. Gene frequencies of 2 alleles, allele A (168, 123, 99, 88, 64 and 54 bp fragments) and allele B (123, 104, 99, 88, 64 and 54 bp fragments) were 0.64 and 0.36. The genotypic frequencies of genotypes AA, AB and BB were 0.17, 0.30 and 0.53, respectively. Heterozygote (AB) demonstrated higher magnitude of all immunocompetence traits. Tsp509 I PCR-RFLP of INFG gene at promoter region was suggestive of development of genetic markers for high humoral immune response in chicken.

Key words: Aseel, PCR-RFLP, interferon gamma

T51 Association of BMPR–IB gene polymorphism with breeding value of growth and reproductive traits in Mazandaran native chicken. Sh. Niknafs*, A. Nejati Javaremi, and M. Sadeghi, *Agricultural Faculty, University of Tehran, Karaj, Alborz, Iran.*

The aim of the current study was to investigate A287G SNP of the chicken BMPR-IB gene and its association with the breeding value of growth and reproductive traits. Hence, a sample of 206 individuals including 10 males and 196 females of Mazandaran native chicken were genotyped using PCR-RFLP technique. On the other hand, for estimating breeding value of the traits, phenotypic information of 18 successive generations of selection in breeding station of Mazandaran native chicken (north of Iran) was analyzed using a univariate animal model in ASREML procedure. Investigated traits included body weight at hatch (35287 records), at 8 (43067), at 12 weeks of age (38297), at sexual maturity (31147), egg number (31349), age at first egg (31349), egg weight of first (27249), of 28 (17225), of 30 (19031), of 32 (18955) weeks of age, average egg weight of first 12 weeks of production (18847), egg mass (28725) and egg production intensity (31349). Finally, marker-trait association analyses were performed using estimated breeding value of the traits, as dependent variable, in GLM procedure of SAS 9.1. The significant differences of least squares means were tested with Tukey-Kramer multiple range tests, and a P-value of < 0.05 was considered statistically significant. Two alleles and 3 genotypes were identified. Genotypic frequency of AA, AG and GG were 0.349, 0.544 and 0.107 respectively. Results showed, for all investigated traits, no significant differences among breeding value LSmeans of the genotypes existed ($P < 0.05$). In conclusion, we found no significant association between BMPR-IB gene and breeding value of the growth and egg production traits in Mazandaran native chicken.

Key words: BMPR-IB gene, SNP, growth and reproductive traits

T52 Association of a single nucleotide polymorphism in NPY gene with growth and reproductive traits in Mazandaran native chicken. S. Niknafs*, A. Fatemi, H. Mehrabani Yeganeh, and A. Nejati Javaremi, *Agricultural Faculty, University of Tehran, Karaj, Alborz, Iran.*

The objective of the current study was to investigate a SNP (with accession number of M87298) for the chicken NPY gene and its association with breeding value of growth and reproductive traits in chicken. A breeding station of Mazandaran native chicken was established in 1988 with 2 main objectives: extension and genetic improvement of the local breed. From 1988 to 2009, 18 generations of selection was done for traits of 8-wk BW (BW8), egg number, age at first egg and average egg weight as selection criteria. Recorded traits consisting of body weight at hatch (35287 records), at 8 (43067), at 12 weeks of age (38297), at sexual maturity (31147), egg number (31349), age at first egg (31349), egg weight of first (27249), of 28 (17225), of 30 (19031), of 32 (18955) weeks of age, average egg weight of first 12 weeks of production (18847), egg mass (28725) and egg production intensity (31349). A total of 206 individuals, from generation 17, were selected at random and genotyped for the SNP using PCR-RFLP technique. Phenotypic information of the 18 generations was analyzed genetically to estimate breeding value of the traits for genotyped individuals. Genetic analysis was performed by univariate animal model in ASREML software. Fixed effects of sex, generation and hatch were considered in the model where would have significant effects. Marker-trait association analysis was done using breeding values (as dependent variable) and SNP genotypes (as independent variables) in GLM procedure of SAS 9.1. Three genotypes of BB, Bb and bb with the frequencies of 0.885, 0.100 and 0.015 were respectively identified. Results suggested that there were significant differences among breeding value LSmeans of genotypes for body weight at sexual maturity. In conclusion, chicken

NPY gene may be associated with body weight and may be considered in MAS program to improve growth performance.

Key words: growth and reproductive traits, NPY gene, SNP

T53 Association of a single nucleotide polymorphism from GnRHR gene with growth and egg production traits in Mazandaran native chicken. S. Niknafs*, A. Fatemi, H. Mehrabani Yeganeh, and A. Nejati Javaremi, *Agricultural Faculty, University of Tehran, Karaj, Alborz, Iran.*

Gonadotropin releasing hormone receptor (GnRHR) is mainly associated with the development and function of the reproductive axis in avian species. To study the association of this gene with growth and egg production traits in Mazandaran birds, a total of 206 individuals were selected at random and PCR-RFLP technique was used to genotype chickens for one SNP (accession number AJ506779) of this gene. Three genotypes of AA, Aa and aa with the frequencies of 0.379, 0.469 and 0.152, respectively, were identified. Association of these genotypes with both breeding values and phenotypic records of growth and egg production traits were examined. Breeding values were estimated by a univariate animal model in ASREML methodology using information that pertained to 18 generations of selection in breeding station of Mazandaran native chicken. A total of 206 genotyped chickens for this study belonged to generation 17. Investigated traits included body weight at hatch (35287 records), at 8 (43067), at 12 weeks of age (38297), at sexual maturity (31147), egg number (31349), age at first egg (31349), egg weight of first (27249), of 28 (17225), of 30 (19031), of 32 (18955) weeks of age, average egg weight of first 12 weeks of production (18847), egg mass (28725) and egg production intensity (31349). Marker-trait association analysis showed no significant differences among phenotypic LSmeans of the genotypes. However, least squares means of breeding value for traits of egg number and egg mass demonstrated significant differences among genotypes. More egg number and egg mass were observed for the genotype AA. In conclusion, GnRHR gene may be associated with egg production traits genetically and additively in Mazandaran native chicken.

Key words: GnRHR gene, SNP, chicken

T54 Investigation of three single nucleotide polymorphisms of STAT5B gene and their association with growth and reproductive traits in Mazandaran native chicken. S. Niknafs*, A. Nejati Javaremi, M. Sadeghi, and A. Fatemi, *Agricultural Faculty, University of Tehran, Karaj, Alborz, Iran.*

The objective of the current study was to investigate the association of 3 SNPs of the STAT5B gene with breeding value of growth and reproductive traits in Mazandaran native chicken (north of Iran) breed. A total of 205 individuals were selected randomly and genotyped for 3 SNPs of STAT5B gene (C4535156T, G4533675C and G4533815A) using PCR-RFLP technique. Phenotypic information of 18 generations was employed in estimating breeding value for different traits using univariate animal models in ASREML. Investigated traits included body weight at hatch (35287 records), at 8 (43067), at 12 weeks of age (38297), body weight at sexual maturity (31147), egg number (31349), age at first egg (31349), egg weight of first (27249), at 28 (17225), at 30 (19031), at 32 (18955) weeks of age, average egg weight of the primary 12 weeks of production (18847), egg mass (28725) and egg production intensity (31349). Marker-trait associations analysis were performed with the GLM procedure of SAS 9.1. Significant differences of least squares means were tested with Tukey-Kramer multiple tests correction, and corrected P-values <0.05 were considered statistically significant. Two alleles and 3 genotypes were observed for each SNP. Alleles of A (0.663) and a (0.337) for C4535156T SNP, B (0.646) and b (0.354) for G4533675C SNP, C (0.804) and c (0.196) for G4533815A SNP were identified. Four significant associations of C4535156T SNP with body weight at hatch, G4533675C SNP with egg weight of first and G4533815A SNP with body weight at 8 and 12 weeks of ages were found ($P < 0.05$).

Key words: STAT5B gene, growth and reproductive traits, chicken

T55 Effect of feeding a combination of galacto-oligosaccharides and a *Bifidobacterium* sp. strain on feline intestinal ecosystem. G. Biagi*[1], I. Cipollini[1], M. Grandi[1], C. Pinna[1], A. Pompei[2], M. Zini[3], and G. Zaghini[1], *[1]Department of Veterinary Medical Sciences, University of Bologna, Ozzano Emilia, Italy, [2]Department of Pharmaceutical Sciences, University of Bologna, Bologna, Italy, [3]Department of Biochemistry, University of Bologna, Bologna, Italy.*

Synbiotics (i.e., the combination of a prebiotic and a probiotic) are recognized means to modulate composition and activities of gut microbiota. The aim of the present study was to evalute the effects derived from the oral administration of a combination of galacto-oligosaccharides (GOS) and a *Bifidobacterium pseudocatenulatum* strain, previously isolated from the feces of a healthy adult cat, on composition and metabolism of feline intestinal microbiota. Growth kinetics of the *B. pseudocatenulatum* strain was determined on 4 different prebiotic substances (GOS, fructo-oligosaccharides, lactitol and pectin). Biomass yield was higher ($P < 0.01$) for GOS than for other treatments. Ten adult healthy cats received for 15 d a synbiotic consisting of the freeze-dried *B. pseudocatenulatum* strain (10^8 cfu/d) and GOS at 1% of the diet. Fecal samples were collected from each cat the day before synbiotic administration started (Day 0) and 1 and 10 d after synbiotic withdrawal (Day 16 and 25, respectively), for chemical and microbiological analysis. Results at Day 0, 16 and 25 were analyzed by one-way ANOVA with time as the main factor. While no difference on fecal moisture and pH was detected, ammonia concentrations were reduced on d 16 and 25 compared with trial start (288 and 281 vs. 353 mmol/g of fecal DM; $P < 0.05$). On Day 16, fecal concentration of acetic acid was increased compared with d 0 (17.1 vs. 13.2 mmol/g of fecal DM; $P < 0.05$). Furthermore, on Day 16, fecal concentrations of lactic, n-valeric and iso-valeric acids were lower than on Day 0 and 25 (0.18 vs. 0.30 and 0.30, 0.15 vs. 1.84 and 1.73, 0.35 vs. 0.65 and 0.62 mmol/g of fecal DM, respectively; $P < 0.05$). Fecal counts of *Cl. perfringens*, enterococci, *Bacteroides* spp., *E. coli* and lactobacilli were not influenced by treatment whereas an increase of bifidobacteria counts was observed on Day 16 and 25 compared with trial start (7.98 and 7.52 vs. 5.63 Log cfu/g of fecal DM; $P < 0.01$). Present results show an overall positive influence derived from the synbiotic administration on feline fecal microbiota.

Key words: bifidobacteria, feline intestinal microbiota, synbiotics

T56 Dietary fiber viscosity may affect insulin and GLP-1 secretion, but does not appear to contribute to the "second meal effect" in healthy adult dogs. P. Deng*[1], A. Wolff[1], A. N. Beloshapka[1], B. M. Vester Boler[1], and K. S. Swanson[1,2], *[1]Department of Animal Sciences, University of Illinois, Urbana, [2]Division of Nutritional Sciences, University of Illinois, Urbana.*

Viscous dietary fibers have beneficial effects on postprandial glucose metabolism and insulin secretion. However, the effects of fiber viscosity on the "second meal effect" in dogs are unknown. Our objective was to evaluate the effects of dietary fiber type in a morning meal on glucose, insulin, and glucagon-like peptide 1 (GLP-1) responses to a glucose challenge later in the day. Six healthy adult intact female hounds (mean BW = 25 kg) were used in a replicated 3 × 3 Latin square design consisting of 21 d (3 7-d periods). Dogs were randomly assigned to one of 3 treatments containing equal amounts of fiber: a low-viscosity fiber (LVF) diet containing 8% cellulose; a moderate-viscosity fiber (MVF) diet containing 4% cellulose, 2% psyllium, and 2% pectin; or a high-viscosity fiber (HVF) diet containing 4% psyllium and 4% pectin. Dogs were fed 3 times daily (8 a.m.; 12 p.m.; 4 p.m.) to maintain BW. On the last day of each period, dogs were fed at 8 a.m. as usual, then dosed with 25 g of maltodextrin in 120 mL of water at 12 p.m. Blood samples were collected before (0 min) and 10, 20, 30, 45, 60, 90, 120, and 180 min after dosing, and analyzed for glucose, insulin, and GLP-1 concentrations. Baseline and postprandial incremental area under the curve (IAUC) data were analyzed statistically. Baseline GLP-1 concentrations were greater ($P < 0.005$) in dogs fed HVF, while baseline insulin concentrations in dogs fed HVF were lower ($P < 0.05$) than dogs fed MVF, but not different from dogs fed LVF. There were no differences in baseline GLP-1 and insulin concentrations between dogs fed MVF and LVF. No treatment effects were observed in glucose, insulin, and GLP-1 IAUC responses. This might be due to the timing of meals and baseline insulin and GLP-1 effects. In conclusion, while fiber viscosity did not appear to contribute to a second meal effect, dogs fed highly viscous fibers had altered GLP-1 and insulin concentrations 4 h after the morning meal. Further research to determine the effects of fiber viscosity on gut hormone response and mechanisms of action in dogs is needed.

Key words: viscous dietary fibers, second meal effect, dog

T57 Comparison of fecal microbial communities of healthy adult dogs fed raw meat-based or extruded diets using 454 pyrosequencing. A. N. Beloshapka*[1], S. E. Dowd[3], L. Duclos[4], and K. S. Swanson[1,2], *[1]Department of Animal Sciences, University of Illinois, Urbana, [2]Division of Nutritional Sciences, University of Illinois, Urbana, [3]Research and Testing Laboratory, Lubbock, TX, [4]Nature's Variety Inc., Lincoln, NE.*

It is often presumed that feeding a raw meat-based diet will negatively affect the fecal microbial populations of dogs. However, this question has not been well tested in healthy dogs. Thus, the objective of this experiment was to use 454 pyrosequencing to characterize microbial populations of healthy adult dogs fed raw meat-based or extruded diets. Six healthy adult beagles (5.5 ± 0.5 yr; 8.5 ± 0.5 kg) were first fed a commercially available extruded diet (control), then randomly allotted to 1 of 6 raw meat diets in a Latin square design. Diets had varying protein, fat and carbohydrate (including fiber) composition. Following a 14d adaptation phase, a fresh fecal sample was collected on d15 or d16 for each period. Dogs were fed to maintain BW throughout the study. Genomic DNA was extracted from fresh fecal samples and used to create 16S rDNA amplicons, which were then subjected to 454 pyrosequencing. Predominant bacterial phyla in all dogs included Firmicutes, Bacteroidetes, and Fusobacterium. However, dogs fed raw meat-based diets had lower ($P < 0.01$) Firmicutes and Bacteroidetes, but greater ($P < 0.01$) Fusobacteria and Proteobacteria populations. Actinobacteria were also present at low quantities (1.5%), but unchanged by diet. *Clostridium*, *Fusobacterium*, and *Bacteroides* were predominant bacterial genera in all dogs. Dogs fed raw meat-based diets had greater ($P \leq 0.05$) *Fusobacterium* (25.6 vs. 14.8%), but lower ($P \leq 0.05$) *Fecalibacterium* (0.3 vs. 9.7%), *Lactobacillus* (0.02 vs. 8.9%), *Prevotella* (0.2 vs. 8.8%), *Eubacterium* (1.4 vs. 2.8%), and *Enterococcus* (0.2 vs. 1.2%) populations as compared with dogs fed the extruded diet. Although gastrointestinal distress was not observed in dogs fed raw meat-based diets, the dietary changes resulted in great shifts in fecal microbiota. Future studies are required to determine

whether dietary macronutrient composition or form of diet resulted in such changes, and how they may affect long-term health.

Key words: gut microbiota, raw diets, pyrosequencing

T58 Processing techniques to maintain low glycemic index of peas. J. Fouhse*[1], J. Adolphe[2], L. Weber[2], and M. Drew[1], *[1]University of Saskatchewan, Saskatoon, Saskatchewan, Canada, [2]Western College of Veterinary Medicine, Saskatoon, Saskatchewan, Canada.*

Peas have a low glycemic index (GI) due to their low content of rapidly digestible starch (RDS) and high content of slowly digestible (SDS) and resistant starch (RS) fractions. Low GI foods are thought to protect against cardiovascular disease, diabetes and obesity thus, the use of peas as a starch source in dog foods may improve the health of dogs. However, peas intended for canine diets require processing to increase palatability and digestibility, which may affect the GI of peas. An experiment was performed to determine the effect of extrusion processing on pea starch fractions RDS, SDS and RS. The trial used a completely randomized 2 × 2 × 2 × 2 factorial design with 2 levels of temperature (110 vs. 150°C), moisture (20 vs. 28%), particle size (288 vs. 407μm) and cooling method (freezing vs. drying). Extrudates were analyzed for their RDS, SDS and RS contents. Particle size significantly affected RS and RDS portions ($P < 0.05$). There was a significant negative correlation between particle size and RDS and SDS fractions ($P < 0.05$) and a trend toward particle size being positively correlated with RS content ($P = 0.059$). RDS was also positively correlated with temperature ($P < 0.05$). Subsequently, 4 of the 16 extruded pea treatments were selected for the measurement of GI in beagles (n = 6): 1) 150°C, 288 μm, 20% H_2O, dried; 2) 110°C, 288 μm 20% H_2O, dried; 3) 150°C, 407 μm 28% H_2O, frozen; 4) 110°C, 407 μm, 28% H_2O, frozen. All test diets were fed in amounts that provided 10g of available carbohydrate. A 20% glucose solution was used as a control. There was no relationship between GI and particle size, moisture content or cooling rate ($P < 0.05$). However, GI was negatively correlated with temperature ($P < 0.05$). These results suggest that in vitro starch fractions are not good predictors of GI in dogs. However, starch fractions and GI may be manipulated by controlling processing temperature. Further studies are needed to determine the effect of multiple temperatures on the GI of various starch fractions.

Key words: glycemic index, pea starch, extrusion

T59 Acute effects of carbohydrates in dogs. J. L. Adolphe*[1], J. M. Fouhse[2], M. D. Drew[2], and L. P. Weber[1], *[1]Department of Veterinary Biomedical Sciences, Western College of Veterinary Medicine, University of Saskatchewan, Saskatoon, Saskatchewan, Canada, [2]Department of Animal and Poultry Science, College of Agriculture and Bioresources, University of Saskatchewan, Saskatoon, Saskatchewan, Canada.*

In humans, diets containing low glycemic index (GI) carbohydrate sources appear to be protective against cardiovascular disease, diabetes and obesity. However, the effect of carbohydrates on health in dogs is poorly characterized. The purpose of this research was to examine the acute effect that high and low glycemic ingredients and dog foods have on glycemic, insulinemic and cardiovascular responses in dogs. Laboratory beagles (n = 6–7) were used in 2 crossover experiments. First, the GI of 4 carbohydrate sources (corn, barley, rice and peas) was determined. Second, the GI was determined for 2 extruded dog diets containing either a high or low GI carbohydrate source. A glucose solution was used as the control food and foods were fed in amounts that provided 10 g available carbohydrate. Flow-mediated dilation (FMD), a measure of endothelial function and predictor of cardiovascular health, was performed before and 60 min after feeding. The mean GI (±SEM) of the carbohydrate sources were: peas 29 ± 5; corn 47 ± 10; barley 51 ± 7; and rice 55 ± 6. Thus, the peas (lowest GI) and rice (highest GI) were used as the carbohydrate source to formulate the extruded diets in experiment 2. The GI for the extruded pea and rice diets were 46 ± 7 and 63 ± 9, respectively. The area under the insulin response curve was significantly higher for the glucose compared with the carbohydrate sources or extruded diets, but no difference was observed between the carbohydrate sources or diets. FMD did not differ between the carbohydrate sources or diets, but was lowest 60 min after feeding glucose in both experiments. A negative correlation between FMD and serum glucose was found 60 min after feeding the carbohydrate sources ($r = -0.3$; $P = 0.02$), but not for extruded diets ($r = -0.08$; $P = 0.6$). In both studies, peas resulted in a decreased glycemic response. However, once formulated into an extruded dog food, the GI of the peas and rice increased suggesting that the properties of the carbohydrate source were altered due to the presence of other ingredients and/or extrusion. Future studies are needed to determine if the lower GI pea diet offers health benefits in the long-term.

Key words: glycemic index, cardiovascular, flow-mediated dilation

T60 Effects of protease enzyme on diets for growing mink (*Mustela vison*). E. S. Dierenfeld*[1], E. Keith[1], R. Johnson[2], C. Falco[2], B. Roeder[3], and N. Odetallah[1], *[1]Novus International, Inc., St. Charles, MO, [2]FBAC, Sandy, UT, [3]Brigham Young University, Provo, UT.*

Enhanced protein digestion/diet utilization through the use of exogenous enzymes was investigated for application to commercial mink production. A preliminary in vitro study was conducted to determine effects of time (0, 2, 3 or 4 h), temperature (23°, 30°, 35° or 40°C), and enzyme inclusion (0, 0.05% or 0.1%) upon diet matrix viscosity to mimic practical handling/storage/ranch conditions associated with bulk diet preparation, transport to feeding sites, and environmental temperatures of feed on cages. Healthy growing mink kits (n = 24) were assigned randomly to one of 4 diet treatments with 6 replicates. Animals were housed individually in metabolism cages, acclimated for 2 wk and fed a blended diet (150 −230 g) twice daily, with water available ad libitum. Diets were identical with the exception of protease enzyme (CIBENZA DP100) added at 0 (Control), 0.05, 0.1 or 0.2% (wt/wt). Apparent digestibility (D_a) was measured over a 5-da trial using Cr_2O_3 (0.1%) as a marker; daily feed intake and weekly BW were recorded. Kits fed diets containing 0.1% enzyme gained more weight (76 g; $P = 0.11$), demonstrated higher ADG (41 vs. 30 g/d), and consumed less food (20 g/d) than controls, resulting in improved F:G ratios (9 vs. 13; $P = 0.05$). Additionally, they tended toward higher DM digestibility (85.5 vs. 83%; $P = 0.11$) and improved crude protein D_a. Inclusion of 0.1% protease thus resulted in improved utilization of practical diets for growing mink. In the laboratory studies, time ($P < 0.001$) and enzyme concentration ($P < 0.05$, for all temperatures except 35°C) had significant impacts on diet matrix consistency. Direction of change was temperature dependent, suggesting varying protein fractions may have been affected at different temperatures. For minimal effects upon physical characteristics of mink diet containing exogenous CIBENZA DP100, maintain long-term storage at ≤ 4°C, and when feeding, ensure diet is kept at ≤ 30°C for no longer than 2–3 h before consumption.

Key words: mink, protease enzyme

T61 Influence of feeding a fish oil containing diet to mature overweight dogs: Effects on lipid and protein metabolism, postprandial glycemia, and body weight. M. R. C. de Godoy*, K. R. McLeod, and D. L. Harmon, *University of Kentucky, Lexington.*

The aim of this study was to assess the mechanism by which fish oil may alter lipid and protein metabolism, postprandial glycemia, and body weight in mature overweight dogs. Seven female dogs were randomly assigned to 1 of 2 isonitrogenous and isocaloric diets, control (CO) or 2% fish oil (FO), in a crossover design. Experimental periods were 69 d, separated by a wash out period of 30 d. At the beginning of the experiment, and at 30 and at 60 d of feeding the experimental diets, the dogs were infused with D-glucose (2 g/kg body weight) through the intravenous catheter. Blood samples were collected for 3h to perform a glucose tolerance test. Nitrogen balance began at 0700 on d 63 of each experimental period, and ended at 0700 on d 69. On d 66 of each period a single dose (7.5 mg/kg) of ^{15}N-glycine was administered orally to each dog via a gelatin capsule. From d 66 at 0700 through d 69 at 0700 an additional 25% of acidified urine from each dog was separated, composited and frozen for later analysis for ^{15}N enrichment and determination of protein turnover. Incremental area under the curve and glucose concentration at peak did not differ between treatments or overtime within treatment. Glucose clearance from plasma was increased ($P < 0.05$) in the FO treatment on d 30 when compared with baseline (d 0). β-Hydroxybutyrate, NEFA and triglycerides did not differ within or between treatments. Cholesterol decreased ($P < 0.05$) on the FO treatment on d 30, d 60 and d 69 when compared with d 0, as well as on d 60 when compared with d 30 of the same dietary treatment. High density lipoprotein (HDL) decreased in the FO treatment on d 69 when compared with d0. Body weight, food intake, fecal excretion, dry matter and nitrogen digestibilities, nitrogen balance, as well as protein turnover were not different between diets. Overall, the FO diet improved the rate glucose tissue uptake and decreased cholesterol and HDL concentrations in mature overweight dogs.

Key words: dog, fish oil, postprandial glycemia

T62 Influence of feeding a fish oil containing diet to adult lean dogs: Effects on lipid and protein metabolism, postprandial glycemia, and body weight. M. R. C. de Godoy*, C. E. Conway, K. R. McLeod, and D. L. Harmon, *University of Kentucky, Lexington.*

The aim of this study was to assess the mechanism by which fish oil may alter lipid and protein metabolism, postprandial glycemia, and body weight in lean adult dogs. Eight female Beagles were randomly assigned to 1 of 2 isonitrogenous and isocaloric diets, control (CO) or 2% fish oil (FO), in a crossover design. Experimental periods were 69 d in length, separated by a wash out period of 30 d. At the beginning of the experiment, and at 30 and at 60 d of feeding the experimental diets, a baseline blood sample was collected and the dogs were, subsequently, fed their daily ration. Postprandial blood samples were collected for 3h to perform a glycemic response. Nitrogen balance began at 0700 on d 63 of each experimental period, and ended at 0700 on d 69. On d 66 of each period a single dose (7.5 mg/kg) of ^{15}N-glycine was administered orally to each dog via a gelatin capsule. From d 66 at 0700 through d 69 at 0700 an additional 25% of acidified urine from each dog was separated, composited and frozen for later analysis for ^{15}N enrichment and determination of protein turnover. Incremental area under the curve and glucose concentration at peak did not differ between treatments or overtime within treatment. Triglycerides were increased ($P < 0.05$) in both dietary treatments on d 69 when compared with baseline (d 0). Cholesterol was increased ($P < 0.05$) on the CO treatment on d 69 when compared with d 0. Body weight and food intake did not differ between dietary treatments. Dry matter digestibility was decreased ($P < 0.05$) and fat digestibility tended ($P < 0.10$) to decrease in the FO treatment. Nitrogen digestibility and balance, as well as protein turnover were not different between dietary treatments. Overall, feeding a FO containing diet did not appear to improve protein and lipid metabolism, and postprandial glycemia in adult lean dogs.

Key words: dog, fish oil, postprandial glycemia

T63 In vivo and in vitro procedures for measuring coat quality after dietary manipulation in dogs. G. González-Ortiz[1], L. Castillejos*[1], R. Franco-Rosselló[1], J. J. Mallo[3], J. Alcañiz[3], M. A. Calvo[2], and M. D. Baucells[1], *[1]Nutrition and Welfare Service, Department of Animal and Food Science (UAB), Bellaterra, Spain, [2]Departament de Sanitat i d'Anatomia Animals (UAB), Bellaterra, Spain, [3]Norel, S.A., Spain.*

A standardized methodology, noninvasive and practical procedure to asses coat quality in companion animals has not been described in the literature. Beneficial effects of probiotic supplementation on animal and human health have been reported. The objective was to determine whether probiotic supplementation could improve coat quality in healthy dogs using noninvasive procedures. Sixteen beagles were divided in 2 groups of 8 dogs: control (T1) and treatment (T2) supplied with 1 g/kg of ingested food of a mixture of *Bacillus amyloliquefaciens* CECT 5940 and *Enterococcus faecium* CECT4515 (5×10^8 cfu/g each strarin) from Norel S.A. Procedures were carried out after the supplementation period (D1) of 39 d and after 56 d of non probiotic supplementation (D2). Each animal was evaluated by 4 trained observers who recorded different scored parameters (visual brightness, softness and optimum coat feel). These scores resulted in a final hair condition score (HCS) between 3 (less valued) and 7 (more valued). Colorimetry was used for measuring light intensity (L*) in the parietal area by MiniScan 45/0 Lav of HunterLab. Hair samples were taken to perform an in vitro challenge. The ability of Microsporum canis to degrade hair's structure and develop drilling organs was used as resistance or susceptibility indicator. Data was analyzed using the MIXED procedure of SAS. On D1, T1 and T2 had similar HCS (5.34 vs. 5.36). T2 showed lower HCS in D2 than D1 ($P = 0.02$) whereas no differences were found in T1. Concerning L*, the interaction of the main factors was statistically significant ($P = 0.047$). T2 showed greater L* in D1 than D2 (39.19 vs. 36.83 ± 1.873; $P = 0.054$). However, L* values in T1 were not different between days. No drilling organs were observed in T2 on D1, but on D2 they were detected in half of T2 samples. However, T1 showed drilling organs in both sampling periods. Data suggest differences in the coat quality after the nonprobiotic supplementation period. The combination of hair condition score, colorimetry and in vitro hair culture could be used to evaluate changes on hair quality in dogs related to dietary manipulation.

Key words: dogs, hair quality, probiotic

T64 Evaluation of a mixture of *Bacillus amyloliquefaciens* CECT 5940 and *Enterococcus faecium* CECT4515 in adult healthy dogs. G. González-Ortiz[1], L. Castillejos*[1], J. J. Mallo[3], J. Alcañiz[3], M. A. Calvo[2], and M. D. Baucells[1], *[1]Nutrition and Welfare Service, Department of Animal and Food Science (UAB), Bellaterra, Spain, [2]Departament de Sanitat i d'Anatomia Animals (UAB), Bellaterra, Spain, [3]Norel, S.A., Spain.*

Probiotic supplementation has demonstrated beneficial effects such as reestablishment of unbalanced intestinal microbiota, enhanced resistance to colonization by enteropathogens and improving intestinal barrier, among others. The objective of this study was to evaluate the potential effect of a mixture of 2 probiotic strains (*Bacillus amyloliquefaciens* CECT 5940 and *Enterococcus faecium* CECT 4515 at 5×10^8 cfu/g each strain) in adult healthy dogs. Sixteen beagles (8 males and 8 females; between 1 and 7 years of age) housed at the UAB facilities were used. Animals were divided into 2 groups of 8 dogs: control (T1) and treatment (T2) group received daily 1 g of probiotic mixture per kg of the same dry diet for 39 consecutive days. Daily food consumption, weekly body weight and body condition score and fecal score (3 times a week) were assessed as health indicators. Fresh fecal samples were collected on d 1, last day of supplementation period (d 39) and after a withdrawal period of 6 d (d 45). By means of conventional plating methods, total aerobic mesophilic bacteria, *Enterobacteriaceae* spp., *Escherichia coli*, *Clostridium perfringens*, lactic acid bacteria and the 2 probiotic strains were analyzed. Fecal pH was determined. Total fecal samples were collected during 6 d to perform a digestibility trial during the supplementation period according to FEDIAF (2008). Differences were tested by PROC MIXED (SAS, 2002). The 2 probiotic strains were recovered after the supplementation period from fresh fecal samples, but not after the withdrawal period. No statistical differences were detected in any health indicators measured or in digestibility coefficients. No statistical differences were found in microbiota analyzed. However, C. perfringens counts were significantly reduced in T2 after the supplementation period (5.64 vs. 2.94 ± 0.53 log cfu/g feces; $P < 0.0001$). Bacterial counts were in the same range as baseline after the withdrawal period and no differences were detected in fecal pH. The use of probiotics could stabilize dog fecal microbiota, by decreasing pathogenic populations.

Key words: dogs, microbiota, probiotic

T65 Effect of increasing levels of mannoprotein in humoral immunity in dogs. A. F. Chizzotti*, F. M. O. B. Saad, F. S. Ebina, R. C. Silva, J. S. R. Reis, and M. C. Kadri, *Universidade Federal de Lavras, Lavras, MG, Brazil.*

The advances of health sciences have provided a deeper understanding of cellular and molecular mechanisms for normal and abnormal physiological states. At the same time, the relationship between nutrition and health has been studied through the discovery of nutrients and non-nutrients capable of interfering in the pathological process. Nutraceuticals can improve organism functions and some are used as immunomodulators. Nutrients denominated immunonutrients or immunomodulators, such as mannoprotein, obtained from external cell wall of *Saccharomyces cerevisiae*, have shown the ability to preserve the intestinal mucus integrity, improving the immunological response. The aim of this study was to evaluate the effect of increasing levels of fractions of mannoprotein in dog's immune system. This study was conducted at the Department of Animal Science of Federal University of Lavras, Brazil. Twenty-four adult Beagle dogs were randomly assigned to 4 treatments: commercial diet (control) and control plus 300, 600, 900 ppm of fractions of mannoprotein, on dry matter basis. Diets were formulated according to NCR (2006) recommendations, and mannoprotein were added to the diets in capsules. Diets were fed for 37 d. Blood samples were collected from jugular vein on d 0, 10, 23 and 35 in a syringe and were centrifuged to obtain serum which was kept refrigerated until clinical analysis. The blood assessments included complete blood count, quantification of antibodies against leishmaniasis, immunoglobulin IgA, IgG and IgM concentrations, platelets, fibrinogen and C-reactive protein. The animals were exposed to antigen challenge by vaccination against leishmaniasis on d 7. Data were analyzed as repeated measurements in time using PROC MIXED of SAS 9.1. No treatment differences were detected over all variables measured ($P > 0.05$). The use of mannoprotein fractions up to 900 ppm in the diet did not influence humoral immunity of dogs.

Key words: immunonutrients, nutraceuticals, canines

T66 Effect of dietary starch level on protein metabolism in domestic cats. T. J. Wester*[1], K. Weidgraaf[1], M. Hekman[1], N. J. Cave[2], and M. H. Tavendale[3], *[1]Institute of Food, Nutrition and Human Health, Massey University, Palmerston North, New Zealand, [2]Institute of Veterinary, Animal and Biomedical Sciences, Palmerston North, New Zealand, [3]AgResearch Ltd., Palmerston North, New Zealand.*

Cats evolved eating meat-based diets high in protein and very low in carbohydrates and consequently have high AA requirements and high obligate AA catabolism. Cats must also use AA to produce glucose when dietary carbohydrate is limited. Metabolism may be affected at low protein intake when there is a conflict between AA use for protein synthesis and gluconeogenesis. This study was undertaken to test whether protein utilization in cats would be enhanced if glucose, from dietary starch, is used to replace gluconeogenesis from protein. Adult cats (n = 12) were allocated to either low or high starch diets (0 or 25% starch as-fed) with 15% ME as CP. Diets were fed at maintenance for 3 wk, and then cats were fitted with saphenous and cephalic vein catheters. On the following day, they received primed continuous infusions of [^{13}C]bicarbonate, [1-^{13}C]Leu, and [$^{15}N_2$]urea and [6,6-d_2]glucose from 0 to 120, 120 to 480, and 0 to 480 min, respectively. Cats were fed hourly during infusion and Leu entry rate from diet was calculated. Breath was sampled at 0, 100, 110, 120, 440, 460, and 480 min to measure $^{13}CO2$, with blood sampled at 0, 440, 460, and 480 min to measure ^{13}C enrichments in Leu and ketoisocaproate, and urea and glucose fluxes. There were no differences between treatments for non-oxidative Leu disposal (NOLD, an indicator of protein synthesis), Leu rate of appearance in plasma (Ra, an indicator of protein degradation), and Leu oxidation (Table 1). However, Leu flux and urea production rate (an indicator of net protein catabolism) tended to be lower ($P < 0.1$) in cats fed 25% starch diets indicating that protein utilization for anabolism may be more efficient in cats fed starch.

Table 1.

	Diet (% starch as fed)			
	0	25	SEM	P <
Leu flux, μmol/(kg•h)	243.8	207.6	12.85	0.07
Leu NOLD, μmol/(kg•h)	150.4	129.7	12.67	0.28
Leu Ra, μmol/(kg•h)	157.1	126.1	13.19	0.13
Leu oxidation, μmol/(kg•h)	93.5	77.9	11.82	0.37
Urea production, μmol/(kg•h)	519.0	396.8	46.56	0.09
Glucose flux, μmol/(kg•h)	1,065.3	1920.7	103.74	0.001

Key words: feline nutrition, protein metabolism, urea flux

T67 Effect of glucose infusion and dietary protein level on urea production in the domestic cat. T. J. Wester*[1], K. Weidgraaf[1], M. Hekman[1], N. J. Cave[2], and M. H. Tavendale[3], *[1]Institute of Food, Nutrition and Human Health, Massey University, Palmerston North, New Zealand, [2]Institute of Veterinary, Animal and Biomedical Sci-*

ences, Palmerston North, New Zealand, [3]AgResearch Ltd., Palmerston North, New Zealand.

Cats are unique among domestic animals as they are obligate carnivores that have evolved eating diets high in protein and very low in carbohydrate. As a carnivore eating a meat-based diet, cats are reliant on gluconeogenesis from protein to meet their glucose requirement even when protein intake is low or at the requirement (15% ME as CP). This study was undertaken to examine the effect of glucose infusion on AA catabolism in cats fed at and above their protein requirement. Our hypothesis was that once the glucose requirement was met by endogenous administration, urea production would reach a minimum. Adult cats (n = 18) were allocated to one of 3 very low carbohydrate diets with 15, 45 or 65% ME intake as CP and fed at maintenance for 3 wk. Cats were then fitted with saphanous and cephalic vein catheters and fasted overnight. The following day they received a primed continuous infusion of [$^{15}N_2$]urea from 0 to 720 min. Starting at 120 min, glucose was continuously infused into the cephalic vein at 0, 0.75, 1.5, 4.0, and 8.0 mg/kg•min for 2 h at each level. Blood was sampled in the last 30 min of each level of glucose infusion. Urea production rate increased with increasing dietary protein ($P < 0.001$), but decreased as glucose level increased only at 45 and 65% ME as CP ($P < 0.001$; Table 1). This drop in urea production as rate of glucose infusion increased was greater at 65 vs. 45% CP as ME ($P < 0.001$). When dietary protein was supplied at its requirement, AA catabolism was low and not affected by glucose infusion. The minimum level of urea produced when glucose was supplied in cats fed 15% ME as CP may represent obligate AA catabolism.

Table 1. Urea production (μmol/kg•h) in cats fed diets containing varying levels of ME intake as CP

Glucose infusion, mg/kg•min	Diet (% ME as CP)		
	15	45	65
0	32.60	466.2	598.8
0.75	325.74	439.8	556.2
1.5	315.56	418.2	510.6
4.0	302.90	401.4	473.4
8.0	307.74	394.2	447.0

Fixed effects of protein level, glucose infusion, and protein×glucose were significant ($P < 0.001$; SEM = 25.08).

Key words: feline nutrition, protein metabolism, urea flux

T68 Effects of sow stocking rate and season on bermudagrass (*Cynodon dactylon*) ground cover. S. Pietrosemoli*[1], J. C. Guevara[2], and J. T. Green[3], [1]*Animal Science Department, North Carolina State University, Raleigh,* [2]*Alternative Swine Research and Extension Project, Raleigh, NC,* [3]*Crop Science Department, North Carolina State University, Raleigh.*

Sustainable outdoor swine production faces management challenges to minimize potential environmental impacts, including the deterioration of vegetative ground cover, soil disturbance, irregular nutrient dispersion and high nutrient loads that can cause soil and water pollution and risk of N-leaching and ammonia volatilization. Ground cover reduces erosion by increasing infiltration, trapping sediments, stabilizing the soil, and reducing the effects of intense rainfall. High stocking rates can accelerate degradation. At the Center for Environmental Farming Systems (CEFS) in Goldsboro, NC, the effects of 3 stocking rate (SR; 10, 15 and 25 sows/ha) on bermudagrass ground cover were evaluated during 3 seasons (S; Jan-March 09 [W09]; Sept-Oct 09 [F09] and Apr-May 10 [S10]). Paddocks of 2020m^2 were divided into 9 sections, with the central section being defined as a heavy use area where shelter and water were provided and with permanent access by the animals. The other sections were managed in a weekly rotational pattern. Yorkshire sows (avg BW: W09: 294; F09: 212; S10: 186 kg) were restrictedly fed concentrate daily in the morning (3 kg, 15% CP). Ground cover components (percent of live vegetation (LV), dead residue (DR), bare soil (BS), and vegetative ground cover (VGC) changes were recorded weekly following a step point technique on transect lines evenly distributed across all sections. The VGC was the sum of LV and DR. The experimental design was a randomized complete block, with 2 field replicates. The SR affected LV (P = 0.09; 41.71^a, 27.97^b and 28.0^b %, respectively, for 10, 15 and 25 sows/ha) whereas BS did not change (P = 0.31; 23.6, 32.7 and 34.4%, respectively, for 10, 15 and 25 sows/ha). Season had a pronounced effect on VGC components: LV W09: 7.2^a, F09: 38.2^b; S10: 52.3^c%; P = 0.0005) and DR (W09: 67.2^a, F09: 23.3^b; S10: 17.9%^{b}; P = 0.0002). Conversely, S had no effect on BS (W09: 22.5; F09:38.4; S10: 52.3%; P = 0.14). Under the conditions of these experiments, S had a more pronounced effect on vegetative ground cover than SR.

Key words: *Cynodon dactylon*, swine, stocking rate

T69 Cradle-to-farm gate analysis of milk carbon footprint. A critical review. G. Pirlo*, *Consiglio per la ricerca e sperimentazione in agricoltura, Centro di ricerca per le produzioni foraggere e lattiero-casearie (CRA-FLC), Cremona, Italy.*

Objectives, methods and results of life cycle assessment (LCA) studies about milk production have been examined. The studies considered refer to milk production only and do not include milk transportation to dairies, processing and distribution. Otherwise, the parts of the studies down the milk production have been excluded. Emissions of GHG (CO2, CH4 and N2O) only have been considered, ignoring other environmental impacts such as acidification, eutrophication, land use, energy use, water use, eco-toxicological and human-toxicological pollutants, desertification, biodiversity, PM10 etc. Studies have been classified according to the country, the farm data source (real farms, simulated representative farms, national statistics), functional unit, allocation criteria, LCA tools (databases, models, literature), kind of comparison (milk ability, year, conventional versus organic farming, grazing versus confined, system intensification grade, herd size). Comparisons show a large variability among the GHG emissions associated to the functional unit, caused also by the different methods used in the analyses. Study showed the important role played by production system, stocking rate, and milk ability. LCA seems to be a tool for several scopes: international benchmark, economic and social planning, eco-labeling, verification of technical innovations. Further studies on farm characteristics, consumptions and emissions associated with milk production are needed in order to make LCA a practical tool.

Key words: GHG, LCA, CFP

Dairy Foods: Microbiology

T70 Fluid milk quality survey. C. Boeneke*, J. Vargas, and K. Aryana, *Louisiana State University Agricultural Center, Baton Rouge.*

Whole and 2% milks were received from 17 dairy processing plants located in the west, midwest, and southern regions of the United States in duplicates. All milks were shipped overnight in Styrofoam coolers filled with ice to maintain the temperature of the samples. The samples were pasteurized at the processing plants by high-temperature short-time pasteurization. The first set of milk samples was evaluated for standard plate count, coliforms, and psychrotrophic counts using a standard method as well as a rapid method, heat-resistant spore-forming psychrotrophs, aerobic spores, HR testing (HR-1, HR-2 and HR-3), fat percentage, protein percentage, somatic cell count and a sensory evaluation immediately upon arrival. Milks were evaluated for flavor using the Collegiate Dairy Products Evaluation Score Sheet. The duplicate set was evaluated for standard plate count, coliform count and a sensory evaluation at the end of 2 weeks storage time at 7°C. Three replications were conducted. Five percent of the 2% milk samples presented psychrotrophic counts (3 samples in the first replication of the study, 2 samples in the third replication) with a mean values of approximately 2 cfu/ml. For heat resistant spore forming psychrotrophs, 10% of the samples showed the highest counts of approximately 1 cfu/ml, mainly in the second replication of the study. Ninety percent of the samples showed zero counts. Sensory evaluation scores ranged from 1 to 10 out of 10 possible points. The most common flavor criticism found by the panelists was a cooked off-flavor as well as rancid and oxidized criticisms.

Key words: fluid milk, shelf life, flavor

T71 Seasonal variation of psychrotrophic bacteria isolated from raw milk in South Korea. H. A. Lee*, J. H. Myung, Y. H. Park, and Y. K. Shin, *Institute of Dairy Food Research, Seoul Dairy Cooperative, Ansan, Kyunggi, South Korea, 425-838.*

The aim of this study was to examine the distribution and diversity of psychrotrophic bacteria from raw milk sampled from 9 provinces in South Korea by seasons. Raw milk was collected from farms in the central, eastern, western, southern, northern, northern east, southern east Kyunggi, Ansan and Incheon province at 4 different seasons. The samples were diluted and plated on sterile plate count agar and incubated at 7°C for 10 d. Then, 20 colonies per province every season were randomly selected and subcultured at least 3 times at 30°C for 48 h. For bacterial sequencing, 16s rDNA region was amplified using RT-PCR, then the products were sequenced using the 3130 Genetic analyzer. As a result, psychrotrophic counts were higher in winter than in other seasons as 5.43 log cfu/mL ($P < 0.05$). Among 9 provinces, the population in raw milk sampled from Incheon province was in significantly greater numbers and from the western Kyunggi province was in significantly lower numbers than from any other provinces, 5.38 log cfu/mL and 3.56 log cfu/mL, respectively ($P < 0.05$). Among 720 bacterial isolates, the predominant class was Gammaproteobacteria (84.01%) and genus was *Acinetobacter* (36.99%), especially *Acinetobacter johnsonii* (17.24%).

Key words: psychrotrophic bacteria, raw milk, seasonal

T72 Influence of multilayer packaging on pasteurized milk quality. M. da Silva Pinto, A. F. Carvalho*, J. Y. Suda, A. C. P. Silveira, and A. C. dos Santos Pires, *Food Science Department, Federal University of Viçosa, Viçosa, MG, Brazil.*

The type of packaging used for pasteurized milk can substantially affect their quality characteristics by directly controlling the amount of oxygen and light which comes into contact with food or for providing perfect isolation to avoid post-processing contamination by microorganisms. In this study, we tested 3 different high density polyethylene (HDPE) multilayer films and one HDPE monolayer film with the objective to evaluate the effects of the 4 different packaging types on milk quality: (1) multilayer with high barrier to light, high oxygen barrier, high tensile strength; (2) multilayer with high oxygen barrier; (3) multilayer with high barrier packing light, high tensile strength and (4) monolayer. The milk stored in each type of packaging was analyzed as the microbiological (mesophilic and psychrotrophic bacteria), physicochemical (pH, titratable acidity, dry matter content, protein content, fat content, lactose content, density and cryoscopy) and nutritional (fat oxidation and vitamin degradation) characteristics besides sensory acceptance of pasteurized milk stored at 5°C for 21 d. Three replications were analyzed using the general linear models procedure of SAS (SAS Institute Inc., Cary, NC) version 9.1, licensed by University Federal of Viçosa, 2008. The milk quality was in accordance with the Brazilian legislation. The various film properties provided by the different packaging systems demonstrated similar milk characteristics ($P > 0.05$) during the 21 d of storage at 5°C, although there were differences between the barrier packaging. All packaging materials evaluated can provide sufficient protection to the quality of pasteurized milk that can achieve a shelf life of 21 d/ 5°C, considering the conditions of the quality of the raw material and the integrity of the entire cold chain.

Key words: packaging, shelf-life, milk quality

T73 Microbiological quality of UHT dairy products analyzed by rapid, reference, and ATP bioluminescence methods. A. F. Cunha[1], A. D. Lage[1], M. M. P. Araújo[1], C. F. Abreu[2], A. R. Tassinari[2], M. R. Souza[1], C. F. A. M. Penna[1], L. M. Fonseca[1], M. O. Leite[1], and M. M. O. P. Cerqueira*[1], *[1]Universidade Federal de Minas Gerais, Belo Horizonte, Minas Gerais, Brazil, [2]3M do Brazil, Sumaré, São Paulo, Brazil.*

Besides traditional methods used for microbiological analysis of UHT dairy products, rapid methodologies based on ATP bioluminescence have been developed to detect contamination of these products in a shorter time. The use of these new approaches for monitoring the quality of UHT products such as Brazilian flavored milk and milk cream was compared with the traditional microbiological methods. Sixty-six samples of UHT dairy products, from different sources, incubated at 48, 72, and 168 h, were analyzed for the counts of mesophilic and psychrotrophic aerobic microorganisms using plate count agar (PCA) and brain heart infusion (BHI) agar and also PetrifilmAC plates. The data were compared with results of the ATP bioluminescence technique performed by the 3MMicrobial Luminescence System expressed in RLU and submitted to the MacNemar test at 95% of confidence. At all incubation times, the majority of UHT dairy samples showed low counts of mesophilic and psychrotrophic microorganisms and values lower than 150 RLU by ATP bioluminescence. Only one sample showed mesophilic count above the limit established by the Brazilian legislation - 100 cfu/mL - in PCA (2.6×10^2 cfu/mL) and PetrifilmAC (1.1×10^2 cfu/mL) at 168 h. These high counts were also detected by the ATP bioluminescence (416 RLU) and were mathematically equal.

It can be concluded that the ATP bioluminescence results were similar to those obtained by traditional methods. For the dairy industry, the ATP bioluminescence using the MLS system may become an important tool for rapid monitoring of microbiological quality of UHT dairy products, releasing the products in a shorter time than that established by the Brazilian legislation.

Key words: UHT dairy products, ATP bioluminescence, quality

T74 Phylogenic analysis and characterization of bacterial sporeformer isolates obtained from raw milk, pasteurized milk, and dairy farm environments. R. A. Ivy*, M. L. Ranieri, N. H. Martin, H. C. den Bakker, B. M. Xavier, M. Wiedmann, and K. J. Boor, *Cornell University, Ithaca, NY.*

The presence of psychrotolerant bacterial sporeformers represents a major challenge to extending the shelflife of pasteurized dairy products. The objective of this study was to identify prominent phylogenetic groups of psychrotolerant dairy-associated sporeformers from a collection sporeformer isolates from dairy systems (i.e., raw and pasteurized milk and dairy farm environments). Partial *rpoB* sequences of 1425 sporeformer isolates had been obtained previously, and partial 16S rDNA sequencing was used to assign species identifications to unique *rpoB* allelic types (ATs). A maximum likelihood phylogenetic tree was constructed for 288 unique *rpoB* ATs. Major *rpoB* clades consisted of Bacillaceae (i.e., *Bacillus* spp., *Lysinobacillus* spp., and *Viridibacillus* spp.) and *Paenibacillus* spp. Most Bacillaceae isolates grouped into clades with known contaminants of raw milk or with species associated with high altitudes, soil, and organic material. Major *Paenibacillus* clades were identified as *P. ordorifer*, *P. amylolyticus*, and *P. graminis*, and many uncharacterized *Paenibacillus* species were identified. Among the 8 major Bacillaceae clades, only 2 included isolates that grew to >4 log (cfu/ml) in skim milk broth (SMB) at 6°C, whereas 6 out of 8 major *Paenibacillus* clades contained isolates that grew to >4 log(cfu/ml) in SMB at 6°C. Though all *Paenibacillus* clades tested positive for β-galactosidase activity at 32°C and most Bacillaceae clades tested negative, *Bacillus licheniformis* (13% of Bacillaceae isolates) showed variable β-galactosidase activity. β-galactosidase activity alone, therefore, could not reliably distinguish between Bacillaceae and *Paenibacillus*. Therefore, consensus sequences of predominant *Paenibacillus rpoB* ATs indentified in this study will be used to design a DNA-based system to rapidly and specifically detect these psychrotolerant sporeformers in fluid milk and dairy ingredients (e.g., milk powders).

Key words: sporeformers, dairy microbiology, *Paenibacillus*

T75 Spores in dairy products: Characterization and destruction by pulsed light. A. Laubscher* and R. Jimenez-Flores, *California Polytechnic State University, Dairy Products Technology Center, San Luis Obispo.*

The USDA has reported an increase in the consumption of nonfat dry milk and skim milk powders due to the opening of international markets for these products. However, the main limitation to international sales is the spore counts in dairy powders. The objective of this study was to examine the characteristics of the spores in California milk powders, and to evaluate the potential quality improvement using pulsed light covering all wavelengths. We designed our experiments around 4 liquid matrices in which to contain the spores: sterile nanopure water, sterilized whey, non-fat UHT milk, and 2% UHT milk. In addition we tested dry matrices in 6 commercial skim milk and buttermilk powders. The bacteria used to inoculate these medias include ATCC reference strains (*Geobacillus* spp. and *Paenibacillus* spp.) and a collection of aerobic spore-forming bacteria isolated from California milk powders. These strains were selected because they were considered to be highly heat-resistant after exposure to excessive heat treatments. UV treatments with the Xenon pulsed lamp consisted of 4 different levels (1 burst, 2 bursts, 3 s, and 20 s) and included a post 4°C incubation and HTST pasteurization. Protein profiles were obtained for each strain used, and compared before and after treatments. With pure water we observed a seven logarithmic reduction in spores with two bursts of pulsed UV light. However, cloudy solutions were much less permissive of the lethal action of light. These matrices had the same seven logarithmic reductions but only after 3 seconds. Powders were treated with variable success, and much detriment to the flavor and chemical structure. However, while the same reduction of spore viability was achieved, the powder buttermilk was significantly more resistant to off flavor development.

Key words: spores, pulsed light, milk quality

T76 The effect of different sweeteners on growth and survival of *Lactobacillus rhamnosus* GR-1 in milk. S. Hekmat*[1,2] and G. Reid[2], *[1]Brescia University College, London, Ontario, Canada, [2]Canadian Research and Development Center for Probiotics, London, Ontario, Canada.*

There has been an increasing demand by consumers for low-calorie and low-sugar products with functional properties. *Lactobacillus rhamnosus* GR-1 is a probiotic agent with therapeutic properties. The objective of this study was to monitor growth and survival of *L. rhamnosus* GR-1 in milk sweetened with various sweetening agents during storage period. Six formulations of milk (1% fat) with 7% xylitol (X), 0.04% stevia (ST), 5% sucrose (S), 0.04% stevia-inulin-chromium mixture (SIC), 1.25% sucralose (SU) and one with no sweetening agents (C) were prepared. The mixtures were autoclaved for 15 min, cooled to 37°C and inoculated with 1% of starter culture. The samples were then incubated anaerobically at 37°C overnight. Selective MRS agar containing 0.015 g/L fusidic acid was used to enumerate *L. rhamnosus* GR-1 after 1, 14, and 28 d of storage at 4°C. All sweetening agents supported the growth and survival of *L. rhamnosus* GR-1; however, it showed a higher survival rate ($P < 0.05$) in the ST and SIC treatments. After 1 d of storage, the total colony counts of treatments ST and SIC for *L. rhamnosus* GR-1 were 7.4×10^9 and 1.1×10^9 cfu/mL, respectively. The total colony counts for all treatments decreased slightly after 28 d of storage. The results indicate that *L. rhamnosus* GR-1 can remain viable in presence of various sweetening agents during the storage period and there is potential for incorporating these sweetening agents in other probiotic dairy products.

Key words: probiotics, sweeteners, milk

T77 Detection and transfer of the glutamate decarboxylase gene in *Streptococcus thermophilus*. G. Somkuti*, J. Renye, and D. Steinberg, *Eastern Regional Research Center/USDA, Wyndmoor, PA.*

γ-Aminobutyric acid (GABA) is generated from glutamate by the action of glutamic acid decarboxylase (GAD) and characterized by hypotensive, diuretic and tranquilizing effects in humans and animals. The production of GABA by lactic acid starter bacteria would enhance the functionality of fermented dairy foods including cheeses and yogurt. The survey of 42 strains of the yogurt starter culture *Streptococcus thermophilus* by PCR techniques indicated the presence of

a glutamate decarboxylase gene (*gad*) in 15 strains. DNA sequencing data indicated that in the genome of GAD+ *S. thermophilus* strains the *gad* as a rule is flanked by a transposase gene (5′) and a HD-superfamily hydrolase gene (3′). Specific primers were designed to amplify a 1.75-kb genomic fragment in *S. thermophilus* to include *gad* and its putative promoter region. The resulting PCR product was inserted into the 5.48-kb pMEU5a shuttle vector which was used to transform *Escherichia coli* DH5α. Subsequently, the recombinant plasmid pMEU5a-1/*gad* (7.24 kb) was transferred by electroporation into the GAD-negative strain *S. thermophilus* ST128. The ST128 transformants carrying the plasmid-encoded *gad* produced fully functional GAD enzyme as evidenced by the conversion of glutamate to GABA at a rate similar to strains with *gad* located on the chromosome. The results demonstrated the potential to equip non-GABA producing strains *S. thermophilus* and possibly other lactic acid bacteria with the capacity to produce GAD to improve culture performance in the development of functional foods.

Key words: γ-aminobutyric acid, *Streptococcus thermophilus*

T78 Development of a real-time PCR assay for rapid detection of spoilage *Paenibacillus* spp. in fluid milk. M. L. Ranieri*, W. R. Mitchell, R. A. Ivy, N. Martin, M. Wiedmann, and K. J. Boor, *Cornell University, Ithaca, NY.*

Psychrotolerant sporeforming bacteria, specifically *Paenibacillus* spp., represent the current biological limit to the extension of fluid milk shelf-life. *Paenibacillus* have been found in farm environments, raw milk, processing plant environments, and in pasteurized fluid milk across the United States. While typically present at low levels in raw milk, *Paenibacillus* spores can survive conventional pasteurization temperatures, germinate, and grow to numbers capable of negatively impacting the sensory characteristics of refrigerated milk products. A real-time PCR assay was designed to detect *Paenibacillus* spp. in fluid milk and discriminate between *Paenibacillus* and other closely related sporeforming bacteria. Partial 16S rDNA sequences, representing a total of over 1400 *Paenibacillus* and *Bacillus* spp. isolated from dairy farms, milk processing plants, and fluid milk products, were compared with identify appropriate primer and probe regions specific to *Paenibacillus* spp. To confirm specificity, genomic DNA from 16 *Paenibacillus* and 17 *Bacillus* isolates were tested with the assay; these isolates represented the 9 most frequently isolated *Paenibacillus* and *Bacillus* allelic types, plus additional allelic types to include genetic diversity. All 16 *Paenibacillus* isolates were detected with a mean cycle threshold (Ct) of 19.14 (±0.54). While 14/17 *Bacillus* isolates showed no signal (Ct > 40), 3 *Bacillus* isolates showed very weak positive signal (Ct = 38.66 [±0.80]). When total genomic DNA was also extracted from milk samples inoculated with *Paenibacillus*, we found a detection limit of 1,000 *Paenibacillus* cfu/mL. We also showed that this assay could be used to screen colonies collected from standard plate count agar, using crude colony lysates. Despite the additional incubation time necessary to develop colonies on plate media, this method eliminates the time and cost associated with genomic DNA preparations. Overall, this assay represents a specific and rapid tool to identify *Paenibacillus* spp. and therefore provides a method for determination of sources or milk containing spoilage bacteria.

Key words: fluid milk, spoilage, *Paenibacillus*

T79 Genetic analysis of a novel plasmid encoded durancin locus in *Enterococcus durans* 41D. L. Du[1], G. Somkuti*[2], and J. Renye[2], [1]*Nanjing University of Finance and Economics, Nanjing, China,* [2]*Eastern Regional Research Center/USDA, Wyndmoor, PA.*

Enterococcus durans is commonly found in the intestinal tract in humans and animals and several strains are known to produce bacteriocins. Durancin GL, a novel bacteriocin of *Enterococcus durans* 41D with antilisterial activity was isolated from artisanal cheese samples and its genetic determinants were characterized. The bacteriocin operon included the structural (durA) and immunity (durB) genes among the 9 putative ORFs identified on pDGL1, an 8.3-kb plasmid which was fully sequenced. The deduced DurA protein was a 71-amino acid peptide with 74% identity to the class II bacteriocin BacA of *E. faecalis*. DurA had a potential signal peptidase cleavage site indicating the involvement of a sec-dependent transport system in yielding a 7.97 kDa mature peptide. The mature DurA peptide had the typical structure of subclass IIa bacteriocins, including a conserved YYGNG motif and a hydrophobic C-terminal region. The immunity gene (durB) encoded a 94-amino acid peptide with 85% identity to the BacB immunity gene. The minimum requirement for durancin GL production was defined by translationally fusing a 547 bp fragment containing the durAB genes with the *Streptococcus thermophilus* chromosomal promoter P2201 by PCR, and subcloning in vector pMEU5a. Isolates of the yogurt starter culture *S. thermophilus* electrotransformed with the recombinant plasmid pMEU5a-1 secreted durancin GL into the medium and inhibited the growth of *Listeria*. The results showed the possibility of transferring the durancin GL gene into food-grade lactic acid bacteria to serve as the source of a natural bioprotective agent for *Listeria* control.

Key words: durancin, *Listeria*, *Streptococcus thermophilus*

T80 Development of a qPCR method for monitoring strain dynamics during yogurt manufacture. D. Miller*, E. G. Dudley, and R. F. Roberts, *The Pennsylvania State University, University Park.*

Starter cultures used in the manufacture of yogurt consist of multiple strains of *Lactobacillus delbrueckii* ssp. *bulgaricus* (LB) and *Streptococcus thermophilus* (ST). Existing tools for monitoring ST and LB levels during yogurt manufacture rely on conventional plating methods, which require 48–72 h of incubation and do not allow for quantification of individual strains. The objectives of the present work were to i) design and evaluate primers for quantification of individual strains in a commercial starter culture by quantitative polymerase chain reaction (qPCR), ii) to identify an external control for DNA isolation and qPCR, iii) to prepare standard curves with individual starter culture strains and combinations of starter culture strains spiked in bulk starter base, and iv) to evaluate strain balance in bulk starters prepared at 3 different temperatures. Strain-specific primers were designed for 2 ST strains (ST DGCC7796 and ST DGCC7710), one LB strain (DGCC 4078) and one *Lactobacillus delbrueckii* ssp. *lactis* strain (DGCC4550). Primers for the individual ST strains were designed to target unique DNA sequences in clustered regularly interspersed palindromic repeats (CRISPR, GenBank Accession no. EF434468 and EF434469). LB primers targeted a CRISPR locus based on sesquence information provided by the culture supplier. Primers for LL were designed to target mannitol-specific IIbC component of the PTS system (GenBank Accession no. AF496224.1). *Lactobacillus farciminis* ATCC 29644^T (LF) was selected as an external control for the DNA extraction procedure and qPCR because it has a similar peptidoglycan structure as the LB and LL strains. Following evaluation of primer specificity, standard curves relating cell number to cycle threshold (Ct) were prepared for each strain individually and for each strain in 3-strain combinations when spiked bulk starter base, and no significant

differences in the slopes were observed ($\alpha = 0.05$). Strain balance data was collected for bulk starter cultures prepared at 37, 41, and 43°C to demonstrate the potential application of this method for evaluation of the influence of fermentation conditions on strain balance.

Key words: yogurt, qPCR, LB and ST

T81 Binding and efficacy of a natural biopreservative (nisin) in different food matrices. R. Niewohner*, S. Anand, and R. Nauth, *South Dakota State University, Brookings.*

Nisin is a natural biopreservative produced by lactic acid bacteria. We explored its ability to bind in different food matrices and to protect them from bacterial spoilage in ranch sauce, vegetable soup, and hot dogs with a well plate assay. Skim milk was used as a control for these studies. Challenge studies were also conducted by spiking specific spoilage bacteria such as *Lactobacillus plantarum* in ranch sauce and hot dogs, and *Bacillus cereusi* in vegetable soup. The hypothesis of this experiment was that the more recovery of nisin over time of the sample matrix, the fewer bacteria will be able to grow, since the "free nisin" is not bound and available to act against the bacteria. *Lactococcus lactis ssp. cremoris* was used as a test culture in the entire study. All experiments were replicated thrice. In the first part of the experiment, a nisin standard was established using 10, 100, 1,000, and 10,000 IU Recovery studies were conducted at 0 and 24 h intervals in each of the food matrices, including milk, by spiking 1000 IU of nisin. The Dunnett multiple comparisons showed that skim milk had the highest recovery. Ranch sauce showed a slight decrease with about 900 IU recovered, however, in vegetable soup only 20 IU could be recovered. Hot dogs showed a slight decrease, but it was not significantly different from the milk. After 24 h, the ranch sauce and the hot dog proved to not be significantly different than the milk. However, the vegetable soup showed a decreased recovery over time with a final estimate of 5 IU of nisin. In the ranch sauce challenge study, with nisin addition at 1,000 IU, a decrease in *L. plantarum* counts were observed up to 24 d of the storage studies from an initial count of 10^9 cfu/g of the sample. The hot dogs with 1,000 IU of nisin showed a decrease in the number of *L. plantarum* up to 10 d of the storage studies. On the other hand, *Bacillus cereus* (10^4 cfu/g) in vegetable soup challenge test did not show any reduction by nisin at 1,000 IU. The study thus demonstrated variations in the binding of nisin to different food matrices with variable protective effect.

Key words: recovery of nisin, preservative, ranch sauce, hot dog, and vegetable soup

T82 Resistance of membrane biofilms to cleaning and sanitation treatments. D. Singh* and S. K. Anand, *Midwest Dairy Foods Research Center, Dairy Science Department, South Dakota State University, Brookings.*

Previous studies conducted in our lab have established the formation of bacterial biofilms on reverse osmosis (RO) whey concentration membranes. In the present study we evaluated the effectiveness of different chemicals of a cleaning in place (CIP) protocol against the constitutive microflora of biofilms formed on whey RO membranes. Different bacterial isolates that were a part of biofilm consortia of 2 to 12 mo old membranes included *Bacillus* sp., *Escherichia coli*, *Klebsiella oxytoca, Enterococcus* sp., *Streptococcus* sp., *Staphylococcus* sp., *Micrococcus* sp., *Aeromonas* sp., *Corynebacterium* sp., and *Pseudomonas* sp. The CIP protocol tested against the planktonic and 12-h-old biofilms of above microflora included 5 treatment steps based on; alkali, surfactant, acid, enzyme, a second surfactant, and a weekly sanitizer application. The results confirmed the resistance of isolates in both planktonic and embedded states against most of the 5 treatment steps. The only effective step was acid based treatment, which resulted in 5–8 logs reduction in case of planktonic cells, and 2–5 logs reduction against embedded cells in 12 h old biofilms formed under lab conditions. The sanitizer treatment step also showed similar results and caused a reduction of 6–8 logs against planktonic cells. On the other hand, it was much less effective against the embedded cells in biofilms, and resulted in a reduction of only 1 to 3 log counts. *Bacillus* sp. showed highest resistance in planktonic cell, as well as, embedded cell state. Differences were noticed in the resistance pattern of biofilm isolates as the membranes aged. In general, isolates from the older membranes showed higher resistance to CIP chemicals and sanitizer treatment. Data were statistically analyzed using the SAS program. On the basis of these results, it can be concluded that the biofilms formed on the RO whey concentration membranes were resistant to the CIP protocol being used.

Key words: planktonic, biofilm, embedded

T83 Effect of low sonication intensities on the growth of *Streptococcus salivarius* ssp. *thermophilus* ST-M5 subjected to different temperatures. M. Moncada* and K. Aryana, *School of Animal Sciences, Louisiana State University Agricultural Center, Baton Rouge.*

Whether low sonication conditions stimulate the growth of bacterial cultures is not clearly understood. The objective was to study the influence of low sonication intensities on the growth characteristics of *Streptococcus salivarius* ssp. *thermophilus* at different temperatures. 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 4 sonication intensities of 8.07, 14.68, 19.83 and 23.55 Watts/cm^2 randomized over 3 different temperatures (4, 22 and 40°C) of inoculated peptone water before sonication. The energy input (1500 J) was kept constant in all treatments. Control samples did not receive any sonication treatment. Growth of treatment and control samples was determined hourly during 12 h of incubation at 37°C. Data were analyzed using proc mixed model of statistical analysis system (SAS). At all 3 temperatures growth of *Streptococcus thermophilus* ST-M5 subjected to low sonication intensities were significantly ($P < 0.05$) better than control. At 4 and 40°C all low sonication intensities showed better growth than control. At 22°C 8.07, 14.68 and 19.83 Watts/cm^2 showed higher ($P < 0.05$) viable counts than control and 23.55 Watts/cm^2. Some low sonication intensities improved growth of *Streptococcus salivarius* ssp. *thermophilus* ST-M5.

Key words: mild sonication, probiotic

T84 Low sonication intensity influences on the protease activity of *Lactobacillus delbrueckii* ssp. *bulgaricus* LB-12 at different temperatures. M. Moncada* and K. Aryana, *School of Animal Sciences, Louisiana State University Agricultural Center, Baton Rouge.*

Low sonication intensity is an acoustic energy which involves the conversion of an electrical signal into a physical vibration. It uses the sound for modifying the permeability of the cell plasma membrane. *Lactobacillus delbrueckii* ssp. *bulgaricus* is a widely used bacterium used for the production of some fermented dairy products. The objective was to study the influence of low sonication intensities on protease activity of *Lactobacillus delbrueckii* ssp. *bulgaricus* LB-12 at different

temperatures. 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 4 sonication intensities of 8.07, 14.68, 19.83 and 23.55 Watts/cm^2 randomized at 3 different temperatures (4, 22 and 40°C) of inoculated peptone water before sonication. The energy input (1500 Joules) was kept constant in all treatments. Control samples did not receive any sonication treatment. Protease activity was determined at 0, 12 and 24 h of incubation spectrophotometrically at 340 nm. Differences of least squares means were used to determine significant differences at $P < 0.05$ for main effect (low sonication intensity) and interaction effect (low sonication intensity * time * temperature). At 4°C the sonication intensities of 14.68, 23.55 and 19.83 W/cm^2 significantly ($P < 0.05$) increased protease activity compared with the control. At 22°C the sonication intensities of 23.55 and 19.83 W/cm^2 had protease activities significantly ($P < 0.05$) higher than the control. The optical density (OD) values for control bacterium and culture sonicated at 19.83 and 23.55 W/cm^2 at 12 h were 0.38, 0.46 and 0.59 absorbance units respectively. The OD at 24 h for control bacterium and bacterium sonicated at 19.83 and 23.55 W/cm^2 were 0.68, 0.92 and 0.96 absorbance units. At 40°C all treatments exhibited significantly ($P < 0.05$) higher protease activity than control. Protease activity of *Lactobacillus delbrueckii* ssp. *bulgaricus* LB-12 was improved by some low sonication intensities.

Key words: mild sonication, probiotic

T85 Influence of low sonication intensities at different temperatures on the bile tolerance of *Streptococcus salivarius* spp. *thermophilus* ST-M5. M. Moncada* and K. Aryana, *School of Animal Sciences, Louisiana State University Agricultural Center, Baton Rouge.*

Low sonication intensity condition is a non-destructive technique that uses sound waves to cause cavitation in aqueous solutions and may improve the permeability of membrane, speed up the transfer of substrates and promote cellular growth and propagation. Bile tolerance is an important probiotic characteristic. *Streptococcus salivarius* spp. *thermophilus* is widely used in the fermentation of dairy products. The objective was to determine the effect of various low sonication intensities at different temperatures on bile tolerance of *Streptococcus salivarius* spp. *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 4 sonication intensities of 8.07, 14.68, 19.83 and 23.55 W/cm^2 randomized over 3 different temperatures (4, 22 and 40°C) of inoculated peptone water before sonication. The energy input (1500 J) was kept constant in all treatments. Control samples did not receive any sonication treatment. Bile tolerance of samples were determined hourly for 12 h of incubation. Data were analyzed using the using proc mixed model of statistical analysis system (SAS). At 22°C culture sonicated at 19.83 W/cm^2 and at 4°C culture sonicated at 8.07 and 14.68 W/cm^2 showed similar bile tolerance compared with control. At 40°C bacterium subjected to intensity of 14.68 W/cm^2 showed significantly ($P < 0.05$) higher bile tolerance at hours 6 to 12 compared with control.

Key words: mild sonication, probiotic

T86 Screening of mild pulsed electric field parameters for enhancing acid tolerance of *Streptococcus salivarius* spp. *thermophilus* ST-M5. N. Najim and K. Aryana*, *School of Animal Sciences, Louisiana State University Agricultural Center, Baton Rouge.*

Aim of the present study was to screen mild PEF conditions for increasing acid tolerance. Freshly thawed frozen concentrated culture of *Streptococcus salivarius* spp. *thermophilus* ST-M5 was suspended in 0.1% (wt/vol) sterile peptone water and treated in pilot plant PEF system. A range of mild PEF treatments included positive and negative square unipolar pulse widths of 2, 3, and 4 µs, pulse periods of 0.3 and 0.6 s, voltages of 1 and 3 kV/cm at 2 temperatures, 21.6°C and 40.5°C. The control was run through the PEF system without receiving any pulsed electric field condition. The flow rates of both the control and PEF treated samples were kept constant at 60 mL/min. Samples were individually inoculated in acidified M17 broth at pH 2.0. Samples were plated in duplicates and incubated aerobically at 37°C for 48 h. The acid tolerance was determined at 0, 30, 60, 90 and 120 min of incubation. Three replications were conducted for each experimental condition. The acid tolerances using the 3 positive square unipolar pulses of 2, 3 and 4 µs for both pulse periods of 0.3 and 0.6 s and voltage of 1 kV/cm at both 21.6°C and 40.5°C PEF treatment temperatures were significantly the highest compared with both the control and negative square unipolar pulses at the same PEF conditions. The acid tolerance with positive square unipolar pulse width of 3 µs for both pulse periods of 0.3 and 0.6 s using voltage of 1kV/cm at 40.5°C PEF treatment temperature was significantly higher than both pulses of 2 and 4 µs. Furthermore, the same PEF conditions at 40.5°C PEF temperature showed significantly higher acid tolerance than pulses of 2, 3 and 4 µs at 21.6°C. The acid tolerances using positive square unipolar pulse widths of 2, 3 and 4 µs for both pulse periods of 0.3 and 0.6 s with voltage of 1 kV/cm were significantly higher than both the control and those subjected to voltage of 3 kV/cm at the same PEF conditions. Positive square unipolar pulses significantly improved acid tolerance compared with the negative square unipolar and square bipolar pulses.

Key words: mild pulsed electric fields, probiotic

T87 Mild pulsed electric field conditions identified for improving growth, protease activity and acid tolerance of *Lactobacillus delbrueckii* ssp. *bulgaricus* LB-12 and *Lactobacillus acidophilus* LA-K. N. Najim and K. Aryana*, *School of Animal Sciences, Louisiana State University Agricultural Center, Baton Rouge.*

The objective was to determine the effect of mild pulsed electric field (PEF) conditions on acid tolerance, growth and protease activity of *Lactobacillus delbrueckii* ssp. *bulgaricus* LB-12 and *Lactobacillus acidophilus* LA-K. Freshly thawed frozen concentrated cultures were individually inoculated in 0.1% (wt/vol) sterile peptone water and treated in pilot plant PEF system. The treatment was positive square unipolar pulse width of 3 µs, pulse period of 0.5 s, voltage of 1 kV/cm, delay time of 20 µs and flow rate of 60 mL/min at 40.5°C PEF treatment temperature. The control was passed through the PEF system at the same flow rate (60 mL/min) without receiving any pulsed electric field condition. The acid tolerance was determined every 30 min for 120 min of incubation in acidified MRS broth at pH 2. Growth of the cultures was determined hourly for 32 h of incubation of *Lactobacillus acidophilus* LA-K and for hourly for 25 h of incubation of *Lactobacillus delbrueckii* ssp. *bulgaricus*LB-12. Protease activity was determined at 0, 12, 24, 36 and 48 h of incubation. Three replications were conducted. The viability of the control *Lactobacillus delbrueckii* ssp. *bulgaricus* LB-12 was lost after 30 min of incubation in acidified MRS broth (pH 2), whereas, the bacterium subjected to mild PEF treatment was acid tolerant until the end of 120 min of incubation.

Mild PEF treated cultures of both *Lactobacillus acidophilus* LA-K and *Lactobacillus delbrueckii* ssp. *bulgaricus* LB-12 reached the logarithmic growth phase an hour earlier than the control. Mild PEF treatment significantly ($P < 0.0001$) enhanced the protease activity of both *Lactobacillus delbrueckii* ssp. *bulgaricus* LB-12 and *Lactobacillus acidophilus* LA-K compared with the control. Mild PEF conditions studied significantly improved acid tolerance, growth and protease activity of *Lactobacillus delbrueckii* ssp. *bulgaricus* LB-12 and *Lactobacillus acidophilus* LA-K.

Key words: mild pulsed electric fields, probiotic

T88 Impact of mild pulsed electric field conditions on improving bile tolerance, protease activity and growth of *Streptococcus salivarius* ssp. *thermophilus* ST-M5. N. Najim and K. Aryana*, *School of Animal Sciences, Louisiana State University Agricultural Center, Baton Rouge.*

Certain mild pulsed electric field (PEF) conditions show promise in enhancing probiotic characteristics and need to be further explored. In an earlier study on screening mild PEF conditions for enhanced acid tolerance, a condition was identified that enhanced acid tolerance. Aim of the present study was to evaluate the identified mild PEF conditions' influence on the bile tolerance, growth and protease activity of this probiotic bacterium. Freshly thawed frozen concentrated culture of *Streptococcus salivarius* ssp. *thermophilus* ST-M5 was suspended in 0.1% (wt/v) sterile peptone water and treated in pilot plant PEF system. Treatment was positive square unipolar pulse width of 3 µs, pulse period of 0.5 s, voltage of 1 kV/cm, delay time of 20 µs and flow rate of 60 mL/min at 40.5°C PEF treatment temperature. Control was passed through the PEF system at the same flow rate (60 mL/min) without receiving any pulsed electric field condition. Growth and bile tolerance of the control and PEF treated samples were determined hourly throughout 20 and 16 h of incubation respectively. Protease activity was determined at 0, 12, 24, 36 and 48 h of incubation at 37°C. Three replications were conducted. The mild PEF conditions had non significant influence on the bile tolerance of *Streptococcus salivarius* ssp. *thermophilus* ST-M5 throughout the entire incubation time period of 16 h. The control and mild PEF treated samples had the same counts of 10.97 (+/− 0.25) log cfu/ml at 0 h of growth. Mild PEF treated samples reached the logarithmic growth phase an hour earlier than the control. Mild PEF treated samples had significantly higher counts compared with the control for all the time points over the logarithmic phase but had nonsignificant ($P > 0.05$) difference for all the time points over both the stationary and the decline phases of the growth curve. *Streptococcus salivarius* ssp. *thermophilus* ST-M5 subjected to mild PEF throughout the incubation time points of 12, 24 and 36 h had significantly enhanced proteolytic activity compared with the control.

Key words: milk pulsed electric fields, probiotic

T89 Resistance of *E. coli* and *L. rhamnosus* to acid stress is affected by the presence of pepsin-treated caseinomacropeptide. G. Robitaille, C. Lapointe, D. Leclerc, and M. Britten*, *Food Research and Development Centre, Agriculture and Agri-Food Canada, St Hyacinthe, Quebec, Canada.*

Caseinomacropeptide (CMP) is a 7 kDa phosphoglycopolypeptide released from κ-casein during milk digestion and during chymosin-induced renneting of caseins. The objective of the study was to analyze the effect of pepsin-treated CMP from cow and goat milk on the resistance of *E. coli* and *L. rhamnosus* during acid stress. Bacterial cells in exponential growth phase were suspended in acidified phosphate buffered saline with or without pepsin-treated CMP. Viability was determined during a 90 min incubation period. Pepsin-treated CMP exhibited bactericidal activity at pH 3.5 when added in a dose dependent manner to *E. coli*, reducing survival by more than 90% within 15 min at 0.25 mg/mL. At pH >4.5 the bactericidal activity was lost indicating that pepsin-treated CMP was efficient at low pH only. The effectiveness of pepsin-treated CMP at pH 3.5 was not affected by the presence of glycoconjugates linked to CMP or by the bovine or caprine origin of milk. In contrast, *L. rhamnosus*, a probiotic, was more resistant to acid stress when pepsin-treated bovine or caprine CMP was added to the media. The viability reached 50% after 60 min incubation at pH 3 compared with 5% survival without additive. Neither the glycosylation extent nor the sequence variations between CMP from bovine and caprine milk affected the protective activity of hydrolysed CMP toward *L. rhamnosus*. This suggests that encrypted bioactive peptides released by the pepsin treatment of CMP was antibacterial toward *E. coli*, and improved acid stress resistance of *L. rhamnosus* in an acidic media that mimicked gastric environment.

Key words: caseinomacropeptide, antibacterial, acid stress

T90 Effect of microencapsulation on survival of *Lactobacillus acidophilus* La5 during simulated gastrointestinal conditions of stirred yoghurt after refrigerated storage. M. C. E. Ribeiro, K. S. Chaves, C. G. M. S.C. Tenório, F. N. Souza, C. R. F. Grosso, and M. L. Gigante*, *State University of Campinas, Campinas, SP/Brazil.*

Microencapsulation is an effective method for maintaining high viability of probiotic bacteria, as it protects probiotics both during food processing and storage as well as in gastric conditions. The aim of this study was to evaluate the viability of *Lactobacillus acidophilus* La5 in both free and microencapsulated forms in stirred yogurt during simulated gastrointestinal transit. Probiotic bacteria were microencapsulated using pectin and whey protein, associating ionotropic gelation and complex coacervation. Three batches of stirred yogurt were made with *L. acidophilus* incorporated into the product in different states: free (1% v/v), moist microcapsules (10% w/v) and rehydrated freeze-dried microcapsules (13% w/v). After 35 d of storage the survival of *L. acidophilus* during the passage through the gastrointestinal tract was determined by exposing the yogurts at 37°C for 420 min to a simulated gastric juice (pH 3.0) containing pepsin and, subsequently, to a simulated intestinal juice (pH 7.0) containing pancreatin, and by monitoring changes in total viable counts. Bile tolerance (1%) at pH 7.0 was evaluated for 300 min. The experiment was repeated 3 times and the results were evaluated by ANOVA and Tukey′s mean comparison tests ($P \leq 0.05$). During the simulation of the passage through gastrointestinal conditions, the counts of viable cells in probiotic yogurts with free *L. acidophilus* reduced 0.38 log cycles while this reduction was 0.17 and 0.18 log cycles when the probiotic was added to the yogurt in moist and rehydrated freeze-dried microcapsules, respectively. After 5 h exposed to a bile solution, there was a reduction of 3.5 log cycles in the viability of *L. acidophilus* when incorporated in yogurt in free form, 1.37 and 0.98 log cycles in yogurt with moist and rehydrated freeze-dried microencapsulated *L. acidophilus*, respectively. Therefore, microencapsulation of *L. acidophilus* La5 can be considered a potentially useful technique for delivering probiotics to the gastrointestinal tract of humans.

Key words: probiotic yoghurt, microencapsulation, gastrointestinal resistance

T91 Viability of free and microencapsulated *Lactobacillus acidophilus* La5 in stirred yoghurt during refrigerated storage. M. C. E. Ribeiro, C. G. M. S.C. Tenório, K. S. Chaves, F. N. Souza, C. R. F. Grosso, and M. L. Gigante*, *State University of Campinas, Campinas, SP/Brazil.*

The aim of this study was to evaluate the characteristics of probiotic stirred yogurt added of *Lactobacillus acidophilus* La5 in both free and microencapsulated forms during refrigerated storage. The probiotic microorganism was microencapsulated by association of ionotropic gelation with Ca^{2+} and complex coacervation using low methoxyl amidated pectin and whey protein as wall materials. The yogurts were manufactured with sterilized, homogenized and standardized milk added of 2.5% (v/v) yogurt starter culture and submitted to the following treatments: 1) addition of 1% (v/v) of free *L. acidophilus*; 2) addition of 10% (w/v) of moist microcapsules containing *L. acidophilus* and 3) addition of 13% (w/v) of rehydrated freeze-dried microcapsules containing *L. acidophilus*. Incubation was carried out at 42°C until fermentation reached pH 4.8 ± 0.05. Yogurts were evaluated once a week over the 5-week storage period for pH and viability of starter culture and probiotic microorganism. A Split-Plot design in a 3 × 6 factorial, in completely randomized blocks, was used with 3 replications. Results were evaluated by ANOVA and Tukey′s mean comparison tests ($P \leq 0.05$). The samples with free cells and with moist microcapsules showed fermentation time of 180 min, while this period was 200 min for microencapsulated rehydrated freeze-dried cells. The yogurts added by microencapsulated *L. acidophilus* showed less post-acidification and higher survival of probiotic microorganism after 35 d storage than yogurt added by free probiotic. The number of free cells was reduced by 0.98 log cycles, while in microencapsulated form for both moist and rehydrated freeze-dried forms the reduction was 0.2 log cycles. The microencapsulation of *Lactobacillus acidophilus* La5 by association of ionotropic gelation with Ca^{2+} and complex coacervation using pectin and whey protein as wall materials provides protection to the microorganism during refrigerated storage of probiotic yogurt.

Key words: probiotic, yoghurt, microencapsulation

T92 In vitro property evaluation of *Propionibacterium* cultures for probiotic applications. W. Y. Yang*, A. Hostetler, C. Nolan, and H. S. Kim, *Culture Systems Inc., Mishawaka, IN.*

The potential use of propionibacteria as a probiotic is getting attention for both humans and animals. Some of the benefits include aiding in the prevention of colon cancer for humans and weight gain for animals. Certain properties are needed for maximizing probiotic effectiveness, such as tolerance in acidic and bile salt conditions and maintenance of viability. The objective of this study was to isolate and screen *Propionibacterium* strains from healthy cow rumen fluid and cheese, and to evaluate their effectiveness as probiotic cultures. The tolerance of propionibacteria strains to acidic environments and bile salt conditions was tested. In addition, the antibiotic susceptibility and growth in a limited fermentation medium were assessed. Finally, the stability of the freeze-dried cultures during storage at 25°C was analyzed. These tests resulted in the selection of 2 *Propionibacterium freudenreichii* strains: *P. freudenreichii* ssp. freudenreichii CS36 and *P. freudenreichii* ssp. shermanii CS39. No loss of viable cell count was observed in any of the *P. freudenreichii* strains during a 3-h treatment at pH 4 or 3. Bile salt at 0.5% concentration had no apparent effect on the cell count of the strains. There was no atypical antibiotic resistance by the 2 strains. The highest concentration of propionic acid was obtained with the limited growth medium. Cell count was stable at 25°C for a one year storage period when strains were properly packaged as a freeze-dried powder. In conclusion, 2 strains of propionibacteria, CS36 and CS39, meet some of the basic property requirements for the use as probiotics or direct fed microbial products.

Key words: propionibacteria, probiotics, colon cancer

T93 Can high quality raw milk have enough microbial load to show a reduction of organisms in a pasteurization adjunct? J. A. Zonneveld*, A. M. Lammert, and R. Jimenez-Flores, *California Polytechnic University, San Luis Obispo.*

UV light treatment may be used in adjunct to pasteurization to further decrease microbial load in milk. The purpose of this study was to determine if fresh raw milk could be used to evaluate the reduction in microbial load of milk treated by pasteurization and UV light and to determine if the microbial reduction was significant. Sixteen hundred gallons of raw Holstein and Jersey milk from the Cal Poly Dairy were standardized to 3.5% fat and stored in a 4.4°C raw milk bulk tank. Control samples were obtained from the raw milk tank and stored without air or agitation. Every 24 h for 4 d milk control samples and raw milk bulk tank samples were analyzed for coliform and aerobic plate counts. The raw bulk tank milk was processed using UV light treatment in addition to pasteurization using traditional pasteurization controls to determine boundaries for future testing. Samples were taken after each variable to determine microbial kill efficiency. After 4 d in the raw milk bulk tank, the aerobic plate counts and coliform counts were >500,000 cfu/mL and 2175 coliforms/mL, respectively, and much higher than the 39,000 cfu/mL and 195 coliforms/mL, respectively, from the initial batch tank samples. Microbial disinfection worked well with all processing methods evaluated. Every variable of treated milk had 0 coliforms/mL and aerobic plate counts below 50 cfu/mL, when combined with pasteurization. Even the minimal UV treatment lowered both aerobic plate counts and coliforms greatly prior to pasteurization; however, the maximum level UV treatment came much closer to traditional pasteurization in effectiveness. When milk was processed with UV light first followed by traditional pasteurization, aerobic plate counts decreased greater than 2 log and coliforms were essentially eliminated from milk leaving only a few cfu/mL if any. This work indicates that 4 d old day raw milk treated with UV light and pasteurization may be used to successfully lower the microbial counts of aerobic bacteria and coliforms.

Key words: fluid milk, ultraviolet light

T94 Effects of prolactin on the expression of genes related to milk protein synthesis in bovine mammary epithelial cells. X. Y. Li, J. Q. Wang*, H. Y. Wei, X. M. Nan, D. P. Bu, P. Sun, 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 reveal the role of prolactin (PRL) on the expression of important genes related to milk protein synthesis in bovine mammary epithelial cells. Mammary epithelial cells were isolated from a 3 year old Chinese Holstein dairy cow in mid-lactation (ca.100 d relative to parturition) and cultured in the medium containing a combination of hydrocortisone, insulin, transferrin, bovine epithelial growth factor and PRL (5μg/m L). No PRL was added in medium of control groups. Expressions of genes were measured by RT-qPCR. The content of caseins and lactose were detected by Casein ELISA Kit and HPLC, respectively. All experiments repeated 3 times. The results showed that after treatment with PLR casein synthesis was increased by 20% and lactose synthesis was increased by 25%. The expression of prolactin receptor (PRLR) was significantly increased ($P < 0.01$). *CSN3* and *LALBA* were the most highly expressed casein genes ($P < 0.01$),followed by *CSN1S1*, *CSN2* and *CSN2S2*, but these genes were not increased significantly ($P > 0.05$). The expression of genes related to *JAK2-STAT5* pathway were upregulated, and *JAK2* and *ELF5* expression increased significantly ($P < 0.01$). This study revealed that PRL was necessary for high levels of milk protein genes expression and milk protein synthesis.

Key words: prolactin, bovine mammary epithelial cells, genes expression

T95 The best ratio between lysine and methionine on milk protein synthesis in bovine mammary epithelial cells. X. Y. Li, J. Q. Wang*, H. Y. Wei, X. M. Nan, D. P. Bu, P. Sun, and L. Y. Zhou, *State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China.*

This study took the bovine mammary epithelial cells as a model to determine the best ratio between lysine and methionine, focusing on the effects of additional lysine and methionine on the regulation of genes related to milk proteins, genes related to amino acid transporters, and genes related to milk protein synthesis. The expression of important genes related to milk protein synthesis process included the genes of the *JAK2-STAT5* pathway and the *mTOR* signaling pathway. The experiment was conducted with a 5 × 3 factorial design: with lysine (1.0, 1.2, 1.4, 1.5, 1.6 m mol/L in DMEM/F12 medium) and methionine (0.4, 0.5, 0.6 m mol/L in DMEM/F12 medium). All experiments repeated 3 times. The expression of genes and caseins content were detected by RT-qPCR method and Casein ELISA Kit, respectively. Data were analyzed with the PROC GLM and PROC ANOVA. The results showed that when the concentration of lysine was 1.2 m mol/L and the concentration of methionine was 0.4 m mol/L, the content of casein in medium increased significantly ($P < 0.01$) and peaked at 2.95ppm. We measured the genes expression at this ratio (3:1). *CSN1S1* and *LALBA* were the most highly expressed genes encoding caseins and increased more than 2-fold ($P < 0.01$), followed by*CSN2*, *CSN3* and *CSN2S2*, and these genes expression were also upregulated ($P < 0.01$). The expression of genes related to *JAK2-STAT5* pathway were upregulated, and *JAK2*and *ELF5* expression increased significantly ($P < 0.01$).The expression of genes related to *mTOR* signaling pathway was increased, but *S6K* was not significantly ($P > 0.05$). *EIF4E-BP1* expression was significantly downregulated ($P < 0.01$). The expression of amino acid transporter *CAT-1* and *ASCT-2* had no change. These observations together with the fact that genes expression changed in the cells with the ratio between lysine and methionine revealed that the lysine, methionine and the ratio between lysine and methionine may directly regulate the expression of genes related to milk protein transcription and translation, leading to improved milk protein synthesis.

Key words: lysine, methionine, milk protein

T96 Development of safe glue sticks containing whey protein. G. Wang and M. Guo*, *The University of Vermont, Burlington.*

The major whey proteins are small globular proteins that may be undesirable for application in adhesives. However, their structures can be modified using chemical and physical means such as heating. Commercial glue sticks on the market may contain toxic chemical components, which can pose potential health hazards to users. In this study, a new safe glue stick product was developed using whey protein isolate (WPI), polyvinylpyrrolidone K90, propylene glycol, stearic sodium, and sucrose. WPI was first dissolved in distilled water, and then other ingredients were added. The mix was heated to 93–95°C with constant stirring for 30 min until it became homogenous, and then was filled into the push–up tubes. The new product was analyzed for bonding strength and hardness in comparison with a commercial product as a control. Bonding strength of the prototype was 247.63 ± 11.73 N, which was higher than that of the control (241.60 ± 9.49 N), but the difference was not significant ($P > 0.05$). The bonding strength remained stable after 3 mo of storage at 23°C or 40°C. Hardness of the prototype (23.31 ± 2.51 N) was comparable to that of the commercial glue (20.30 ± 1.09 N). The content of total solids of the prototype (52.17 ± 0.67%) was higher ($P < 0.05$) than the control (36.46 ± 0.29%). The new product was easy to be applied on paper, extended and retracted in push–up tubes. There was no growth of mold and yeast on the sticks after 3 mo of storage at 40°C. In conclusion, the new safe glue stick prototype containing whey proteins was comparable to the commercial control in bonding strength and hardness. Shelf life tests are being carried out to determine the storage stability of this new product.

Key words: glue stick, whey protein, safe

T97 Isolation and characterization of prosaposin from milk from four goat breeds. A. Robertson-Byers*, M. Worku, and S. Ibrahim, *North Carolina A&T State University, Greensboro.*

Increased scientific knowledge related to the nutritional, functional and biological activities and health benefits of goat milk is needed to further promote goat farming, goat milk and traditional or innovative neutrceuticals as a basis for socio-economic benefit. Prosaposin, a protein in goat milk is the precursor of the sphingolipid activator proteins. Saposins are small lysosomal proteins required for the hydrolysis of sphingolipids. Prosaposin is important in development and maintenance of the nervous system. Genetic variation may impact nutraceutical properties of milk by altering the biological function of bioactive peptides and antigens. The objectives of this study were to detect prosaposin and the sphingolipid activator proteins (saposins A, B, C, and D) in milk from different breeds of goats. Raw milk was collected at North Carolina A&T State University farm from Alpine, Spanish, Boer, Spanish × Boer goats and from a Holstein Friesian

cow. Whey fractions were separated by centrifugation. Extracts were analyzed by electrophoresis and immunoblotting with anti-prosaposin and anti-saposin HRP conjugated antibodies. Specific proteins were identified using a tetramethylbenzidine substrate. Multiple proteins were observed in whey fractions from all animals tested. Antibodies detected a 65 kDa prosaposin band and a 29 kDa saposin C band. Saposins and their precursor prosaposin are present in milk from different breeds of goats. The possible effect of genetic variation on concentration need further study. These studies will contribute to our knowledge of the therapeutic benefits of goat milk to aid producers in maintaining breeds with the potential to produce prosaposin.

Key words: prosaposin, neutraceutical, goats

T98 Poultry offal meal traceability in meat quail tissues using the technique of stable carbon-13 and nitrogen-15 Isotopes. C. Mori*[2], E. A. Garcia[1], C. Ducatti[1], J. C. Denadai[1], and K. Pelicia[1], *[1]São Paulo State University, Botucatu, São Paulo, Brazil, [2]São Paulo State University, Registro, São Paulo, Brazil.*

Studies on detection of animal byproducts in poultry meat are rare, and non-existent on quail meat. This study aimed at detecting increasing levels of poultry offal meal (POM) in quail meat, using carbon ($^{13}C/^{12}C$) and nitrogen ($^{15}N/^{14}N$) stable isotopes technique. Sixty 4 one-day-old male quails derived from commercial farm were fed experimental diets containing 0, 1.5, 3.0, 4.5, 6.0, 7.5, and 15% of POM. Diets were formulated to contain equal energy, protein, and amino acid levels. Four individuals per treatment were sacrificed at 42 d of age for breast muscle (pectoralis major), keel, and tibia, and subsequently prepared and submitted for isotopic analysis of C and N. Isotopic analyses of feed ingredients, feeds, and tissues were carried out at the Center of Stable Environmental Isotopes of the Biosciences Institute (CIE/IB), UNESP, Botucatu campus. Isotopic carbon ($^{13}C/^{12}C$) and nitrogen ($^{15}N/^{14}N$) ratios were determined in an isotopic ratio mass spectrometer (IRMS) type DELTA-S (Finnigan Mat) coupled to an Elementary Analyzer (EA 1108 CHN). The obtained isotopic results were submitted to multivariate analysis of variance (MANOVA) using GLM (General Linear Model) procedures of SAS statistical software. Data were generated by error matrices for each tissue, which were later graphically distributed in regions (ellipses) with 95% confidence of observing possible differences between experimental treatment means and control treatment means. The inclusion of animal byproducts in quail diets was detected by ^{13}C and ^{15}N analyses in the tissues of the birds, with the lowest detection level of 3% dietary inclusion of poultry offal meal. It was concluded that quail meat can be certified by the technique of stable isotopes.

Key words: quail, stable isotopes, traceability

T99 Use of stable isotopes of carbon-13 and nitrogen-15 in quail eggs. C. Mori*[2], C. Ducatti[1], C. C. Pizzolante[3], S. K. Kakimoto[3], and J. C. Denadai[1], *[1]São Paulo State University, Botucatu, São Paulo, Brazil, [2]São Paulo State University, Registro, São Paulo, Brazil, [3]São Paulo Agency of Agribusiness Tecnology, Brotas, São Paulo, Brazil.*

The objective was to trace the inclusion of bovine meat and bone meal (BMBM) in the diet of quails through the analysis of eggs and their fractions (yolk and albumen), using the stable isotope carbon ($^{13}C/^{12}C$) and nitrogen ($^{15}N/^{14}N$) technique. It was used 120 quails were used in 5 treatments and 4 replications of 5 birds each. After 42 d, 20 eggs were randomly selected per treatment over 3 consecutive days. From these collected eggs, 10 were used for yolk and albumen sampling and the other 10 for the total egg sampling. Treatments were: a control diet based on corn and soybean meal (T0) and other 5 diets containing inclusions of BMBM, namely: 1, 2, 3, 4 and 5%. Isotopic analyses of feed ingredients, feeds, and tissues were carried out at the Center of Stable Environmental Isotopes of the Biosciences Institute (CIE/IB), UNESP, Botucatu campus. Isotopic carbon ($^{13}C/^{12}C$) and nitrogen ($^{15}N/^{14}N$) ratios were determined in a isotopic ratio mass spectrometer (IRMS) type DELTA S (Finnigan Mat) coupled to an Elementary Analyzer (EA 1108 CHN). The obtained isotopic results were submitted to multivariate ANOVA (MANOVA) using GLM (General Linear Model) procedures of statistical software. Data were generated by error matrices for each tissue, which were later graphically distributed in regions (ellipses) with 95% confidence of observing possible differences between experimental treatment means and control treatment means. In the final product (eggs and their fractions) it was possible to detect the inclusion of 1% of BMBM in the diet. Thus, the technique of isotope carbon-13 and nitrogen-15 is able to track the inclusion of 1% of BMBM in diets of laying quails, through the analysis of eggs and their fractions, ensure safe information about the product be consumed, but also allows the certification of origin government agencies.

Key words: egg quail, stable isotopes, traceability

T100 Adsorption capacity and efficacy assessment of bamboo charcoal an alternative adsorbent for aflatoxin B1 in a ruminal batch culture. H. J. Yang* and Y. H. Jiang, *State Key Laboratory of Animal Nutrition, College of Animal Science and Technology, China Agricultural University, Beijing, China.*

Fifty milligrams of bamboo charcoal (BC), activated charcoal (AC) and smectite power (SP) were weighed into tubes containing 4.5 mL McDougall′s buffer (pH 6.8) in the presence of 4 mg/L aflatoxin B1 (AFB1) and incubated at 39°C. The 5 replicate tubes were incubated for 1, 3, 6, 12, 24, 48 or 72 h, then removed to assess the AFB1 adsorption capacity (Q) and adsorption rate (Y). The mean value of Q did not differ between AC and BC (0.383 vs 0.381 mg/g), which Q means were greater than that of SP ($P < 0.05$). No differences of Y were observed between AC and BC (0.958 vs. 0.955), and a low Y (0.931) occurred in SP ($P < 0.01$). In a separate batch culture (75 mL, rumen fluid: McDougall′s buffer = 1: 2), a 2-factor randomized block design was applied in vitro with 2 binder blocks (SP and BC) at dose rates of 0, 0.1, 1, 10 g/L in the cultures to investigate effects of the binders on fermentation of a grain-rich substrate (*Leymus chinensis* hay: maize meal = 1: 4) in the presence of 1.0 mg/L AFB1. After a 72 h incubation, cumulative gas production was fitted to an exponential model: $Y = A \times [1\text{-}e^{-c \times (\text{time-lag})}]$, and the asymptotic gas production A was greater in BC than in SP ($P < 0.01$), and it increased linearly ($P < 0.01$) and quadratically ($P < 0.01$) against the binder dose rates. Both lag time (h) and the average gas production rate (AGPR, mL/h) did not differ between SP and BC. The residual AFB1 concentration in both binders decreased against the dose rates before a methanol washing procedure ($P < 0.05$), and it was greater in BC than SP after the washing ($P < 0.01$). No differences for pH and ammonia N were observed between the binders or their dose rates. Total VFA was lower in SP than BC ($P < 0.01$). The addition of SP numerically decreased total VFA production, but the addition of BC comparatively increased it. The addition of the binders quadratically increased molar propionate proportion ($P < 0.05$), and molar acetate proportion was greater in BC than SP ($P < 0.01$). These results suggested that the effectiveness of BC was comparable to SP, and that it could be an effective AFB1 sequestering agent.

Key words: bamboo charcoal, aflatoxin B1, rumen fermentation

T101 Occurrence of mycotoxins in feedstuffs and feed samples from 2009-2010. U. Hofstetter*, K. Naehrer, and I. Rodrigues, *Biomin Holding GmbH, Herzogenburg, Austria.*

A survey about the most important mycotoxins in feedstuffs from different countries/regions all over the world, specifically Asian-Pacific, Europe, Middle-East, Africa and Americas was initiated with the objective to identify major mycotoxin occurrence. From January 2009

until December 2010, a total of 3961 samples were analyzed for the presence of aflatoxins (Afla), zearalenone (ZON), deoxynivalenol (DON), fumonisins (FUM) and ochratoxin A (OTA). Samples tested ranged from cereals, to processing by-products (e.g., DDGS) and other fodder like silage or finished feed. Analyses were performed by HPLC (high performance liquid chromatography), ELISA (enzyme-linked immunosorbent assay) or TLC (thin-layer chromatography) according to the standard procedures. For the purpose of data analysis, non-detect levels are based on the quantification limits (LOQ) of the test method for each toxin. The majority of the analyses were performed at Romerlabs (Austria, Singapore, USA) and SAMITEC (Brazil). From all survey samples 33%, 36%, 51%, 55% and 28% tested positive for Afla, ZON, DON, FUM and OTA, respectively. The most frequently detected mycotoxins were the *Fusarium* sp. toxins FUM and DON with an average contamination of all tested samples of 1280 µg/kg (median of all samples tested positive 1034 µg/kg, maximum 53700 µg/kg) and 434 µg/kg (median of all samples tested positive 460 µg/kg, maximum 29300 µg/kg), respectively. In the case of ZON a mean of 83 µg/kg (maximum 16712 µg/kg) was verified. The average contamination of Afla and OTA was 22 µg/kg and 4 µg/kg, respectively. Data were grouped according to occurrence of mycotoxins in different geographical regions, on the occurrence in diverse raw materials and on the co-occurrence of different mycotoxins. From all samples sourced worldwide, only 24% were below the respective detection limits of the analyzed mycotoxins. 76% of all analyzed samples were contaminated with one mycotoxin and 41% were contaminated with more than one mycotoxin.

Key words: mycotoxins, survey

T102 Horizontal transfer of Stx2 gene from *E. coli* O157:H7 to non-pathogenic *E. coli* occurred under feedlot conditions. W. F. Yue, M. Du, W. J. Means, and M. J. Zhu*, *Department of Animal Science, University of Wyoming, Laramie.*

Shiga toxins (Stx) are the key virulence factors of *Escherichia coli* O157:H7 which is responsible for hemorrhagic colitis and serious renal failure. It is commonly believed that *E. coli* O157:H7 picked up stx genes through bacteriophages. *E. coli* O157:H7 genome contains a pool of defective lambdoid prophages including prophages carrying stx genes. We hypothesized that strong UV radiation in combination with high temperature associated with global warming accelerates stx prophages activation, which facilitates the dissemination of stx genes into non-pathogenic *E. coli* in feedlots. Plaque analysis showed that UV radiation increased prophage activation in *E. coli* O157:H7 (EDL933), which was further enhanced by high temperature. Activated prophages were capable of converting non-pathogenic *E. coli* (MG1655) to Shiga toxigenic *E. coli* in culture media. To further confirm horizontal transfer of stxs, EDL933 and kanamycin resistant (Kan^R) MG1655 were mixed into fresh cattle feces and incubated at 37°C for 12 h. Kan^R-MG1655 was recovered by kanamycin antibiotic selection, which were further subjected to in situ hybridization to examine the possible presence of stx2. In situ hybridization results indicated that stx2 were horizontal transferred from EDL933 to MG1655. In summary, data implicated that high temperature combined with UV radiation accelerates the spread of stx genes through enhancing prophage activation. Cattle feedlot sludge is frequently exposed to UV radiation, in combination with elevated temperature associated with global warming, which may provide an environment promoting generation of new Shiga toxigenic *E. coli*. (USDA AFRI, 2010–65201–20599, Agricultural Experiment Station at University of Wyoming, NIH-INBRE P20RR016474).

Key words: *E. coli* O157:H7, prophage, Stx2

T103 Antagonistic intestinal microflora produces antimicrobial substance inhibitory to *Pseudomonas* species and other spoilage organisms. B. Hatew*[1,2], T. Delessa[1,3], V. Zakin[1], and N. Gollop[1], *[1]Agricultural Research Organization of Israel, Bet-Degan, Israel, [2]Wageningen University, Wageningen, the Netherlands, [3]Swiss Federal Institute of Technology, Zurich, Switzerland.*

Today an increase in consumers demand for fresh, natural and chemical preservative-free foods have enhanced attention to antimicrobial substances from Generally Recognized as Safe bacteria. Chicken intestines harbor a vast number of bacterial strains that play an important role in the health of chickens. Many of these bacterial strains produce antimicrobial substances which are active against aerobic spoilage bacteria of refrigerated poultry meat, especially *Pseudomonas* spp. In the present study, an antimicrobial substance produced by lactic acid bacteria isolated from the gastrointestinal tract of healthy chickens was isolated, characterized and purified. Based on 16S rRNA sequencing the bacteria strain was identified as *Lactobacillus plantarum*, and designated as *L. plantarum*-vN. The antimicrobial substance exhibited a broad-spectrum of activity against many important pathogenic and spoilage microorganisms including *Pseudomonas aeruginosa*, *Staphylococcus aureus*, *Micrococcus luteus*, *Salmonella typhimurium* and *Erwinia amylovova*. The antimicrobial substance was found to be thermostable, insensitive to pH values ranging from 2.0 to 8.0, resistant to various organic solvents and to enzymatic inactivation. The inhibition kinetics displayed a bactericidal mode of action. This study revealed a new type of antimicrobial substance with low molecular mass of less than 1 kDa and having features not previously reported for lactic acid bacteria isolated from the chicken intestines. The novelty of the substance and its potential to inhibit gram-negative bacteria of spoilage and health significance, not normally inhibited by the majority of bacteriocins of lactic acid bacteria, may be of potential interest to food safety and preservation.

Key words: *Pseudomonas*, antimicrobial substance, *Lactobacillus plantarum*

T104 Microencapsulated feed additives to reduce *Salmonella* shedding. E. Grilli*[1], R. Bari[1], A. Piva[1], B. Tugnoli[1], and T. R. Callaway[2], *[1]University of Bologna, Ozzano Emilia, BO, Italy, [2]Food and Feed Safety Research Unit, ARS/USDA, College Station, TX.*

The reduction of *Salmonella* prevalence in food animals in Europe is regulated by EU Reg. 2160/2003, EU Reg. 1003/2005 and others. The purpose of these regulations is to detect and control *Salmonella* strains that represent a threat to public health and to ensure that preventive measures at each stage of production are taken. In this context, tailored nutritional strategies are now a priority, along with improved management and biosecurity. Aim of the study was to investigate the efficacy of an experimental microencapsulated blend of sorbic acid and naturally identical compounds (SAB) against *S. Typhimurium* in pigs. The active principles of SAB were dissolved in TSB and serial dilutions were prepared to reach final concentration of: 0, 200, 400, 600, 800, 1000, 2000, 3000, 4000, and 5000 mg/L. Each dilution tube was inoculated with *S. Typhimurium* at 10^6 cfu/ml initial concentration. Compared with controls, after 24 h of incubation, SAB at 2000 and 3000 mg/L reduced ($P < 0.05$) *Salmonella* growth by 4–5 Log_{10}, respectively, and SAB at 4000 and 5000 mg/L completely inhibited ($P < 0.05$) its growth. Forty (n = 40) pigs housed in 20 pens were assigned to 4 dietary treatments: control group (challenged, not treated), and 3 treatment groups treated with 300, 3000, 30000 g/ton of SAB, respectively). After 1 week of adaptation pigs were challenged with 10^7 cfu of *S. Typhimurium* mixed to the feed and a second challenge was

repeated via gavage after 7d. After 2d, and every 4d thereafter, fecal samples were collected from each pig and analyzed for *S. Typhimurium* qualitatively and quantitatively. Results demonstrated that 3000 and 30,000 g/ton SAB reduced ($P < 0.05$) *S. Typhimurium* prevalence by 40% and 50% after 2 wk, and at the end of the third week 100% of the animals in the same groups resulted negative for *S. Typhimurium*. This study demonstrated that intestinal delivery of microencapsulated sorbic acid and naturally identical compounds can result in a reduction of *S. Typhimurium* prevalence and fecal shedding in pigs. In-field trials are currently under exploitation to confirm our preliminary small-scale observations.

Key words: *Salmonella*, pig, microencapsulation

T105 Improving voluntary oral interaction of dairy cattle with manila ropes to facilitate *E. coli* O157:H7 monitoring on dairies.
A. F. Pedroso*[2,1], O. C. M. Queiroz[1], and A. T. Adesogan[1], *[1]Department of Animal Sciences, Institute of Food and Agricultural Sciences, University of Florida, Gainesville, [2]Brazilian Agricultural Research Corporation, Embrapa Cattle-Southeast, 13560-970, São Carlos, SP, Brazil.*

This trial aimed to improve the efficacy of the manila rope method for *E. coli* O157:H7 detection on dairy herds. In an initial test, untreated and molasses-treated (3 min immersion in a autoclaved molasses solution - 8.5% in water) manila ropes (0.64 × 80 cm) were tied at alternate positions (30 cm apart) on the railing over feed bunks in 2 pens containing 22, 13.5 mo dairy heifers each. Seven ropes per treatment were placed immediately before feeding (0930 h) and observed from 0940 to 1130 h. Treatment with molasses resulted in a 16% increase in the total number of times the ropes were visited (chewed, licked or touched with the muzzle) in each pen, and in a 19% increase in an "efficacy index" estimated by multiplying the number of visits by the percentage of heifers visiting the ropes (85 and 83%, respectively, for ropes with and without molasses). Subsequently, the effect of rope to animal ratio was evaluated using 89, 11 to 22 mo heifers stratified by weight into 4 pens (19 to 26 animals/pen) and randomly assigned to 4 treatments. Ratios of 1, 3, 6 and 9 ropes/25 animals were tested in each pen. Molasses-treated manila ropes were placed in the pens as mentioned before and monitored from 0800 to 1100 h every 4 d. Increasing the rope to animal ratio linearly increased the percentage of heifers visiting the ropes, increased quadratically the number of visits per pen, and increased exponentially the efficacy index (Table 1). Molasses treatment and increasing rope to animal ratio in pens potentially makes the method more effective.

Table 1. Effect of rope to animal ratio on measures of oral interaction of heifers with manila ropes

No. ropes/ 25 animals	% heifers visiting ropes	No. visits/ pen	Efficacy
1	32.6 ± 6.98^{b}	11.0 ± 9.73^{c}	4.8 ± 8.68^{c}
3	45.6 ± 6.98^{b}	23.5 ± 9.73^{c}	12.0 ± 8.68^{bc}
6	71.8 ± 6.98^{a}	40.8 ± 9.73^{b}	32.3 ± 8.68^{b}
9	83.7 ± 7.82^{a}	72.6 ± 10.79^{a}	62.5 ± 9.74^{a}
Equation	$y = 17.9x - 3.9$	$y = 4.75x^2 - 12.95x + 18.45$	$y = 0.9251e^{0.8582x}$
R^2	0.978	0.997	0.995

[a,b,c]Means within a column with different letters differ ($P < 0.05$) by the Tukey test.

Key words: *E. coli* O157:H7, manila ropes

T106 Effects of predipping practices on milk iodine concentrations.
S. I. Borucki-Castro[1], R. Berthiaume[1], A. Robichaud[2], and P. Lacasse*[1], *[1]AAFC-Dairy and Swine Research and Development Centre, Sherbrooke, QC, Canada, [2]Food Directorate, Health Canada, Longueuil, QC, Canada.*

A study was conducted to determine the effects of udder preparation before milking on milk iodine concentrations. The study compared the use of pre-dip and post-dip solutions; and determined the effect of an incomplete removal of pre-dip solution on milk iodine. Thirty-two lactating cows were assigned to 4 treatments: no pre-dip (udder wash without iodine; control); pre-dip with a pre-dip solution containing 0.5% iodine (Theratec, GEA Farm Technologies) + complete cleaning with paper towel (complete); pre-dip with a post-dip solution 1% iodine (Teat-Kote, GEA Farm Technologies) + complete cleaning with paper towel (post); and pre-dip with a pre-dip solution 0.5% iodine (Theratec) + incomplete cleaning with paper towel (incomplete). Incomplete cleaning was achieved by cleaning only 3 of the 4 teats. All cows received a diet without goitrogenic feeds, and an iodine concentration of 0.50 mg /kg of feed offered. During the 14d pre-experimental and the 19d experimental periods, non-iodized sanitizers were used for post-milking dipping or flushing of the milking units. The first 2 weeks were used for adaptation to treatments and measurements were done on the final week to ensure a plateau in the milk iodine response. During the pre-experimental period, milk iodine concentrations were similar for all groups and averaged 160.4, 167.3, 157.0 and, 153.0 ± 17.3 µg/kg for control, complete, post and, incomplete; respectively. During the last week of treatment, milk iodine averaged 164, 189, 218 and, 252 ± 9.8 µg/kg for control, complete, post, and incomplete, respectively. Pre-planned orthogonal contrasts indicated that pre-dipping with a 0.5% iodine pre-dip solution (complete) tended to increase milk iodine content above that of control ($P = 0.08$) and, that iodine content of post ($P < 0.05$) and incomplete ($P < 0.001$) were higher than that of the complete treatment. These results indicate that pre-dipping is an acceptable practice but must be performed with the appropriate product and completely wiped out before milking.

Key words: iodophore, milking, milk safety

T107 Effects of natural beta-acids extracted from hops on *Salmonella* and *Campylobacter* pure culture.
N.A. Krueger*[1], R. C. Anderson[1], J. A. Byrd[1], M. D. Flythe[1], and D. J. Nisbet[1], *[1]Food and Feed Safety Research Unit, United States Department of Agriculture, Agriculture Research Service, College Station, TX, [2]Forage Animal Production Research Unit, United States Department of Agriculture, Agriculture Research Service, Lexington, KY.*

Salmonella and *Campylobacter* are important foodborne pathogens that may colonize the gut of food-producing animals. The objective of this experiment was to evaluate the effects of a hops β-acid solution on *S.typhimurium* and *C. jejuni* pure cultures. Nine-milliliter volumes with approximately 10^{-4} colony forming units (cfu) of overnight grown *S. typhimurium* (in tryptic soy broth; TSB) or *C. jejuni* (in Mueller Hinton; MH) added in triplicate to screw top tubes previously loaded with 1 mL MH, TSB, or hops β-acid extract solution to achieve 0, 62.5 (H1) or 125 ppm (H2) hops and were incubated anaerobically at 40°C. After 0, 3 and 6 h incubation, 1 mL sample from each culture was serially diluted and plated to XLT4 or Campy-Cefex agar for quantification of *S. typhimurium* and *C. jejuni*. Log_{10} transformations of *S. typhimurium* colonies enumerated after 24 h incubation and *C. jejuni* colonies enumerated after 48 h microaerobic (85% N_2, 10% CO_2, 5% O_2) incubation were subjected to Mixed Model repeated

measures ANOVA to assess affects of treatment over time. Tubes containing *S. typhimurium* initially contained 3.35 ± 0.202 $\log_{10}$ cfu/mL. Concentrations of *S. typhimurium* in control and H1 cultures increased ($P < 0.05$) by 6 h incubation (5.80 ± 0.175 and 4.97 ± 0.227, respectively); however, S. Typhimurium concentrations in H2 cultures did not differ over time ($P > 0.05$). *Campylobacter jejuni* cultures initially contained 4.41 ± 0.135 log10 cfu/mL. Concentrations of *C. jejuni* in control cultures did not differ ($P > 0.05$) over time whereas *C. jejuni* concentrations in H1 and H2 treated cultures were reduced to below our limit of detection ($\log_{10}$ 1.5) by 3 h incubation and did not recover by 6 h incubation. Results of this study demonstrate that hops β-acids can effectively reduce *C. jejuni* but not *S. typhimurium* concentrations in vitro.

Key words: *Campylobacter*, *Salmonella*, natural beta-acids

T108 *Staphylococcus aureus* virulence and metabolism are dramatically affected by *Lactococcus lactis* in cheese matrix. M. Cretenet[1,2], S. Nouaille[3,4], J. Thouin[1,2], L. Rault[1,2], L. Stenz[5], P. François[5], J. A. Hennekinne[6], M. B. Maillard[1,2], J. Fauquant[1,2], P. Loubière[3,4], S. Lortal*[1,2], Y. Le Loir[1,2], and S. Even[1,2], *[1]INRA, STLO, Rennes, France, [2]Agrocampus Ouest, STLO, Rennes, France, [3]Université de Toulouse; INSA, Toulouse, France, [4]INRA, UMR792, Toulouse, France, [5]University of Geneva Hospitals, Geneva, Switzerland, [6]ANSES, LERQAP, Maisons-Alfort, France.*

In complex environments such as cheeses, the lack of relevant information on the physiology and virulence expression of pathogenic bacteria and the impact of endogenous microbiota has hindered progress in risk assessment and control. Here, we investigated the behavior of *Staphylococcus aureus*, a major foodborne pathogen, in a cheese matrix, either alone or in the presence of *Lactococcus lactis*, as a dominant species of cheese ecosystems. The dynamics of *S. aureus* was explored in situ by coupling a microbiological and, for the first time, a transcriptomic approach. *L. lactis* affected the carbohydrate and nitrogen metabolisms and the stress response of *S. aureus* by acidifying, proteolysing and decreasing the redox potential of the cheese matrix. Enterotoxin expression was positively or negatively modulated by both *L. lactis* and the cheese matrix itself, depending on the enterotoxin type. Among the main enterotoxins involved in staphylococcal food poisoning, sea expression was slightly favored in the presence of *L. lactis*, whereas a strong repression of sec4 was observed in cheese matrix, even in the absence of *L. lactis*, and correlated with a reduced saeRS expression. Remarkably, the agr system was downregulated by the presence of *L. lactis*, in part because of the decrease in pH. This study highlights the intimate link between environment, metabolism and virulence, as illustrated by the influence of the cheese matrix context, including the presence of *L. lactis*, on 2 major virulence regulators, the agr system and saeRS.

Key words: *Staphylococcus aureus*, cheese, bacterial interactions

T109 Characterization of risk of food pathogens in Minas Frescal cheese. R. Freitas[1], A. F. Carvalho*[1], L. A. Nero[1], G. G. Netto[1], and M. A. V. Brito[2], *[1]Federal University of Viçosa, Viçosa, MG, Brazil, [2]EMBRAPA CNPGL, Juiz de Fora, MG, Brazil.*

This work aimed to carry out a characterization of the risk found in the food pathogens *Staphylococcus aureus*, *Listeria monocytogenes* and *Salmonella* sp., in Minas Frescal cheese. The prevalence and level of contamination by microbial agents was studied as well as the presence of microorganisms indicators of hygienic conditions (total coliforms and *Escherichia coli*), in relation to cheese making methods (lactic acidification, acidification by lactic acid and curd) and inspection stamp (federal, state or municipal) to which they were submitted. The magnitude of ingesting this type of cheese by Viçosa consumers for the qualitative estimate of risk of contracting diseases after consuming this product was investigated. Of 99 cheese samples analyzed, 20 were contaminated with *S. aureus*, with microorganism enumeration in 65% being higher than 1.0×10^3 cfu/g. The pathogen *L. monocytogenes* was isolated from one cheese sample, while *Salmonella* sp. was not identified in any of the samples analyzed. High contamination of the product by *E. coli* was also verified in 30.3% of the cheese samples analyzed, in values above the limit allowed by the current legislation, rendering these samples improper for consumption. A high level of cheese ingestion by the population was verified for consumption frequency and amount consumed. Of the total of 400 persons interviewed, 15.5% were in the age range between 11 and 20 years old, 77.5% between 21 and 60 years old and 7% above 60. Among the individuals interviewed, 84 informed that they consumed Minas Frescal cheese, 177 stated they consumed between 2 and 7 d per week, with the 11 to 20 year old, the 21 to 60 and the over 60 groups corresponding, respectively, to 11.9%, 77.4% and 10.7% of high cheese intake. Based on the use of the product by the population surveyed and the presence of S. aureus, Minas Frescal cheese consumption has the potential to contribute to the occurrence of intoxication cases in the population exposed to it, mainly when risk groups are considered. However, for *L. monocytogenes* and *Salmonella* sp. the risk of infection from consuming the product is low.

Key words: Minas Frescal cheese, risk characterization, quality

T110 Inhibition of *Listeria monocytogenes* growth in cheddar cheese by nanofiltration retentate of tryptic extract of whey proteins. V. Demers-Mathieu[1,2], G. Robitaille[1], D. St-Gelais[1], S. Gauthier[2], and M. Britten*[1], *[1]Food Research and Development Centre, Agriculture and Agri-Food Canada, St Hyacinthe, QC, Canada, [2]Centre de recherche STELA & INAF, Département de Sciences des Aliments et de Nutrition, Québec, QC, Canada.*

The objective of the study was to investigate the efficiency of a nanofiltration retentate (RT_{NF}) of trypsin-hydrolyzed whey proteins to control the food-borne pathogen *Listeria monocytogenes* and the non-pathogen *Listeria innocua* in Cheddar cheese models. Reconstituted Cheddar cheeses (37% humidity) containing 0, 10 or 20 mg/g of RT_{NF} and 3.5 or 1.75% salt/Humidity (S/H) were prepared from irradiated cheese powder, and were inoculated with 10^3-10^4 cfu/g of *Listeria* and 10^7 cfu/g of commercial lactic acid starter strains (*Lactococcus lactis* ssp. *cremoris*, *L. lactis* ssp. *lactis* and *Leuconostoc cremoris*). Cheeses were stored 7 d at 30°C or 28 d at 4°C, and bacterial counts during the storage were carried out for *Listeria* species and for lactobacilli. The presence of RT_{NF} in model cheese significantly decreased the survival of *Listeria* strains in a dose-dependent manner. The antimicrobial activity of RT_{NF} in Cheddar cheese was greater against *L. monocytogenes* than against *L. innocua* and was higher at 30°C than at 4°C. Moreover, the combination of 20 mg/g RT_{NF} and 1.75% S/H in cheeses incubated at either 30°C for 7 d or at 4°C for 28 d was the most efficient condition. For instance, *L. monocytogenes* bacterial counts significantly ($P < 0.001$) decreased by 1.1 and 1.5 log, respectively, when compared with model cheeses containing 1.75% or 3.5% S/H without RT_{NF}. Lactobacilli bacterial counts decreased during storage according to salt content, but was not affected by RT_{NF} ($P > 0.05$). It is suggested that the presence of higher lactobacilli content in cheeses containing 1.75% S/H contributes to the decrease of *Listeria* bacterial

content in synergy with RT_{NF}. In conclusion, antimicrobial peptides from trypsin-hydrolyzed whey proteins could be useful as natural preservative to control *L. monocytogenes* growth in reduced-salt cheeses.

Key words: *L. monocytogenes*, antibacterial, cheese

T111 Investigating contamination of bulk tank milk with *Listeria monocytogenes* on a dairy farm. J. C. F. Pantoja*, A. C. O. Rodrigues, C. Hulland, D. J. Reinemann, and P. L. Ruegg, *University of Wisconsin, Madison.*

The objective of this study was to identify the source of bulk tank milk (BTM) contamination with *Listeria monocytogenes* on a dairy farm with a history of isolation of this pathogen from unpasteurized BTM. The herd was comprised of 711 cows that produced an average of 36 kg of milk per day, with BTM SCC of 250,000 cells/mL. Cows were milked in a parallel parlor and milk was stored in 2 bulk tanks after passing through a plate cooler. Free stalls were bedded with sand or manure solids. The farm was visited between September and November, 2010, in 2 study phases. Each phase consisted of 3 weekly visits performed to assess the presence of *L. monocytogenes* in the following samples: environmental (feces, bedding, silage, and water from troughs, hoses, and wells); milking machine (milk filters and swabs from the inner surface of liners, milk hoses, milk meters, milk line, gaskets, and receiver jar); in-line milk of each pen milked; mammary glands; and BTM. Daily BTM and milk filters were also collected. Of all samples collected during the 2 study phases (n = 299), *L. monocytogenes* was isolated from 66% of milk filters (19 of 29), 16% of BTM (7 of 44), 6% of water samples (2 of 33) and 1 of 18 in-line milk samples. No other samples were positive for *L. monocytogenes*. A subset of 27 pairs of BTM and milk filter samples collected on the same day was used to assess the agreement between the isolation of *L. monocytogenes* from these 2 sources. Of 18 *L. monocytogenes*-positive milk filter samples, only 4 (22%) were also BTM positive. Based on these results, the authors recommended that the milk filter be changed at mid-milking, after which daily milk filter and BTM samples were collected for 3 weeks as a follow-up assessment of the prevalence of *L. monocytogenes* in the BTM. No follow-up milk filter (n = 23) or BTM (n = 15) samples were positive. Although a specific on-farm source of BTM contamination could not be identified based on these preliminary data, results suggest that the milk filter is a point of concentration of this zoonotic pathogen.

Key words: listeria, milk quality, zoonosis

T112 Prediction the growth of *Staphylococcus aureus* in raw milk using modified Gompertz and Logistic models. B. Li[2], C. Man[1], M. Guo*[3], Y. Shan[1], F. Zhao[2], S. Yang[2], Y. Jiang[2], Y. Lang[2], and Y. Jiang[1,2], [1]*National Dairy Engineering and Technology Research Center, Northeast Agricultural University, Harbin, Heilongjiang, China,* [2]*Department of Food Science, Northeast Agricultural University, Harbin, Heilongjiang, China,* [3]*Department of Nutrition and Food Sciences, The University of Vermont, Burlington.*

Staphylococcus aureus in dairy foods could cause foodborne illness. Raw milk may be to be kept incorrect temperatures in developing countries where cold storage facilities are lacking. The objective of this study was to predict the growth of *S. aureus* in raw milk produced in different seasons. Nine raw milk samples were collected in winter, spring, and summer, confirmed *S. aureus* free using 3M Petrifilm Staph Express Count Plates and inoculated with *S. aureus* (ATCC 13565) at a final concentration of 10^2 cfu/mL. The inoculated milk samples were incubated at 15°C, 25°C and 37°C with different incubation time and sampling interval according to the temperature. The enumerations of *S. aureus* were carried out in triplicates using the same method mentioned above. Growth data of *S. aureus* were analyzed with both a modified Gompertz model (mG model) and a modified Logistic model (mL model). The performance of each model were evaluated by calculating the root mean square error (RMSE), the Accuracy factor (A_f) and the Bias factor (B_f) between the observed and predicted values. Results showed that the A_f values of the mG model (1.0492_{Sum} and 1.0432_{Win}) were closer to 1.0 than those of the mL model (1.0851_{Sum} and 1.0663_{Win}) during summer and winter. As for the B_f values, the mG model also superior to the mL model (0.9764_{Sum} and 1.0056_{Win} vs. 1.0293_{Sum} and 1.0198_{Win}). The RMSE values of the mG model (0.1032_{Sum} and 0.0936_{Win}) were lower than those of the mL model (0.1857_{Sum} and 0.1498_{Win}). The results indicated a more accurate fitting between measured and predicted values by the mG model in both seasons. The A_f values and RMSE values of the mG model were better than those of the mL model (1.0562 and 0.1057 vs. 1.0945 and 0.1926) for samples collected in spring, although the B_f values of the mL model were closer to 1.0 than those of the mG model (0.9905 vs. 0.9890). The results showed that the mG model seems to be accurate for predicting the growth of *S. aureus* in raw milk of different seasons. This work was supported by the National Key Technology R&D Program of China (2009BADB9B06).

Key words: *Staphylococcus aureus*, prediction, raw milk

T113 Rapid detection of viable *Listeria monocytogenes* in milk by loop-mediated isothermal amplification coupled with propidium monoazide treatment. Y. Jiang[2], C. Man[1], M. Guo*[3], Y. Lu[1], F. Zhao[2], Y. Liu[2], B. Li[2], S. Yang[2], and Y. Jiang[1,2], [1]*National Dairy Engineering and Technology Research Center, Northeast Agricultural University, Harbin, Heilongjiang, China,* [2]*Department of Food Science, Northeast Agricultural University, Harbin, Heilongjiang, China,* [3]*Department of Nutrition and Food Sciences, The University of Vermont, Burlington.*

Listeria monocytogenes is a common foodborne pathogen in dairy foods. DNA-based loop-mediated isothermal amplification (LAMP) method cannot distinguish viable cells from dead ones, resulting in overestimate of *L. monocytogenes* contamination. Propidium monoazide (PMA) inhibits amplification of LAMP due to its ability of tightly binding to the DNA of dead cells. The objective of this study was to develop a procedure using LAMP method coupled with PMA treatment to detect viable *L. monocytogenes* in milk. *L. monocytogenes* (CMCC 54006) was cultured in tryptone soy broth containing 0.6% yeast extract at 37°C to logarithmic growth phase. Part of the cultured suspension was heated at 95°C for 3 min to obtain dead cells. The dead cell suspension was mixed with the viable cell suspension at a ratio of 9:1. The mix was inoculated in UHT sterilized milk with final concentrations of viable cells up to 10^7 cfu/mL. The inoculated milk was treated with PMA (50 μmoL, final concentration) in the dark for 5 min, subsequently exposed to a 650W halogen lamp for 3 min. Then DNA extracted from the PMA treated samples as templates for LAMP. A set of 4 primers, including forward-inner, backward-inner, forward outer, and backward outer, were designed for LAMP to target 6 distinct regions on the hlyA gene of *L. monocytogenes*. The LAMP analysis was carried out in a reaction mixture containing the 4 primers and DNA templates at 63°C for 1 h and heated at 80°C for 2 min to terminate the reaction. The amplified samples were then analyzed by a 1.5% agarose gel electrophoresis and the gel was stained with ethidium bromide. The detection limit for viable *L. monocytogenes* in steril-

ized milk by the PMA-LAMP method was 6.37×10^1 cfu/ml in only 90 min. Results showed that the PMA-LAMP method is a rapid and sensitive technique to detect viable *L. monocytogenes* in milk. This work was supported by the National Key Technology R&D Program of China (2009BADB9B06).

Key words: *Listeria monocytogenes*, milk, detection

T114 Simultaneous analysis of anions Cl^-, NO_2^-, SO_4^{2-}, NO_3^- and PO_4^{3-} in milk with ion chromatography. D. Liu and Z. Chen*, *Analysis and Testing Center, Shandong University of Technology, Zibo, Shandong Province, China.*

The amount of anions is an important index of milk quality control. Some methods have been reported to determine the concentration of milk anions. However, some methods are time-consuming and susceptible to interference, and only one element can be determined at a time. Ion chromatography (IC) has been developed for the simultaneous analysis of cations and anions in the water, food, atmosphere, etc. Chromatography can yield the precise and reproducible data when the experimental condition is kept constant. In the present studies, the packaged milk was bought in the market, and the anions (Cl^-, NO_2^-, SO_4^{2-}, NO_3^- and PO_4^{3-}) in milk were determined with the technique of IC. A Dionex ICS-2000 ion chromatograph with a Dionex gradient pump, eluent degassing module and conductivity detector was used. Anions were separated on an AS 11 HC ionexchange column, with an AS 11 HC guard column, and detected after suppression with an ASRS 300 anion electrical self-regenerating suppressor. The relative standard deviation (R.S.D.) for Cl^-, NO_2^-, SO_4^{2-}, NO_3^- and PO_4^{3-} was 3.44%, 9.52%, 2.38%, 1.67% and 3.48%, and the percent recovery was ranged from 80.21% to 120.24%. In addition, the concentration of 5 anions in the milk was detected, and the data were expressed as mean ± SD. Statistical analysis was performed by one-way ANOVA followed with comparison test. The concentration of Cl^-, NO_2^-, SO_4^{2-}, NO_3^- and PO_4^{3-} in the milk sample was 440.39 ± 0.15 mg/L, 8.33 ± 0.01 mg/L, 95.14 ± 0.02 mg/L, 2.14 ± 0.01 mg/L and 953.11 ± 0.33 mg/L (n = 6), respectively. There was significant difference among the concentration of Cl^-, NO_2^-, SO_4^{2-}, NO_3^- and PO_4^{3-} ($P < 0.05$). The results indicate that the IC technique is suitable for the rapid, precise and accurate determination of major anions in milk samples. Acceptable detection limits are obtained for the anions, and the time of anions analysis is significantly shortened with the technique of IC.

Key words: ion chromatography, anion, milk

T115 Evaluation of a screening test for detecting antimicrobial residues in milk by visual reading and by reader equipment. M. M. P. Araújo, M. A. Guerra, A. D. Lage, A. F. Cunha, L. M. Fonseca, M. O. Leite, M. R. Souza, C. F. A. M. Penna, and M. M. O. P. Cerqueira*, *Universidade Federal de Minas Gerais, Belo Horizonte, Minas Gerais, Brazil.*

To evaluate the efficiency of Charm MRL BL/TET kit for detecting antimicrobials residues in milk, raw milk samples without antimicrobials were inoculated with 21 drugs in 4 different concentrations including the Brazilian legal limit (MRL) and the detection threshold of the kit. The 21 antimicrobials from 6 different groups and positive and negative controls were tested with 30 repetitions by level. The results obtained by the reader equipment and visual reading were compared by the MacNemar test at 95% of confidence. The temperature of the blocks was monitored and the milk quality was evaluated by total bacterial count; somatic cell count; and fat, protein, lactose, total solids, and solids non fat contents. The temperatures varied from 55 to 57°C in the Charm MRL BL/TET kit and were considered satisfactory. The titratable acidity of the milk samples varied from 14.35 to 16.56°D. Considering all the limit levels of antimicrobial detection (L3) defined by the kit's manufacturer, discrepancies were not observed. The kit detected the different antimicrobials at level 2 that correspond to MRL concentration (Brazilian legislation) and also some detected at level 1 (L1) that was half the L3 concentration. The detection at level 2 (L2) was 100% for the majority of the antimicrobials, exception for cloxacillin (93.3%). Ceftiofur, an important antimicrobial used in Brazil, was detected in 100% of all the milk samples. In relation to L3 level, the Charm MRL Beta/TET kit detected cefalexin in 23.3% and cefapirin in 20.0% of the samples; cefazolin was not detected. Even considered similar ($P > 0.05$), some discrepancies in results evaluated by visual reading and by the kit's reader indicating the presence of antimicrobial residues should be interpreted with caution due to public health hazards and economic problems. It can be concluded that the test kit is efficient for detecting antimicrobials in milk and it can be used as a screening test for monitoring these substances in milk. The kit's reader must be obligatory for screening antimicrobial residues in milk in Brazil.

Key words: milk, antimicrobials, detection

T116 Descriptive statistics for surface and core temperatures measured with infrared imaging and a digital thermometer on commercial Midwestern US silages. J. P. Goeser*, C. Heuer, and C. M. Wacek-Driver, *Vita Plus Corp., Madison, WI.*

Forage temperature is related to silage nutritional status and DM loss, however limited data exists describing commercial forage temperatures in the US. This study surveyed silage surface and core silage temperatures to calculate population statistics reflecting temperature variations on commercial Midwestern US farms. Farms with horizontal silos of corn silage (n=44) and alfalfa silage (n=33) were measured twice, once during January 14 - April 27 and again during May 25 – August 6 in 2010. Range (maximum minus minimum) in surface temperatures was measured using a thermal imaging camera (FLIR Systems model b40, Boston, MA). Core temperatures were measured at approximately 65cm depth using a digital thermometer. Three core measures were taken: 1.5m from the right and left edge (**R/L Edge**) and one in the center; all core measures were taken 1.2m from the ground. Data were summarized using simple population statistics. Results are presented in Table 1. Range in silage temperatures (measured 200mm beneath silage surface) greater than 5°C above the silage central zone has previously been related to decreased nutritional value, however we observed surface temperature ranges greater than 5°C for all silages measured with an infrared camera. The results showed a numerical interaction for season and crop, with winter temperatures higher for corn silage than summer and vice versa for alfalfa silage. Further, silage temperatures greater than 35°C suffer protein losses and we observed core and surface temperatures exceeding 35°C, suggesting commercial forages are likely suffering protein losses due to heat.

Table 1. Forage silo temperature measures (degrees C)

Season	Crop	Measure Location	Mean	Max	Min	SD
Winter	Corn Silage	R/L Edge Core	19.3	39.0	6.0	6.5
		Center Core	22.2	34.0	13.0	6.0
		Surface Range	11.5	43.0	5.0	7.0
Winter	Alfalfa Silage	R/L Edge Core	21.3	38.0	4.0	6.2
		Center Core	24.9	35.0	8.0	6.2
		Surface Range	13.1	35.0	3.0	8.3
Summer	Corn Silage	R/L Edge Core	21.6	37.0	9.0	6.1
		Center Core	20.0	43.0	9.0	6.7
		Surface Range	8.5	21.0	1.0	5.6
Summer	Alfalfa Silage	R/L Edge Core	27.1	42.0	15.0	7.7
		Center Core	27.7	44.0	15.0	8.3
		Surface Range	10.8	28.0	2.0	8.0

Key words: forage, temperature, heating

T117 Intake, digestibility, and internal marker recovery of bermudagrass fed to cattle. J. Kanani*, D. Philipp, K. P. Coffey, E. Kegley, C. West, S. Gadberry, A. Young, and R. Rhein, *University of Arkansas, Fayetteville.*

A study was conducted to evaluate intake (DMI), digestibility (DMD), and fecal recovery of indigestible NDF (INDF) and ADF (INDF) by cattle offered bermudagrass [*Cynodon dactylon* (L) Pers] hays of varied qualities. Eight ruminally cannulated cows (594±100.3 kg) were allocated randomly to 4 bermudagrass-hay diets having a wide range of nutritional value providing two replicates per diet per period(n=24). Crude protein (CP) contents of the four hays offered in each period were 6.8, 10.5, 12.3, and 14.8; 7.8, 11.0, 13.3, and 16.4; and 9.0, 11.8, 13.8, and 18.1% DM; respectively for period 1, 2, and 3. Cows were housed in individual pens and offered their respective hay at 2% of BW in equal feedings at 0800 and 1700 h for a 10-d adaptation period followed by a 5-d total fecal collection period. Duplicate samples of each of the hay, ort, and fecal samples from each period were incubated for 140 h in the rumen of two cows for each of the digestion periods, followed by a sequential analysis of NDF and ADF. Recovery of INDF and IADF was expressed as the ratio of the quantity of marker excreted in the feces per unit of marker consumed. Data were analyzed as a replicated 4 × 4 Latin square design with one period missing using PROC GLM of SAS. Effects of cow, diet, and period were included in the model. Diet affected DMI (1.35, 1.63, 1.82, 1.73% BW, $P < 0.05$) and did not affect apparent DMD (53.0, 58.2, 57.7, 59.1% DM, $P > 0.05$). Marker recovery of INDF (68.2, 77.5, 85.1, 83.3%) was affected by diet ($P < 0.05$). Mean IADF recovery followed the same pattern with a slight increase in percentage of recovery. Mean IADF recovery was 70.0, 79.7, 88.9, and 87.5%; respectively for low, medium low, medium high and high CP content diets. Indigestible NDF and ADF determined by in situ incubation appeared not to be an adequate internal marker for varying quality of bermudagrass hay fed to cattle because of low recovery (less than 95%) and drastic variability across the range of bermudagrass hays tested.

Key words: bermudagrass nutritive value, internal marker, cattle

T118 In vitro gas production and microbial efficiency of *Paulownia tomentosa*. V. Gallardo-Santillan[1], R. Luevano-Escobedo[1], V. M. Llamas-Rodriguez*[1], M. Guerrero-Cervantes[1], H. Bernal-Barragán[2], A. S. Juárez-Reyes[1], and M. A. Cerrillo-Soto[1], *[1]Universidad Juárez del Estado de Durango, Durango,México, [2]Universidad Autónoma de Nuevo León, Nuevo León, México.*

This study was performed to determine the nutritional value of *Paulownia tomentosa* using in vitro estimations. Leaves from trees at three different stages of growth: juvenile (1 year), medium (4 years) and adult (10 years old) were collected during a period of three months. The collected samples were dried and ground through 1 mm screen. The samples (500 mg) were incubated in triplicate in calibrated glass syringes at 39°C. Rumen fluid from fistulated sheep fed alfalfa hay and concentrate (75:25) was used as inoculum. Gas production was recorded at 0, 3, 6, 9, 12, 24, 48, 72, and 96h. Data were fitted to the model $p= a+b\ (1-e^{-ct})$. Additional 24h incubations were utilized to estimate purine contents. The partitioning factor was also calculated from incubation residues which were refluxed with neutral detergent fiber solution. Data were analyzed for a completely randomized design for a 3 × 3 factorial arrangement with 3 maturity levels, (juvenile, medium and adult) and 3 cutting dates (August, September and October, 2010) using the SPSS program. Mean differences were separated using Tukey's test. No interactions were registered in the partitioning factor or fermentation parameters; however, interactions ($P < 0.05$) between maturity level*cutting date for purine contents were recorded. Partitioning factor values were similar during August and September (3.6 ± 0.2 mg substrate truly degraded/mL gas produced $_{24h}$ in vitro) but higher than those registered in October (2.9). Purine content was lower in foliage from adult samples in October (6.3 ± 0.6 µmol) than in medium (13 µmol) and juvenile (14 µmol). An effect of maturity

($P < 0.001$) was registered in the gas produced from the slowly but degradable b fraction; adult samples had lower values (36.5 ± 1.27 ml/500 mg) than juvenile (42 mL) and medium (45 mL). Similarly, the constant rate of gas production c in medium samples was higher (8.7 ± 0.004% h^{-1}) than juvenile (7.5% h^{-1}) and adult (6.3% h^{-1}). Data related to the rate and extent of gas production of the foliage of *Paulownia* at medium stages of growth support the fact this foliage is a promising animal feed resource.

Key words: *Paulownia*, in vitro gas production, purines

T119 Relationships between chemical composition, in vitro dry matter, neutral detergent fiber digestibility, and in vitro gas production of corn and sorghum silages. A. Corral-Luna*[1], D. Domínguez-Díaz[1], M. R. Murphy[2], F. A. Rodríguez-Almeida[1], C. Arzola[1], G. Villalobos[1], and J. A. Ortega-Gutierrez[1], *[1]Facultad de Zootecnia y Ecología, Universidad Autónoma de Chihuahua, Chihuahua, Chihuahua, México, [2]Department of Animal Science, University of Illinois, Urbana-Champaign.*

Five corn (*Zea mays*) and 4 sorghum (*Sorghum bicolor* L. Moench) silages were used to investigate the relationship between chemical composition (CC), in vitro dry matter digestibility (IVDMD), in vitro neutral detergent fiber digestibility (IVNDFD) and in vitro gas production (IVGP). The corn hybrids were harvested at half milk line and sorghum varieties in soft dough stage and ensiled in laboratory silos. Silages were dried in a 60°C forced-air oven, ground to pass a 1 mm sieve and analyzed for CC, IVDMD, IVNDFD and IVGP. The IVDMD and IVNDFD were determined using the ANKOM Daisy^{II} incubator and the IVGP according to the Menke and Steingass technique. The amount of gas produced (AGP) was recorded at 1, 2, 3, 4, 5, 6, 9, 12, 24, 48 and 72 h of incubation using a pressure transducer. The Groot logistic model was fitted to analyze the cumulative AGP for each sample. Pearson correlations coefficients between CC and AGP parameter estimates were calculated. The capability to predict IVDMD and IVNDFD based on CC and AGP data was examined with linear regression analyses. Silage contents of NDF, ADF and lignin were negatively correlated ($P < 0.05$) with IVDMD (−0.52, −0.50 and −0.50, respectively), and CP with asymptotic AGP (−0.42), but positively correlated ($P < 0.01$) with the estimates of parameter B (Time at which the half of asymptotic AGP was reached; 0.85, 0.81 and 0.72, respectively). After 1 h of incubation, AGP was negatively correlated to lignin content ($P < 0.01$) and positively correlated ($P < 0.05$) with non-fibrous carbohydrate (NFC). After 12 h of incubation, the correlations between NDF and ADF with AGP were highest ($P < 0.01$) until 48 h (−0.56 and −0.53, respectively). The CC alone is a good predictor of IVNDFD ($R^2 = 0.66$), and combined with AGP data adequately predicted IVDMD ($R^2 = 0.93$).

Key words: in vitro gas production, chemical composition, in vitro digestibility

T120 Effect of blending ruminal digesta, and filtration procedure on in vitro gas production. M. de J. Marichal*, R. Crespi, M. de los A. Bruni, S. Furtado, and G. Arias, *Departamento de Producción Animal y Pasturas, Facultad de Agronomia, Universidad de la Republica, Montevideo, Uruguay.*

Effect of blending ruminal digesta, and filtering through two or four layers of gauze or cheesecloth on in vitro gas production was evaluated. Rumen contents from two fistulated sheep were collected two hours after the morning meal (alfalfa hay, 1.6 kg DM/d, twice daily). Contents were combined, and blended for up to 1 min or not blended. Filtration was performed using 2 or 4 layers of either gauze or cheesecloth, resulting in eight combinations of inoculum preparation procedures. Samples (500 mg, milled 2 mm) of alfalfa hay (17% CP, 45% NDF) were weighed into 125 ml bottles, and mixed with ruminal fluid (10 ml), buffer (40 ml), and reducing (2 ml) solutions. All manipulations were done at 39$/deg;C, and with consistent CO_2 flushing. Time between rumen fluid collection, and inoculation was 40 min. Three bottles with substrate and three blanks were incubated per treatment. Pressure and gas volume gas were recorded at 1, 2, 3, 4, 6, and 8 h using a pressure transducer and calibrated syringe; venting the gas after each measurement. Gas accumulated at 8 h, and volume at each fermentation time, were analyzed (PROC MIXED, SAS) in a complete randomized design with a 2 × 2 × 2 factorial arrangement of treatments. Treatment effects on accumulated gas at 8 h were observed ($P < 0.01$), but no interactions ($P > 0.15$) among treatments existed. Accumulated gas was greater ($P < 0.001$) when digesta was blended previous to filtration (65 vs. 57 mL gas/g DM, respectively), when filtering through gauze than cheesecloth (65 vs. 59 ml/g DM, respectively), and 2 layers of either material, resulted in greater ($P < 0.01$) gas than 4 (66 and 57 mL gas/g DM, respectively). In all treatments, analysis of gas production at each fermentation time suggested ($P < 0.03$) a lag time of 4 h. When gas from blanks was subtracted from alfalfa gas, results were similar; the only difference was when comparing filtration materials, where no difference ($P = 0.22$) in accumulated gas existed (56 vs. 57 mL gas/g DM, for gauze and cheesecloth, respectively). It is important to consider all aspects of inoculum processing when comparing results of in vitro gas production experiments due to the potential variability between processing methods.

Key words: alfalfa, cheesecloth, layers

T121 Predictive accuracy of near-infrared reflectance (NIR) technology for fat and fatty acids in randomly selected TMR samples. R. T. Ward*[1], S. Weaver[1], and R. A. Patton[2], *[1]Cumberland Valley Analytical Services, Maugansville, MD, [2]Nittany Dairy Nutrition Inc., Mifflinburg, PA.*

Growing realization of the negative impact that consumption of unsaturated fats in general and linoleic acid in particular can have on the production of milk fat has led to a demand for determination of fatty acids, unsaturated fatty acid and linoleic acid in total mixed rations (TMR). At present this is an intensive process. In addition to extraction problems with high fat products, fatty acids must be separated by gas chromatography (GC). Development of an accurate test using NIR could provide a cost effective alternative that would allow more precise measurement and more control of these ration inputs. The objective of this study was to test whether NIR could adequately predict total fat content, total fatty acids, and total unsaturated fatty acids, as well as the C18 saturated and unsaturated fatty acids compared with chemical and GC analysis. Correlation and mean square prediction error (MSPE) were calculated in SAS using the methodology of Bibby and Toutenburg on 17 randomly selected TMR samples submitted in January 2011. Mean fat content of TMR was 4.35 ± 1.01% with a minimum of 2.60% and a maximum of 5.80% of DM. Fatty acid content was 3.87 ± 1.25% on a DM basis. NIR displayed good ability to predict fatty acids in quantities greater than 0.3% of dry matter. Below this level, ability to predict the mean was maintained, but correlation coefficients were decreased, and MSPE as percent of mean (RPE) was increased. Observed mean total unsaturated fatty acids were 2.47 ± 0.91% of DM, while NIR predictions were 2.46 ± 0.73 with a MSPE of 0.054 and R^2 of 0.98. Mean linoleic acid was observed to be 1.64

± 0.62% of DM and NIR predicted to be 1.64 ± 0.57% with MSPE of 0.024 and R^2 of 0.97. Similar value for C18:1 and C18:3 were respectively: mean observed, 0.69 ± 0.32 and 0.26 ± 0.08; mean predicted, 0.69 ± 0.16 and 0.26 ± 0.07; MSPE, 0.035 and 0.004; R^2, 0.89 and 0.64. We conclude that NIR has the potential to adequately predict fat, unsaturated fat and individual fatty acids when quantities are above 0.3% of DM.

Key words: NIR, fat, linoleic acid

T122 Relationships of fermentation characteristics in corn forage. R. Ward*[1] and D. R. Mertens[2], *[1]Cumberland Valley Analytical Services Inc, Maugansville, MD, [2]Mertens Innovation & Research LLC, Belleville, WI.*

Our objective was to study factors affecting the fermentation characteristics of corn forage using a database of analyses from Cumberland Valley Analytical Services, Inc. The initial database contained 4712 samples over 4 years from 41 states with analyses including fermentation characteristics such as titratible acidity (TA), ammonia (NH_3), acetic (Ac), lactic (La), and propionic (Pr) acids (measured chemically). Components such as DM, CP, ash, NDF, ADL, starch (St) and sugar (Su) were determined by chemical or NIR methods. Non-ammonia N (NAN) was calculated by difference between CP and NH_3. Data was analyzed using Proc MIXED in SAS. In order, TA was affected by Ac, La, Pr, NAN, St, Su, NH_3, ash and ADL ($P < 0.0001$). Intercept, Ac and La accounted for 0.61, 0.20 and 0.18, respectively, of the variation explained by the model. The coefficients for Ac, La, and Pr were positive and all other variables had negative coefficients. Average TA was 7.2 in Oct, increased to 8.0 by Jan and was maximum (8.9) in Apr (all different $P < 0.005$). Corn silage NH_3 (% DM) was related (in order) to Ac, La, CP, St, ADL and Pr ($R^2 = 0.54$). Intercept, Ac and La accounted for 0.40, 0.22 and 0.19 of model variation, respectively. All coefficients were positive. Average NH_3 was 0.77 in Oct, increased to 0.90 by Jan and was maximum (1.08) in May (all different $P < 0.0001$). When TA replaced individual acids (La, Ac, Pr) in the model, NH_3 was related (in order) to TA, CP, St and ADL ($R^2 = 0.52$); and TA accounted for 0.73 of model variation. Expressing NH_3 as % of CP, reduced the R^2 (= 0.45) and the influence of CP ($P = 0.093$). When months in storage was added to the NH_3 model with TA, CP, St, and ADL, the R^2 increased to 0.56, and the linear and quadratic effects of storage were significant ($P < 0.0001$). When Ac was grouped by level, DM, St and Su decreased, and fiber and NH_3 increased, as group Ac increased. Region or year had limited effects on any of the results. We concluded that NH_3 in fermented corn forage is related not only to the extent of fermentation as indicated by TA or acids (Ac, La, Pr), but also to time in storage. Fermentation relationships can explain changes in corn forage that affect utilization.

Key words: fermentation, corn silage, forage

T123 Factors affecting estimation of spoilage indices in silage. 1: Effects of culture media, temperature, and duration. J. Leite[1,2], K. G. Arriola[1], N. Cavalcanti[1,2], O. C. M. Queiroz[1], E. N. Muniz*[1,3], and A. T. Adesogan[1], *[1]Department of Animal Sciences, IFAS, University of Florida, Gainesville, [2]Universidade Federal Rural de Pernambuco, Recife, PE, Brazil, [3]Embrapa Tabuleiros Costeiros, Aracaju, SE, Brazil.*

The growth of yeasts and molds reduces silage quality and bunk life and can predispose to mycotoxin production and growth of pathogenic organisms. Little is known about effects of different culture media, temperatures, and durations on the growth of these fungi in silage. This trial was conducted to evaluate effects of 3 culture media, 2 temperatures, and 2 culture durations on the growth of yeasts and molds in corn silage. Fluid was extracted from corn silage (38% DM, 8.4% CP, and 39.8% NDF) and cultured on malt dextrose agar (MEA), potato dextrose agar (PDA) or on 3M film in triplicate at temperatures of 25 or 32°C for 3 or 5 d. The experimental layout was a 3 (media) × 2 (temperatures) × 2 (durations) factorial and the model included these terms and their interactions. Counts of the fungi were log-transformed and statistically analyzed with PROC GLM of SAS. No interaction was significant for mold counts ($P > 0.1$). Mold counts were similar on MEA and PDA, fewest ($P < 0.05$) on 3M film, and unaffected by culture temperature or duration. Culture temperature and duration had no effect on yeast counts on PDA, but yeast counts were fewer when cultured on 3M film at 25°C for 3 d than with other treatment combinations and they were lower when cultured on MEA at 25°C for 5 d than at 32°C for 3 d (media x temperature x duration interaction, $P = 0.007$). On average, yeast counts on MEA were fewer than on other media and counts at 32°C for 3 d were greater than for other temperature and duration combinations. This study shows that experimental conditions markedly affect the outcome of yeast and mold enumeration on silage.

Table 1. Effects of culture temperature, duration, and media on mean counts of molds and yeasts in corn silage

	Mold			
Media	PDA	MEA	3M	
	4.84^{b}	4.40^{b}	$<2^{a}$	
Temperature (°C)	25	32		
	3.31^{a}	2.85^{a}		
Time (days)	3	5		
	3.51^{a}	2.65^{a}		

	Yeast				
	25°C		32°C		
	3 d	5 d	3 d	5 d	Mean
PDA	6.57^{c}	5.04^{bc}	6.48^{c}	5.48^{bc}	5.89^{B}
MEA	2.14^{ab}	$<2^{a}$	4.72^{bc}	2.51^{ab}	2.34^{A}
3M	$<2^{a}$	7.75^{c}	8.02^{c}	5.41^{bc}	5.89^{B}
Mean	2.9^{A}	4.26^{A}	6.41^{B}	4.47^{AB}	

Key words: corn silage, molds, yeasts

T124 Relationship between residual feed intake, performance, and carcass parameters of pasture finished cattle. J. P. S. Neel*[1], E. E. D. Felton[2], S. K. Duckett[3], and W. S. Swecker[4], *[1]USDA-ARS-AFSRC, Beaver, WV, [2]West Virginia University, Morgantown, [3]Clemson University, Clemson, SC, [4]Virginia Tech University, Blacksburg.*

In 2009 and 2010, Angus-crossbred steers (n = 39) were used to evaluate the relationship between residual feed intake (RFI), pasture-finishing performance and carcass parameters. During RFI determinations before pasture finishing initiation in mid-April, animals were fed an alfalfa hay cube diet. Animals were adapted to facilities and cubes for a 10 d period before intake measurements. Intakes were measured utilizing GrowSafe 6000 (GrowSafe Systems, Ltd., Airdrie, Alberta, Canada) feeding nodes (2009 = 30d; 2010 = 56d) for RFI classification of animals. Each animal was assigned an RFI score based on individual intake and performance relative to population. Upon classification, animals were pasture finished on mixed-species pasture until harvest and carcass data collection in early November of each year (338 ± 41kg initial BW; 500 ± 40 kg final BW). During pasture fin-

ishing animals had an ADG of 0.81 ± 0.12 kg. Mean carcass measurements were: hot carcass weight (HCW) 260 ± 24 kg, fat thickness (FT) 0.445 ± 0.177 cm, ribeye area (REA) 67.4 ± 7.3 cm2, KPH 1.1 ± 0.4%, yield grade (YG) 2.0 ± 0.4, and marbling score (MS; 400–500 = slight) 477 ± 62. Data from both years along with Pearson correlation coefficients were utilized to assess RFI relationship with performance and carcass measurements. Residual feed intake was negatively ($P <$ 0.01) correlated with ADG (r = −0.42), and tended ($P = 0.086$) to be positively correlated with KPH (r = 0.28). Residual feed intake was not correlated with initial or final BW, HCW, FT, REA, YG, or MS. Correlations with ADG and KPH need further investigation to determine impact on pasture finishing systems.

Key words: residual feed intake, pasture, finishing

Forages and Pastures: Improving Pasture Quality and Utilization and Animal Performance

T125 Herbage accumulation in *Brachiaria humidicola* subjected to different frequencies and intensities of defoliation. H. H. Vilela[1], D. Nascimento Junior*[1], A. L. Santos[1], D. L. R. Henriques[1], B. D. Faria[1], C. A. S. Freitas[1], and A. F. Sbrissia[2], *[1]Universidade Federal de Vicosa, Vicosa, MG, Brazil, [2]Universidade do Estado de Santa Catarina, Lages, SC, Brazil.*

The experiment was conducted to evaluate the herbage accumulation of *Brachiariahumidicola* cv. Humidicola Common, subjected to different frequencies and intensities of defoliation. Two defoliation intensities, stubble heights of 8 and 16 cm, and two defoliation frequencies [95 and 100% light interception (LI)] were evaluated. The experiment was a completely randomized block design with a 2 × 2 factorial treatment arrangement with 3 replicates. The light interception (LI) was measured using a canopy analyzer (LI-COR LAI 2000) at 4 points per experimental unit (314 m^2). Grazing was carried out by 200 kg Zebu mixed steers. At each point a reading above the sward and 5 readings on the soil surface were taken, resulting in 4 readings above the sward and 20 readings at ground level. Herbage mass was harvested pregrazing using a quadrat of 0.33 × 1.0 m at 3 points in each paddock. Forage was harvested to the stubble height of each residue treatment and weighed immediately after cutting. A sample was force-dried at 65°C for 72 h to determine dry matter (DM) content. After weighing, the herbage mass was calculated from the fresh weight multiplied by the harvested forage DM content. Presented data are from Dec. 2009 to Mar. 2010 and results were compared by the Student's t test, with a significance level of 10%. Herbage accumulation rate was influenced ($P < 0.10$) by the frequencies and intensities of defoliation. Greater herbage accumulation (4191 kg/ha) was observed at higher intensity of defoliation (8 cm). In relation to frequency of defoliation, the highest herbage accumulation (4173 kg/ha) was observed at lower frequency (100% LI). Lower frequency and greater intensity of defoliation presented the highest herbage accumulation rate.

Key words: DM production, light interception, sward target

T126 Sward bulk density in *Brachiaria humidicola* subjected to frequencies and intensities of defoliation. D. Nascimento Junior*[1], H. H. Vilela[1], A. L. Santos[1], B. D. Faria[1], B. M. L. Sousa[1], G. O. Rocha[1], and A. F. Sbrissia[2], *[1]Universidade Federal de Vicosa, Vicosa, MG, Brazil, [2]Universidade do Estado de Santa Catarina, Lages, SC, Brazil.*

The experiment was conducted to assess the forage bulk density of *Brachiariahumidicola* cv. Humidicola comum, subjected to different intensities and frequencies of defoliation. Two defoliation intensities were evaluated, represented by stubble heights of 8 and 16 cm, associated with defoliation frequencies represening 95 and 100% light interception by the sward. Treatments were assigned according to a completely randomized block design with a 2 x 2 factorial treatment arrangement with three replicates. The light interception was measured using a canopy analyzer (LI-COR LAI 2000) at four points per experimental unit. At each point, a reading was taken above the sward and five on the soil surface (within the sward), resulting in four readings above the sward and twenty readings at ground level. Herbage mass was harvested pre-grazing using a quadrat of 0.33 x 1.0 m, at three points in each paddock. The forage was harvested to the residue stubble height for each treatment and the harvested forage was weighed immediately after cutting. A sample was forced- dried at 65°C for 72 h to determine dry matter (DM). Calculated herbage mass was divided by corresponding sward height to determine forage bulk density for each sward. Presented data are for the period of December 2009 to March 2010, and results were compared by Student's t test with a significance level of 10%. The bulk density of forage was influenced by defoliation frequency ($P < 0.10$) and the highest values (161.3±15.2 kg/ha.cm of DM) were obtained at the highest frequency (95% of light interception, LI). Lower frequency of defoliation (100% of light interception, LI) resulted in lower forage bulk density (110.3±15.2 kg/ha.cm of DM).

Key words: sward target, light interception, rotational grazing

T127 Herbage accumulation dynamics in pastures of *Pennisetum purpureum* submitted to grazing severities. D. Nascimento Junior*[1], B. M. L. Sousa[1], H. C. F. Monteiro[1], H. H. Vilela[1], M. C. T. Silveira[1], A. F. Sbrissia[2], and S. C. Da Silva[3], *[1]Universidade Federal de Vicosa, Vicosa, MG, Brazil, [2]Universidade do Estado de Santa Catarina, Lages, SC, Brazil, [3]Escola Superior de Agicultura Luis de Queiroz, Piracicaba, SP, Brazil.*

The experiment was carried out from December 2009 to May 2010 to evaluate the herbage accumulation dynamics of *Pennisetum purpureum* 'Napiergrass' submitted to grazing severities. Three post-grazing heights were evaluated: 30, 50 and 70 cm. Grazing was initiated when the sward reached 95% of light interception during regrowth. A completely randomized block design with three replications was used. Monitoring of the light interception was done using the canopy analyzer (LI-COR LAI 2000). In the beginning of each regrowth period twelve tillers were marked in each experimental unit to evaluate the growth and development dynamics. Additionally, aerial tillers that appeared during the regrowth were monitored. In order to evaluate the herbage accumulation dynamics, on the last day of each evaluation period, all the tillers were cut, separated into stems and leaves, and placed in a forced air oven at 65°C for 72 h. After drying them, the material was weighted and the mass of each one was divided by its respective total length. A conversion factor was generated to transform the linear values (centimeters) of the leaf, stem and leaf senescence rates in weight values to area unit. The herbage accumulation rate was calculated by the difference between values of growth and senescence. The data was submitted to variance analysis using the Mixed Procedure of SAS (Statistical Analysis System) The herbage accumulation rate was influenced by the post-grazing height ($P = 0.0456$) and months of the year ($P < 0.0001$). The highest values were obtained in the post-grazing heights of 50 cm (110.1 kg/ha.day of DM) and 70 cm (119.7 kg/ha.day of DM). March and April in 2010 (105.0 and 112.1 kg/ha.day of DM, respectively) presented the highest values, followed by December in 2009 and January in 2010 (86.9 and 85.0 kg/ha.day of DM, respectively). February and March (66.3 and 70.7 kg/ha.day of DM, respectively) presented the lowest values. A:\\post-grazing height of 30 cm can drastically reduce the pasture accumulation rate.

Key words: post-grazing height, post-grazing height, light interception

T128 Pre-and post-grazing targets for mulato grass subjected to rotational stocking management. M. C. T. Silveira[1], D. Nascimento Junior*[1], S. C. Da Silva[2], K. S. Pena[1], C. S. Rodrigues[1], S. J. Souza[2], V. A. Limao[2], L. M. Barbero[2], and B. M. L. Sousa[1], *[1]Universidade Federal de Vicosa, Vicosa, MG, Brazil, [2]Escola Superior de Agricultura Luiz de Queiroz, Piracicaba, SP, Brazil.*

The objective of this experiment was to evaluate pre- and post-grazing condition targets on mulato grass subjected to rotational stocking management. The experiment was carried out at E.S.A. "Luiz de Queiroz" Universidade de Sao Paulo, from January 2008 to April 2009. Treatments corresponded to combinations between two pre- (95% and maximum canopy light interception - LI) and two post-grazing (15 and 20 cm residue) conditions, and were allocated to experimental units according to a 2 × 2 factorial arrangement in a randomized complete block design, with four replications. Canopy light interception was monitored using the LAI 2000 canopy analyser (LI- COR) at ten locations per experimental unit (1200 m^2 paddocks) and were followed by measurements of sward height at 100 points per paddock using a sward stick. Herbage mass and herbage morphological composition at pre- and post-grazing were estimated using three 0.90 x 0.37 m metallic frames per paddock. Data were analyzed as repeated measurements and means compared using t Student test at 5% significance. Post-grazing heights were consistently close to targets on swards managed at 95% LI, the same response did not occur on those managed at maximum LI (99%), particularly for the 15 cm target that became 20 cm after the first three grazing cycles. That was mainly due to increased accumulation of stem and dead material on swards managed at maximum relative to those managed at 95% LI. This was caused by intense competition for light when canopy light interception was allowed to increase beyond 95%, and caused difficulties to graze paddocks down to residue targets, deteriorating sward structure with potential negative effects on nutritive value and intake of the produced herbage. Pre-grazing height was larger on swards managed at maximum relative to those managed at 95% LI, regardless of post-grazing height for most of the experimental period, and values were relatively stable and around 30 and 40 cm. The results indicate that mulato grass should be grazed when paddocks reach 30 cm pre-grazing height (95% LI) using post-grazing heights of 15 to 20 cm.

Key words: *Brachiaria* sp. 'Mulato', canopy light interception, sward target

T129 Balance between the emergence and mortality of tiller in *Brachiaria decumbens* pastures under continuous stocking. M. E. R. Santos[1], V. M. Gomes[2], D. M. Fonseca[2], D. Nascimento Junior*[2], and A. F. Sbrissia[3], *[1]Universidade Federal de Uberlandia, Uberlandia, MG, Brazil, [2]Universidade Federal de Vicosa, Vicosa, MG, Brazil, [3]Universidade do Estado de Santa Catarina, Lages, SC, Brazil.*

The experiment was conducted to evaluate 2 different strategies for managing *Brachiaria decumbens* under continuous stocking. From June 2008 to March 2009, the *B. decumbens* pastures were evaluated at the Departamento de Zootecnia of the Universidade Federal de Vicosa located in the State of Minas Gerais, Brazil. The experimental site was located at 651 m altitude, 20° 45′ S and 42°51′ W. Annual precipitation is around 1,340 mm. Maximum and minimum temperatures are 22.1°C and 15.0°C, respectively. The experimental area was made up of 8 plots (experimental units) of 0.3 ha. In one management strategy, *B. decumbens* pasture was maintained at height of 25 cm during the trial. In the other, the pasture was kept at an average of 15 cm high during the winter (July to September 2008), and at 25 cm from the beginning of winter until the summer (October 2008 to March 2009). The experiment was carried out using a randomized block design with 4 repetitions and subdivided plots. Both management strategies for the pasture correspond to the plots. The seasons of the year are the subplots. In each experimental unit, all tillers inside the frames with 0.0625 m^2 were counted and marked with colored plastic coated wire. Every 30 d, all tillers were recounted and new tillers were marked with a different wire color. The collected data was used to calculate the balance between the emergence and mortality of tiller (BAL). The BAL was lower ($P < 0.10$) in the winter (0.1%) and higher ($P < 0.10$) in the spring (22.3%) and summer (26.2%). These results characterize a high *B. decumbens* tiller turnover in the spring and the summer, resulting in more young tillers in the pasture. Lowering the pasture height to 15 cm in the winter increased ($P < 0.10$) the BAL (21.1%) if compared with the one kept at 25 cm (BAL equal to 11.3%). For lower canopies, the higher light incidence at the base of the plants stimulates tillering. Hence, to optimize the turnover of tillers, *B. decumbens* should be managed, under continuous stocking, to have 15 cm in height in the winter and 25 cm in the spring and summer.

Key words: grazing management, seasons of the year, sward height

T130 Forage utilization efficiency estimated in *Pennisetum purpureum* submitted to grazing severities. D. Nascimento Junior*[1], B. M. L. Sousa[1], H. C. F. Monteiro[1], F. C. Gomes[1], C. Z. Assis[1], H. H. Vilela[1], A. F. Sbrissia[2], A. L. Santos[1], and M. C. T. Silveira[1], *[1]Universidade Federal de Vicosa, Vicosa, MG, Brazil, [2]Universidade do Estado de Santa Catarina, Lages, SC, Brazil, [3]Escola Superior de Agicultura Luis de Queiroz, Piracicaba, SP, Brazil.*

The experiment was carried out from December 2009 to May 2010 in order to estimate the forage utilization efficiency of *Pennisetum purpureum* 'Napier' submitted to different grazing severities. Three post-grazing heights were evaluated: 30, 50 and 70 cm. The grazings were performed when the sward reached 95% of light interception during regrowth. A completely randomized block design with three replications was used. The monitoring of the light interception was done using the canopy analyzer (LI-COR LAI 2000). In the beginning of each regrowth period, twelve tillers were marked in each experimental unit to evaluate the growth and development dynamics. Aerial tillers that appeared during the regrowth were also monitored. In the last day of each evaluation period, all the tillers were cut, separated into stems and leaves, and dried in a forced air oven at 65°C for 72 h, then weighed and the mass of each compound was divided by its respective total length. A conversion factor was generated to transform the linear values (cm) of the leaf, stem and leaf senescence rates in weight values to area unit. The total growth rate (leaf growth + stem growth) and the pasture senescence rate were calculated. It was possible to estimate the forage efficiency utilization: {(1 â€“ senescence/total growth) x 100}. The data was submitted to variance analysis using the Mixed Procedure of SAS (Statistical Analysis System) and compared by the Student's t-test, with 5% of significance. The forage utilization efficiency estimate was affected by the post-grazing height ($P = 0.0284$) and months of the year ($P < 0.0001$). The post-grazing heights of 70 (82.2%) and 50 cm (86.0%) presented the highest ($P = 0.0284$) forage utilization efficiency estimates, and the residue of 30 cm (73.0%), the lowest. December 2009 presented forage utilization efficiency estimated at 4.5%. This value reduced in January (73.9%) and February (68.8%) in 2010, but increased in March 2010 (80.7%), and reaching

a higher value ($P < 0.001$) in April (87.7%) and May (86.9%) in 2010. The post-grazing height of 30 cm gave the lowest forage utilization efficiency of *Pennisetum purpureum* 'Napier'.

Key words: grazing management, light interception, post-grazing height

T131 Grazing losses and grazing efficiency on mulato grass subjected to strategies of rotational stocking management. M. C. T. Silveira[1], D. Nascimento Junior*[1], S. C. Da Silva[2], C. S. Rodrigues[1], V. A. Limao[2], L. M. Barbero[2], S. J. Sousa[2], K. S. Pena[1], and B. M. L. Sousa[1], *[1]Universidade Federal de Vicosa, Vicosa, MG, Brazil, [2]Escola Superior de Agricultura Luiz de Queiroz, Piracicaba, SP, Brazil.*

This experiment evaluated grazing losses and grazing efficiency on mulato grass subjected to strategies of rotational stocking management. The experiment was carried out at Piracicaba-SP, from January 2008 to April 2009. Treatments corresponded to combinations between 2 pre- (95 and 99% canopy light interception - LI) and 2 post-grazing (15 and 20 cm residue) conditions, and were allocated to experimental units (1200 m^2paddocks) according to a 2x2 factorial arrangement in a completely randomized block, with 4 replications. Litter losses to the soil pathway were considered as all material lying on the ground as well as broken stems and green leaves still attached and hanging onto plants in paddock areas (2 2.0 × 1.0 m sites) previously prepared for measurements before each grazing. Preparation consisted of removal of all surface litter (un-rooted live and dead plant material). Grazing losses were weighed and values calculated as kg/ha. These were also calculated as percentage of the total herbage removed during grazing (difference between pre- and post-grazing herbage masses), and the results used to calculate grazing efficiency as their complement to 100. Data were analyzed as repeated measurements and means compared using Student's *t*-test at 5% significance. Litter losses were smaller ($P < 0.0001$) on swards managed at 95% than on those managed at maximum LI (99%) (795 ± 32.3 and 1305 ± 36.6 kg/ha, respectively), with larger values ($P < 0.0001$) recorded in autumn-winter-early spring (1400 kg/ha ± 134.7 SEM) relative to those recorded in late spring (1265 kg/ha ± 84.6 EPM), summer 2008 (660 kg/ha ± 22.0 SEM) and summer 2009 (880 ± 37.7 SEM). In relation to post-grazing heights, litter losses were larger ($P = 0,0188$) on swards managed at 15 cm relative to those managed at 20 cm (1120 and 980 kg/ha ± 38.1 SEM). Grazing efficiency was 24% larger on swards managed at 95% relative to those managed at maximum LI (70.2 and 56.7% ± 1.4 SEM), suggesting the pre-grazing target of 95% LI as ideal since it was associated with reduced herbage losses due and enhanced grazing efficiency.

Key words: *Brachiaria* sp. 'Mulato', canopy light interception, harvest efficiency

T132 Relationship between canopy light interception and pre-grazing sward height in *Brachiaria humidicola* pastures subjected to frequencies and intensities of defoliation. H. H. Vilela[1], D. Nascimento Junior*[1], A. L. Santos[1], B. M. L. Sousa[1], G. O. Rocha[1], C. A. S. Feitas[1], and A. F. Sbrissia[2], *[1]Universidade Federal de Vicosa, Vicosa, MG, Brazil, [2]Universidade do Estado de Santa Catarina, Lages, SC, Brazil.*

The light interception by the sward is correlated with pre-grazing sward surface height, becoming a practical management tool for farmers. The aim of this work was to evaluate the light interception and pre-grazing sward height of *Brachiaria humidicola* 'Comum' pastures subjected to frequencies and intensities of defoliation. Two defoliation intensities were evaluated (8 and 16 cm), associated with defoliation frequencies represented by 95 and 100% of the intercepted light by the sward. The experiment was assigned according a complete randomized block design in a 2 × 2 factorial arrangement with 3 replicates. The light interception was measured using a canopy analyzer (LI-COR LAI 2000) at 4 points per experimental unit (paddock). A reading was taken above the sward and 5 on the soil surface (within the sward), resulting in 4 readings above the sward and 20 readings at ground level. The evaluation of the sward surface height was performed using a ruler, on the same day the paddocks had their light interception measured. Sward height was measured at 20 points per paddock. The data presented are for the period from December 2009 to March 2010 and means were compared by Student *t*-test, 10% significance. ANOVA was performed on light interception (control variable). The interception of light by pastures in the treatment with the highest frequency was 94.86% and the treatment of lower frequency, 98.05%. The sward height was influenced ($P < 0.10$) only by the frequency of defoliation, with an average of 30.27 cm for the highest frequency (95% LI) and 49.76 cm for lower frequency (100% LI). Pre-grazing stubble height is an important feature on plant and animal performance. In this study, sward height was consistently correlated positively with light interception.

Key words: light interception, rotational grazing, sward target

T133 Tiller population density in *Brachiaria humidicola* pastures subjected to frequencies and intensities of defoliation. H. H. Vilela[1], D. Nascimento Junior*[1], A. L. Santos[1], B. M. L. Sousa[1], G. O. Rocha[1], C. A. S. Feitas[1], and A. F. Sbrissia[2], *[1]Universidade Federal de Vicosa, Vicosa, MG, Brazil, [2]Universidade do Estado de Santa Catarina, Lages, SC, Brazil.*

The maintenance and stability of grasslands can be obtained through appropriate management practices. The use of rotational grazing systems, based on defoliation frequencies determined by canopy light interception can ensure pasture persistence, since this management practice is closely related to the sward ecophysiology. This study was conducted to evaluate basal and aerial tiller population density at post-grazing in *Brachiaria humidicola* 'Comum' pastures subjected to frequencies and intensities of defoliation. Two defoliation intensities were evaluated, represented by stubble height of 8 and 16 cm, associated with defoliation frequencies determined by 95 and 100% of light interception by the sward. A randomized complete block design was adopted with 3 replicates in a 2 × 2 factorial arrangement. The light interception was measured with the canopy analyzer equipment (LI-COR LAI 2000). The assessment of population density of basal and aerial tillers (alive) was held at 3 points in each paddock, by counting the total number of basal and aerial tillers in a quadrat of 0.25 × 0.25 m. The data presented are for the period of December 2009 to March 2010 and results were compared by Student *t*-test with a level of significance of 10%. The population density of basal tillers was influenced ($P < 0.10$) by the intensities and frequencies of defoliation. Highest population density of basal tillers (3205 tillers/m^2 was observed at lower intensity of defoliation (16 cm). Regarding the frequency of defoliation, higher population density of basal tillers (3170 tillers/m^2 was observed at higher frequency (95% light interception). The aerial tiller density was not influenced by treatment ($P > 0.10$). More frequent grazing (95% light interception) and the use of lower intensity defoliation (16 cm), seems to improve stability and persistence of *Brachiaria humidicola* 'Comum'.

Key words: light interception, tillering, sward target

T134 Forage production and leaf area index of tropical grass cultivars under irrigation in the cerrado region of Minas Gerais, Brazil. E. A. da Silva*[1,6], W. J. da Silva[1], J. R. M. Ruas[2,5], D. S. Queiroz[3], M. C. M. Viana[4,6], J. M. V. Paes[1,6], and L. C. da Silva Júnior[7,8], *[1]EPAMIG, Uberaba, Minas Gerais, Brazil, [2]EPAMIG, Janaúba, Minas Gerais, Brazil, [3]EPAMIG, Viçosa, Minas Gerais, Brazil, [4]EPAMIG, Prudente de Morais, Minas Gerais, Brazil, [5]CNPq, Brasília, Federal District, Brazil, [6]FAPEMIG, Belo Horizonte, Minas Gerais, Brasil, [7]FAZU, Uberaba, Minas Gerais, Brazil, [8]FAPEMIG, Belo Horizonte, Minas Gerais, Brazil.*

The Leaf Area Index (LAI) is one of the most important biophysical variables used for crop modeling, and it is directly related to evapotranspiration, yield and light interception. The objective of this work was to estimate LAI of tropical grass cultivars under irrigation on 10 cutting dates. The experiment was carried out from December 2008 to December 2009. The experimental design was a complete randomized block in a split plot with 4 replications. The herbage was considered the main plot and cutting date the subplot. The treatments were: *Brachiaria decumbens* 'Basilisk', *Brachiaria brizantha* 'Marandu', *Brachiaria brizantha* 'Xaraes', *Panicum maximum* 'Mombaça', *Panicum maximum* 'Tanzania' and *Cynodon* spp. 'Tifton 85' and 10 cutting dates. The dry matter percentage and LAI were evaluated. The LAI was calculated as the green leaf area per unit of ground area. The data were subjected to ANOVA and when significant effects for the factors evaluated became the Tukey Test at 5% probability using the statistical package SAS (2001). The dry mass production of forage showed strong relationship with LAI. The dry mass accumulation of cultivars Basilisk, Marandu, Tanzania and Mombaça were superior ($P < 0.05$) to cultivars Tifton 85 and Xaraes production. The LAI showed seasonal variations with lower values in the winter. The cultivars Mombaça and Tifton 85 presented higher and lower LAI ($P < 0.05$), respectively. The satisfactory performance presented by cultivars, associated with other important characteristics of adaptability, show the importance of these cultivars as an alternative pasture for different cattle systems as well as a contribution to their sustainability. The differentiated productive behavior between cultivars must be considered for an adequate management of these grasses. (Research supported by FAPEMIG/CNPq, Brazil)

Table 1. Dry matter (DM) production (t/ha) and leaf area index of different forages

Date	Basilisk	Marandu	Xaraes	Mombaça	Tanzania	Tifton 85
Dec	4^{Bb}	3^{Eb}	8^{Aa}	9^{ABa}	4^{Bb}	2^{Ab}
Jan	8^{Aa}	7^{ABCab}	5^{Aab}	7^{ABab}	7^{ABab}	4^{Ab}
Mar	5^{ABa}	5^{CDEab}	6^{Aa}	6^{BCa}	7^{ABa}	1^{Ab}
Apr	7^{ABa}	3^{Eb}	7^{Aa}	6^{BCab}	6^{ABab}	3^{Ab}
Jun	5^{ABa}	3^{Eab}	5^{Aa}	3^{Ca}	4^{Ba}	3^{Aa}
Set	6^{ABbc}	8^{Bab}	5^{Abc}	9^{Aa}	7^{ABabc}	4^{Ac}
Oct	8^{ABa}	8^{BCa}	5^{Aab}	7^{ABa}	9^{Aa}	3^{Ab}
Dec	9^{Aab}	9^{Aab}	6^{Abc}	10^{Aa}	9^{Aab}	3^{Ac}
DM	51^{a}	43^{ab}	33^{ab}	48^{ab}	43^{cd}	29^{d}

Means followed by different lowercase letters in the same row or capital letters in the same column are significantly different ($P < 0.05$).

Key words: dry matter, tropical forage, season

T135 Morphogenic characteristics of tropical grass cultivars under irrigation in the cerrado region of Minas Gerais, Brazil. E. A. da Silva*[1,5], W. J. da Silva[1], J. R. M. Ruas[2,6], M. C. M. Viana[3,5], D. S. Queiroz[4], J. M. V. Paes[1,5], and L. C. da Silva Júnior[7,8], *[1]EPAMIG, Uberaba, Minas Gerais, Brazil, [2]EPAMIG, Janaúba, Minas Gerais, Brazil, [3]EPAMIG, Prudente de Morais, Minas Gerais, Brazil, [4]EPAMIG, Viçosa, Minas Gerais, Brazil, [5]FAPEMIG, Belo Horizonte, Minas Gerais, Brazil, [6]CNPq, Brasília, Federal District, Brazil, [7]FAZU, Uberaba, Minas Gerais, Brazil, [8]FAPEMIG, Belo Horizonte, Minas Gerais, Brazil.*

The objective of this work was to estimate leaf area index of tropical grass cultivars under irrigation at 10 cutting dates. The experiment was carried out from January to December 2009. The experimental design was a complete randomized block in a split plot with 4 replications. The herbage was considered the main plot and cutting date the subplot. The treatments were: *Brachiaria decumbens* 'Basilisk', *Brachiaria brizantha* 'Marandu', *Brachiaria brizantha* 'Xaraes', *Panicum maximum* 'Mombaça', *Panicum maximum* 'Tanzania' and *Cynodon* spp. 'Tifton 85' and 10 cutting dates. To evaluate the morphogenic characteristics, 3 tillers were marked in each plot. Data were analyzed by ANOVA and means were compared by Tukey test ($P < 0.05$). The number of tillers per area of Tanzania did not ($P > 0.05$) vary with seasons and was 301/m^2. The number of tillers per area was 880, 526, 522, 292, 301 and 1147/m^2 for cultivars Basilisk, Marandu, Xaraes, Mombaça, Tanzania and Tifton 85, respectively. These values are consistent with those reported in the literature. The number of tillers in the sward was a function of grass cultivar and time of the year. The difference in number of tillers was statistically significant at the 5% probability level with the Tukey test. Highest values ($P < 0.05$) of tillers were recorded for Tifton 85 cultivar and the lowest ($P < 0.05$) for the 2 Panicum cultivars, whereas, *Brachiaria brizantha* cultivars ranked intermediate. Tiller population density varied with season of the year and cultivars, with lowest values being consistently recorded during winter. (Research supported by FAPEMIG/CNPq, Brazil)

Table 1. Tillers (m^2) per tropical forages

Date	Basilisk	Marandu	Xaraes	Mombaça	Tanzania	Tifton
Jan	$1{,}053^{ABCa}$	603^{ABab}	264^{Bb}	172^{ABb}	271^{Ab}	624^{Eab}
Mar	528^{Da}	525^{ABa}	370^{Ba}	165^{Ba}	286^{Aa}	595^{Ea}
Apr	765^{BCDab}	270^{Bc}	403^{Bbc}	172^{ABc}	258^{Ac}	928^{CDEa}
Jun	769^{BCDb}	373^{ABbc}	317^{Bbc}	130^{Bc}	176^{Ac}	$1{,}414^{ABCa}$
Set	684^{CDb}	754^{ABb}	465^{ABb}	491^{ABb}	314^{Ab}	$1{,}499^{ABa}$
Oct	$1{,}260^{ABa}$	$4{,}744^{ABc}$	942^{Aab}	676^{Abc}	399^{Ac}	$1{,}159^{BCDa}$
Dec	$1{,}419^{Aa}$	807^{Ab}	524^{ABbc}	524^{ABbc}	356^{Ac}	$1{,}717^{Aa}$

Means followed by different lowercase letter in the same row or capital letters in the same column are significantly different.

Key words: tillering, tropical forage, season

T136 Effect of patch-burning mixed-grass prairie rangeland on cattle performance. S. A. Gunter*[1], T. L. Springer[1], E. T. Thacker[1], and R. L. Gillen[2], *[1]USDA-ARS, Southern Plains Range Research Station, Woodward, OK, [2]Western Kansas Agricultural Research Centers, Kansas State University, Hays.*

Patch burning, a range management tool, has gained favor in recent years to renovate degraded rangelands. By burning a portion of a pasture, it is hypothesized that cattle will concentrate grazing on burned sites and the increased disturbance will encourage forb establishment and lessen grazing in the unburned portion. To evaluate the effect of patch burning on the performance by stocker cattle grazing mixed-grass prairie in northwest Oklahoma, 3 pastures ranging in size from

24 to 13 ha were selected; 2 pastures had been reseeded to native grass <8 yr before the start of the experiment and the third site was go-back land with no record of reseeding since 1939. Each pasture was divided in half and all were burnt in March of 2005 before the start of the 4-yr experiment in 2006; the patch-burnt pastures had 25% burnt each March starting in 2006 through 2009. Each pasture was stocked with steer calves (248 ± 7.6 kg) at a rate of 5l.1 animal-unit-d/ha from mid-January to late-July. From January until mid-April, calves were fed 0.68 to 0.91 kg/steer of a 41% CP cottonseed meal-based supplement; cattle had access to water and plain salt during the entire grazing period. Cattle were weighed in January, mid-April, and late-July after an overnight-shrink without feed or water. Data were analyzed using GLIMMIX in SAS with treatment as the fixed effect and pasture and year as random effects. The ADG of calves on the patch-burned rangeland (0.83 kg) did not differ (P = 0.73) for cattle grazing unburned pastures (0.82 kg). Because BW did not differ (P = 0.77) in January and ADG did not differ, BW at the end of the grazing period in July did not differ (P = 0.88; average BW = 382 ± 12.6 kg). Body weight gain/ha by calves on the patch-burned rangeland (68 kg) did not differ (P = 0.48) for cattle grazing unburned pastures (69 kg). Using the patch-burning tool on mixed-grass prairie in northwest Oklahoma did not have a detrimental effect on cattle performance. If this technique proves to augment the ecological services rangelands provide, it may become widely used by land managers.

Key words: grazing, rangelands, cattle

T137 Estimating pasture growth rates using local weather data. E. B. Rayburn and W. L. Shockey*, *West Virginia University, Morgantown.*

Climatic conditions in the Appalachian region of the US are generally conducive to forage production for use as ruminant livestock feed. Forage growth variations contribute to uncertainty about the number of ruminant livestock that can be supported at any given location in any given year or season of the year. A forage growth model was developed that predicts plant growth rates based on local weather data and Penman-type evapotranspiration. Based on field testing of the forage growth model with in-field weather and clipped forage production over 16 site years the model predicted yield compared with clipped yield with an R^2 of 0.81 and a residual SD of 965 kg/ha. The model was refined to use historical weather data to make a stochastic model that could evaluate yield variability based on historical weather variation. Thirty years of data were collected from 5 weather stations that are representative of a variety of elevations and mean monthly temperatures in northern WV. Data collected were latitude and daily maximum, minimum, and average temperatures, and rainfall. The stochastic model uses the local probability of rainfall frequency and amount to calculate random predictions of weather used in the calculation of the Plant Growth Rate (PGR) for each day of the modeled year for a location. A new model year for PGR is generated with each calculation of the spreadsheet model. By comparing the stochastically modeled PGR estimates which use the variability in the 30-year weather data, one might plan with some confidence, in light of the risk incurred due to variability in pasture growth across years and within the year, the number of animal units that can be supported on a farm that is located in the region supported by its weather station. Because the model estimates PGR for each the day of the year, livestock producers may more accurately plan the timing for changes in stocking rates, mechanical harvest of excess forage, or purchase of supplemental feed relative to the historical risk associated with a given weather station. With appropriate analysis of historical data from additional weather stations this stochastic model could be extended to other areas of the country.

Key words: pasture, weather, plant growth

T138 Impact of feeding strategies on milk production and income over feed cost: A case study of organic, grazing and conventional Wisconsin dairy farms. M. Dutreuil*, M. Wattiaux, R. Gildersleeve, B. L. Barham, and V. E. Cabrera, *University of Wisconsin, Madison.*

A survey was developed to understand feeding practices on Wisconsin dairy farms and their consequences on milk production and milk income over feed cost (IOFC). Farms were randomly selected across 3 management systems: conventional (CON), grazing (GRA) and organic (ORG). Preliminary results from 2 CON, 3 GRA and 3 ORG are presented. No statistical analysis is reported because of these small numbers of farms. Grains were used in similar amounts across the year 2010 on GRA and ORG, whereas CON used less than half grain in summer than in winter. Grains were partially replaced in CON by a protein mix that was used more than double in summer than in winter. Hay was the main component in the winter for all the farm systems, which was partially replaced by grazing during summer. Corn silage, haylage, and baleage were used in similar amounts throughout the year by CON and ORG, whereas GRA used an additional 3.9 kg DM/cow/d in summer. In total, DMI in winter (kg/cow/d) was higher for CON and GRA (24.6 and 23.8, respectively) than for ORG (15.0), which led to differences in milk production (kg/cow/d) and cost of feed, ($/cow/d) for CON (27.3 and 2.6), GRA (20.0 and 1.5), and ORG (10.4 and 1.5). Milk price for ORG ($60/100 kg milk) was about twice as much as CON and GRA. Calculated milk IOFC ($/cow/d) was higher for CON (6.8) in winter and for ORG (7.5) in summer. The use of grazing by ORG during summer improved milk production (+4.6 kg/cow/day) and decreased feed cost (−0.2 $/cow/day), which determined the highest milk IOFC. Our preliminary results indicate that, given 2010 prices, ORG could be as much profitable as CON or GRA systems when including the USDA's National Organic Program grazing standards.

Table 1. Feeding practices, milk production and income over feed cost (IOFC) on Wisconsin dairy farms

	Winter (January)			Summer (June)		
	CON	GRA	ORG	CON	GRA	ORG
Feed (kg DM/cow/d)						
Grain mix	6.3	4.0	4.3	3.0	4.0	4.3
Protein mix	3.6	0.5	0.0	7.7	0.3	0.0
Hay	8.6	13.1	8.0	3.8	3.6	1.3
Corn silage	4.3	3.0	1.3	4.3	3.0	1.3
Haylage/Baleage	1.8	3.0	1.3	1.8	6.9	1.5
Milk production (kg/cow/d)	27.3	20.0	10.4	28.2	22.0	15.0
Cost of feed ($/cow/d)	2.6	1.5	1.5	3.5	1.6	1.3
Milk price ($/100 kg)	34.5	35.8	62.1	32.4	32.3	58.2
Income over feed cost ($/cow/d)	6.8	5.7	5.0	5.7	5.5	7.5

T139 Performance of automatic milking during a whole herd transition to grazing. S. Utsumi*, M. Haan, R. Ashley, and J. Bronson, *Kellogg Biological Station, Michigan State University, Hickory Corners.*

The effect of the length of grazing sessions on the performance of automatic milking systems (AMS), and the milking behavior of a whole herd of Holstein cows transitioned for first time to pastures was evaluated. Two groups of cows (n = 49 ± 3, DIM = 213 ± 1 d, Age = 3.8 ± 01 yr, BW = 611 ± 6 kg) voluntarily milked with single-stall AMS at rates of 4 to 2 milkings/day (based on DIM and milk yield), were exposed to 1-wk adaptation periods of 0, 2, 4, 6, and 8 h of grazing followed by 6 1-wk periods of voluntary grazing for 12 h. Groups grazed at moderate levels (46 ± 8% utilization) on grass-legume strips located within 400 m from the barn. Exit to pasture was permitted via computer-operated gates if prescribed milking intervals (range: 6 to 12 h) were not exceeded. Fetching of cows with 12-h intervals since last milkings was conducted twice per day. Cows received once a day declining amounts of a forage-based TMR (5% orts) in addition to 1 kg of concentrate per 4 kg of milk. Contrast of linear and quadratic effects ($P < 0.05$) of the length of grazing periods on AMS performance and milking behavior of cows was conducted. Total milk, milking visits and the time AMS spent milking decreased linearly as grazing sessions extended. Performance of AMS was likely increasingly limited by lower milkings and milk yield of individual cows exposed to longer grazing sessions. Length of grazing sessions did not affect milk speed or duration of milking visits, but milking time and yield per milking dropped when the length of grazing session was intermediate. Optimization of AMS in pasture-based systems may require strategic planning of dynamic stocking rates to efficiently lessen declines in milking frequency and milk yield per cow.

Table 1. Automatic milking (AMS) performance and milk production of cows

	Grazing session, h						Contrast	
	0	2	4	6	8	12	L	Q
AMS								
Total Milk	1479	1394	1320	1239	1203	1189	**	
Milking visits	143	132	137	125	120	110	**	
Time milking, h/d	17	15	15	14	14	13	*	
Time free, h/d	5	7	7	8	8	9	*	
Time cleaning, h/d	2	2	2	2	2	2		
Cows								
Milk yield, kg/d	30.7	28.6	28.0	26.2	25.6	26.2	**	
Milkings	3.0	2.7	2.9	2.7	2.6	2.4	**	
Yield/milking, kg	10.3	10.5	9.6	9.8	10.0	10.8		**
Milking time, min	3.5	3.6	3.4	3.4	3.4	3.7		*
Milk speed, kg/min	2.5	2.5	2.4	2.4	2.4	2.4		
Fetch rate, %	7	7	7	8	10	12	*	

* = $P < 0.05$; **= $P < 0.01$.

Key words: automatic milking, grazing

T140 Corn and forage yield on degraded pasture recovered by integrated crop-livestock-forest system in the central region of Minas Gerais, Brazil. M. C. M. Viana*[1], M. H. T. Mascarenhas[1], W. M. Albernaz[2], F. M. Freire[1], R. C. Alvarenga[3], E. A. Silva[1], M. M. Gontijo Neto[3], and M. F. F. Teixeira[4,5], *[1]EPAMIG - Minas Gerais Agricultural Research Corporation, Belo Horizonte, Minas Gerais, Brazil, [2]EMATER MG - Minas Gerais Agricultural Assistance and Rural Extension, Belo Horizonte, Minas Gerais, Brazil, [3]Embrapa Maize and Sorghum, Sete Lagoas, Minas Gerais, Brazil, [4]FEAD, Belo Horizonte, Minas Gerais, Brazil, [5]FAPEMIG, Belo Horizonte, Minas Gerais, Brazil.*

The integrated crop-livestock-forest (iCLF) system has been used to recover degraded areas of crop and pastures in Brazil. To evaluate the influence of different eucalyptus arrangements and clones on the corn grain yield and pasture production in the first year of iCLF system a trial was carried out at Belo Horizonte, Brazil (19°28′ SE 45°15′W, 732 m) on *Brachiaria decumbens* degraded pasture. The experimental design was a randomized complete block in a split plot, with three replications. Eucalyptus arrangements: double rows (3 x 2) x 20 m; (2 × 2) × 9 m and single rows (9 × 2m) were distributed in the main plots, with 20 and 9 m between rows and 2 m between tree spacings. Eucalyptus clones: VM 58, GG100 and I144 were tested in the subplots. A corn (hybrid BRS3060) was intercropped with eucalyptus clones and cultivated as monoculture (control). Data were analyzed by ANOVA and means were compared by Tukey test ($P \leq 0.05$). Soil liming (2 t/ha), basal (300 kg/ha 08-28-16) and topdressed (350 kg/ha 20-00-20) corn fertilizations were accomplished. At the corn harvest, plant height, first ear height, number and weight of ears and grain yield were evaluated. Forty days after corn harvest dry matter (DM) production and chemical composition (CP, ADF, NDF and lignin contents) of *B. decumbens* regenerated from the soil seed bank were evaluated. There was no difference ($P \geq 0.05$) between corn in monoculture and corn intercropped with eucalyptus in all arrangements. The average corn grain yield in the iCLF system and as monoculture was 4.76 and 4.28 t/ha, respectively. Also there was no difference ($P \geq 0.05$) between the corn and forage growing under the eucalyptus clones. The DM yield and chemical composition of *B. decumbens* was not affected by the eucalyptus arrangements and clones. The soil liming and fertilizer applied to corn intercropped with eucalyptus contributed to the recovery of the pasture of *B. decumbens*. In the first year of iCLF establishment, the influence of eucalyptus shade is not a limitation to corn and pasture development. (Research supported by FAPEMIG/CNPq, Brazil)

Key words: agroforestry, forage, eucalyptus

T141 Supplement and stocking strategies for heavy-weight fall-born calves backgrounded on Tifton 85 bermudagrass. F. Rouquette*, J. Kerby, G. Nimr, and K. Norman, *Texas AgriLife Research, Overton.*

Fall-born calves weaned at 340 kg in early summer present management challenges for gain on bermudagrass (*Cynodon dactylon*) pastures (BG). Our objectives were to quantify gain/animal and gain/ha due to stocking rates (SR) and supplement (SUP) source and quantity. Simmental-sired calves with F-1 (Angus × Brahman) dams were allotted to SUP treatments in successive years (YR). In YR 1, a 2:1 soybean meal:cracked corn (SBM) 36% protein ration containing Rumensin 80, salt, and minerals was group-fed daily at 0.4% BW (4-SBM) to 3 steers and 2 heifers on each of 2 replicate pastures of Tifton 85 BG stocked at 12, 18.5, and 22 320-kg calves/ha. Calf average daily gain (ADG) from 28 June to 28 September increased ($P < 0.05$) with SUP (0.7 kg/d) compared with pasture only (PAS) at 0.31 kg/d. The ADG differed ($P < 0.01$) between each SR of low (LO) (0.75 kg/d), medium (ME) (0.52 kg/d), and high (HI) (0.32 kg/d). Resultant gain/ac for SUP was 980, 1300, and 1118 kg/ha, respectively, for LO, ME, and HI SR; and for PAS was 690, 470, and 241 kg/ha, respectively. The SUP:extra gain was 3.3:1 for calves on ME or HI SR and 6.2:1 for LO SR. In YR 2, the 4-SBM ration was compared with daily 0.4% BW and 0.8% BW each of 8% protein cracked corn (CRN) (4-CRN, 8-CRN) and pelleted 23% protein corn gluten (GLU) (4-GLU, 8-GLU). Two replicate pastures of the 6 treatments were stocked at LO to ME SR from 22 June to 14 October. With 13.5 320-kg calves/ha, ADG was similar for 8-CRN (0.97 kg/d) and 8-GLU (0.86 kg/d), and similar for 8-GLU, 4-CRN

(0.78 kg/d), and 4-SBM (0.75 kg/d). Calf ADG was similar for all SUP fed at 0.4% BW. The ADG from PAS was lower ($P < 0.01$) at 0.35 kg/d than all SUP. The SUP:extra gain for calves was 3.6:1 (4-CRN), 4.2:1 (4-SBM), 5:1 (8-CRN), 5.1:1 (4-GLU), and 6.1:1 (8-GLU). Gain/ha for 8-CRN was 1385 kg/ha, about 1065 kg/ha for 8-GLU, 4-CRN, and 4-SBM, 900 kg/ha for 4-GLU, and 450 kg/ha for PAS. Economic considerations of calf value, SUP costs, and SUP:extra gain favored ME SR and 0.4% BW SUP of energy (CRN) or protein with Rumensin (SBM) for backgrounding fall-born calves on Tifton 85 BG pastures.

Key words: supplement, bermudagrass, stocking rate

T142 Production of wheat and oats overseeded into Tifton-85 grass at different forage allowances. F. F. Simili*[1], A. C. Ruggieri[2], T. V. Bertolino[2], D. R. Casagrande[3], R. A. Reis[2], and R. Godoy[4], *[1]APTA, Ribeirao Preto, Sao Paulo, Brazil, [2]UNESP, Jaboticabal, Sao Paulo, Brazil, [3]UFAM, Parintins, Amazonas, Brazil, [4]EMBRAPA, Sao Carlos, Sao Paulo, Brazil.*

The overseeded technique has been used successfully for many years in southern Brazil and southern United States and it is considered an appropriate alternative to increase forage production during the winter when there is moisture available in the soil. The objective of the experiment was to evaluate forage mass of annual oat and wheat overseeded into perennial Tifton-85 grass (*Cynodon nlemfluensis* × *Cynodon dactylon*) grazed by sheep, which received three different forage allowances (FA). The experimental design was completely randomized with 3 x 3 factorial scheme and repeated measures (grazing periods), with three repetitions. The treatments were oat (*Avena bysantina*), var. UPF 86081, wheat (*Triticum aestivum* L.) 'BRS Figueira' and the combination of the two species wheat and oats. These grasses were grazed at three FA 4, 7 and 10% of body weight of animals. There was a significant interaction between FA and grazing cycle for all variables ($P < 0.05$). The dry mass production (DMP) by hectare (ha) of Tifton-85 grass was significantly higher ($P < 0.05$) in the third grazing cycle, with an average of 6,728 kg DMP/ha, but there were no differences among FA. The production of annual grass was lower ($P < 0.05$) in the first grazing cycle, with an average of 551.4 kg DMP/ha, but there were no differences among FA. The highest DMP of annual grasses was achieved with 10% of FA in the third grazing cycle, with an average of 2,488.8 kg DMP/ha. These results can be explained by occurrence of rain in October, at the same period of the third grazing cycle. The best ($P < 0.05$) percentage of annual grass plants was observed in the second grazing cycle with an average of 39.6%. However, Tifton- 85 grass presented the highest percentage of plants in all grazing cycles and FA. It was concluded that the overseeded technique to increase DMP for grazing animals was not successful in the environment that was studied.

Key words: *Cynodon*, grazing, winter forage

T143 Effects of lack of shade on Wye Angus brood cows. M. S. Updike* and R. M. Harrell, *University of Maryland, College Park.*

In the Chesapeake Bay watershed, increased environmental regulations will likely result in cattle producers having to fence cattle out of the streams. One side effect of such fencing is that most of the shade (from trees) is provided along the streams and will no longer be available to the cattle. In addition, cost share programs in the Mid Atlantic region for fencing the streams do not include any cost share for adding shade elsewhere on the farms. This study was conducted to determine the effects of lack of shade on mature Wye Angus brood cows that had been adapted to shade in previous years. Forty cow calf pairs (bull calves) were rotationally grazed as normal with access to shade and 40 cow calf pairs (bull calves) were rotationally grazed with no access to shade. To minimize location effects, individual fields were split into paddocks so that shade treatment group had access to trees for natural shade. The study began July 1st which was immediately after the clean up bulls were pulled from the herd. Blood was collected in June before the beginning of the treatments, in July and in August. Cows were checked for pregnancy in the middle of August. Previous research has shown that heat stress causes has a greater impact on early stages of pregnancy. Therefore it was not surprising that 40% of the cattle with no shade were pregnant while 85% of the cattle with shade were pregnant. Blood was analyzed for hematocrit and other blood chemistries. No significant differences were found ($P < 0.05$) and all results were within normal parameters. These results have implications not just for farmers who must contend with changing regulations, but also government agencies and NGOs that are working with farmers to decrease nutrient loss into the watershed.

Key words: cattle, shade, stress

T144 Effect of stocking rate on forage production, soil compaction and root numbers in a swine pasture system. B. Renner*[1], S. Pietrosemoli[1], J.-M. Luginbuhl[1], C. Raczkowski[2], J. T. Green[1], and J. Grossman[1], *[1]North Carolina State University, Raleigh, [2]North Carolina Agricultural and Technical State University, Greensboro.*

Grazing experiments were conducted at the Center for Environmental Farming Systems in Goldsboro, NC from July to August 2008 and 2009 to determine the effect of swine stocking rate on subsequent forage production, soil compaction and root numbers. Pigs (18.4 and 118.5 kg initial and final body weight, respectively) were randomly assigned to each of 12 paddocks sized to equal stocking rates (SR) of 37, 74, 111, and 148 head/ha in a randomized complete block design. Animals had ad libitum access to water and concentrate feed. A winter cereal rye/annual ryegrass (*Secale cereale*/*Lolium perenne*) mixture was sown following removal of the pigs in fall 2009 from a mature bermudagrass (*Cynodon dactylon*) pasture. Forage harvested at early boot stage to 5cm stubble length in spring 2010 was followed by a sorghum-sudangrass hybrid no-till seeded into the plots and harvested at early boot stage to 7cm stubble in August and again at stem elongation stage in October 2010. Soil samples were taken in spring and fall 2010 following the final harvest of each forage crop. Soil compaction and root numbers were determined at depths of 15, 30, 45, 60, 90 cm, and 15, 30, 60, 90 cm, respectively. A Delmi soil penetrometer was used to determine soil compaction and root numbers were determined by counting the roots in the cross-sections of harvested soil cores. In spring, forage yield ($P = 0.72$), soil compaction ($P = 0.4$) and root numbers ($P = 0.8$) did not change with SR, but soil compaction ($P = 0.0001$) and root numbers ($P = 0.0001$) were affected by soil depth. Summer ($P = 0.08$) and fall ($P = 0.7$) sorghum-sudangrass yields were not affected by SR. Fall root numbers were not affected by SR ($P = 0.2$) but strongly affected by soil depth ($P = 0.0001$). Under the conditions of this experiment, SR rate had no effect on subsequent forage yield. Conversely, soil compaction and root numbers were affected by soil depth, the latter being most prevalent in the top 15 cm.

Key words: outdoor pig production, stocking rate, root count

T145 Average annual weight prediction of cows kept four years in a tough regime using a model of simulation. J. M. Tapia[1],

J.C. Martinez[2], H. Diaz[3], A. Moreno[4], J. A. Martinez[1], O. D. Montañez*[1], J. A. Ochoa[1], and G. Rocha-Chavez[1], *[1]CUSUR, U de G, Cd. Guzman, Jalisco, Mexico, [2]Univ Autonom de Tamaulipas, Cd. Victoria, Tamps, Mexico, [3]Univ Auton Agr Antonio Narro, Saltillo, Cohahuila, Mexico, [4]Instituto Tecnologico de Cd Victoria, Cd. Victoria Tamps, Mexico.*

The objective of this study was to predict the average annual weight of cows living in a tough environment using a simulation model. Software STELLA 8, was used and data for the model was obtained from farm systems of the Tamaulipas region in northern Mexico characterized by semi arid climate and low quality pastures including cactus plants. Farmers are usually poor peasants having an average of 3 cows used mostly for subsistence of their families. Cows in the study were 4-year-old crosses (creole-zebu) and were grouped (21 cows per group) into 4 diet regimens: (1) grazing only (buffel and native grass), (2) grazing in a silvopastoral system (mostly bushes), (3) grazing with silage and (4) grazing with corn-molasses nutritional blocks. Silage for supplementing group 3 diets was made with chopped green corn plants that were compressed in a silo and allowed to ferment. The silvopastoral system included grazing over small plants of prosopis farcta and celtis spinosa. Regimen was assessed for 48 mo with 21 simulation cycles totalizing 84 years for each regimen. Analysis of variance was used to compare means and significance was set to $P < 0.05$. As it can be seen in Table 1, the best average weight was for the silvopastoral system whereas the lowest finding corresponds to the grazing only group. No significant differences were found among groups 2 and 3 ($P < 0.05$). Simulation models are useful to predict potential real life scenarios; however, there are several environmental aspects (such as unusual rain) that may influence their outcome.

Table 1. Average annual weight of cows with several types of diets

Diet type	Cycles[1]	Avg annual weight (kg, mean ± SE)
Grazing only	21	331.91±11.32 [a]
Grazing + corn silo	21	343.21±7.90 [b]
Grazing + nutritional block	21	338.33±21.05 [b]
Grazing silvopastoral	21	347.40±10.55 [c]

[1]All values evaluated for each treatment representing a cycle of 48 months totalizing 84 years of evaluation. Different letters in the same column differs significantly ($P < 0.05$).

Key words: weight, cows, prediction

T146 Effects of stocking rate and supplementation on carcass traits of beef cattle grazing winter annual forages. B. C. Williamson*[1], M. L. Looper[2], F. M. Rouquette[3], G. E. Aiken[4], S. F. Tabler[2], J. B. Wolley[2], and C. F. Rosenkrans[1], *[1]University of Arkansas, Fayetteville, [2]USDA/ARS, DBSFRC, Booneville, AR, [3]Texas AgriLife Research, Overton, [4]USDA/ARS, FAPRU, Lexington, KY.*

Environmental and managerial conditions are known to affect subsequent performance and carcass traits of beef cattle. The objective of this study was to document the effect of stocking rate (SR) and supplementation on carcass traits. Steers and heifers (n = 856; BW = 274 ± 46) were allowed to graze 'Maton' rye (*Secale cereale* L.) and 'TAM90' annual ryegrass (*Lolium multiflorum* L.) pastures from January to mid-May of 1999 to 2005. Cattle were allotted to stocking rates (SR) of high (6.7 animals/ha), medium (5.2 animals/ha), or low (3.7 animals/ha), and supplemented (0 vs. 3.0 kg/d corn/cottonseed meal; 16% protein), and finished in commercial feedlots. Body condition score (BCS); ultrasound measurements of intramuscular fat (UIMF), LM area, and rump fat at end of grazing; ADG during stocker (119 d ± 25) and feedlot (125 d ± 28) phases; hot carcass weight (HCW); carcass rib fat; carcass LM area (CLMA); and yield grade (YG) were measured. The ANOVA determined the effects of year, sex, SR, supplementation, and interactions on ADG, ultrasound measurements, and carcass traits . A supplement x SR interaction affected ($P < 0.05$) YG. Cattle tended ($P < 0.10$) to have lower YG when grazed at low SR (YG = 2.7 ± 0.08) compared with cattle grazed at high SR (YG = 3.1 ± 0.08) when supplemented. An SR × sex interaction ($P < 0.05$) affected CLMA. Steer CLMA was not affected ($P > 0.25$) by SR; however, heifers grazed at high SR had the smallest ($P < 0.10$) CLMA. Supplement x SR interaction ($P < 0.05$) affected HCW. Cattle supplemented while grazing had increased ($P < 0.05$) UIMF (1.13%) compared with nonsupplemented cattle (0.94%). High SR cattle had lower ($P < 0.05$) UIMF then medium and low SR (0.79%, 1.05%, and 1.26%, respectively). Cattle allotted to low SR gained more ($P < 0.05$) than cattle on medium or high SR while grazing (1.28, 1.14, 0.77 kg/d, respectively). In the feedlot, cattle at high SR gained more ($P < 0.05$) than cattle at medium or low SR (1.84, 1.67, 1.69 kg/d, respectively). Stocking rate and supplementation of cattle grazing winter annuals affected subsequent performance and carcass traits.

Key words: carcass traits, stocker cattle, ultrasound

T147 Matching hay composition to cow requirements during the winter. W. M. Backus[1], B. T. Campbell[1], A. M. Saxton[1], D. K. Joines[2], and J. C. Waller*[1], *[1]The University of Tennessee, Knoxville, [2]Soil, Plant, and Pest Center, Nashville, TN.*

The objective of this study was to compare the nutrient composition of hays produced in Tennessee and their ability to meet the nutrient requirements of beef cattle during the winter. Crude protein (CP) and estimated total digestible nutrients (TDN) values from 2,076 samples [bermudagrass (*Cynodon dactylon*) - 392; tall fescue (*Festuca arundinacea*) - 607; grass/clover - 200; mixed grass - 793; orchardgrass (*Dactylis glomerata*) - 84] submitted from Jan. 2007 - Dec. 2009 to the Tennessee Forage Testing Lab were used to evaluate available hay for winter feeding. CP levels ranged from 4 to 30% with a mean of 12.98 ± 0.21, TDN levels ranged from 34 to 88% with a mean of 60.77 ± 0.39. Nutrient requirements for 6 herds of 90 cows were established (NRC, 1996), with hay consumption based on published estimates for dry matter intake. Calving distributions from 8 years of spring and fall calving data from the Research and Education Center at Ames Plantation were used to develop the distribution for a 60 d calving season; comprised of 10 6 d periods. Spring and fall herds were grouped into 3 categories by mature size of cows; small cow size (453.6 ± 45.4 kg), medium cow size (544.3 ± 45.4 kg) and large cow size (635.0 ± 45.4 kg), each having an average milking ability of 9.1 kg ± 4.5 kg, with milk production ranging from 4.5 kg to 13.6 kg within each herd. Spring and fall calving seasons began Feb. 1 and Oct. 1 respectively. Hay feeding began Nov. 15 and ended Mar. 15. All hays were compared with individual cow requirements in each 10 d period. Tall fescue comparisons are presented because this is the predominant hay fed to beef cows in Tennessee. The results of matching tall fescue hay to the nutrient needs of the medium cow size spring calving herd indicate that 99% of samples met CP requirements and 93% of samples met TDN requirements of 80% of the herd in Nov., while 57% of samples met CP and 28% of samples met TDN requirements for 80% of the herd in Mar. In the medium cow size fall calving herd 65% of samples met CP requirements and 27% of samples met TDN require-

ments of 80% of the herd in Nov., while 89% of samples met CP and 74% of samples met TDN requirements for 80% of the herd in Mar.

Key words: hay, cow

T148 Total fat and fatty acid composition of steaks from steers finished on three different forage systems in the Gulf Coast Region. G. Scaglia*[1], J. Rodriguez[2], K. McMillin[2], G. Gentry[2], and H. Boland[3], *[1]LSU AgCenter Iberia Research Station, Jeanerette, LA, [2]LSU AgCenter School of Animal Sciences, Baton Rouge, LA, [3]Prairie Unit Mississippi State University, Prairie.*

The objective was to evaluate the effect of 3 forage systems (S1, S2, and S3) on meat characteristics of spring weaned beef steers (n = 54; 257 ± 2.5 kg; 3/8 Gelbvieh, 3/8 Red Angus, and 1/4 Brahman). Steers were divided into 9 groups based on initial body weight (d 0) and randomly assigned to 3 replicates paddocks (average area of 2 ha) within system. Steers in S1 grazed bermudagrass (*Cynodon dactylon*) during summer, ryegrass (*Lolium multiflorum*) and ryegrass sod-seeded into bermudagrass paddocks in winter. Steers in S2 grazed bermudagrass in summer, dallisgrass (*Paspalum dilatatum*)/red (*Trifolium pratense*), white (*Trifolium repens*) and berseem (*Trifolium alexandrium*) clovers (clover mix) during fall and spring, and rye (*Secale cereale*)/ryegrass/clover mix during winter while those in S3 had access to bermudagrass and sorghum-sudan hybrid (*Sorghum bicolor* x *S. bicolor* var. sudanense)/forage soybean (*Glycine max*) during summer, dallisgrass/clover mix during fall and spring, and rye/ryegrass/clover mix during winter. Systems differ in complexity, total forage mass produced and/or nutritive value parameters of forages. Pastures were rotationally stocked with a stocking rate for the systems of one steer per hectare through the grazing period (324 d). Eighteen steers (6 per system) where harvested and steaks obtained for analysis of total fat and fatty acids. Data were analyzed using PROC MIXED with means separation conducted using Tukey (α = 0.05). Total fat (5.4, 4.4, and 4.3%), percent saturated fatty acids (50.4, 51.6, and 54.3%), and percent conjugated linoleic acid in fat (1.3, 1.6, and 1.9%) were not different ($P > 0.05$) between systems (S1, S2, and S3, respectively), but saturated fatty acids were higher than expected. Concentration (as % of total fat) of monounsaturated fatty acids, polyunsaturated fatty acids, omega-6 and omega-3 fatty acids, and omega-6/omega-3 ratio were not different ($P > 0.05$) between systems. Preliminary data indicate that the 3 forage systems for finishing beef in this study did not result in differences in total fat and fatty acids in beef.

Key words: forage-fed beef, forage systems, steers

T149 Effect of molasses or cornmeal on milk production and nitrogen utilization of grazing organic dairy cows. S. Ross*[1], A. F. Brito[1], K. J. Soder[2], K. Greene[1], A. Green[1], and P. Y. Chouinard[3], *[1]University of New Hampshire, Durham, [2]USDA-Agricultural Research Service-Pasture Systems and Watershed Management Research Unit, University Park, PA, [3]Université Laval, Quebec City, Quebec, Canada.*

Pasture is rich in soluble N which is rapidly converted to ammonia in the rumen reducing N utilization in lactating dairy cows. Sucrose is more quickly degraded in the rumen than starch, suggesting that feeding molasses (MOL) to balance energy and RDP supply in the rumen can be strategically used to improve N utilization in grazing dairy cows. Twenty lactating organic Jersey cows (DIM 119 ± 73) were blocked by parity and milk production, and assigned randomly to one of 2 energy sources: 1) liquid MOL (12% diet DM) or 2) cornmeal (CM; 12% diet DM). MOL and CM averaged (% DM), respectively: 5.35 vs. 7.85% CP, 0.12 vs. 68.9% starch, and 50.1 vs. 1.53% sucrose. Cows grazed for approximately 18 h/day on mixed species pasture consisting mostly of orchardgrass, tall fescue, timothy, white clover, red clover and alfalfa from early June to mid-September for a total of approximately 110 d. The energy sources were top-dressed on baleage containing perennial ryegrass, timothy, reed canarygrass, white clover and red clover (18% diet DM) and fed individually twice daily using Calan doors. Cows were split into 2 grazing groups with pasture intake estimated by group using a calibrated rising plate meter to quantify pre- and post-grazing herbage biomass. Data was analyzed using the MIXED procedure of SAS for a completely randomized design with repeated measures over time. Intake of supplement (baleage plus MOL or CM) was significantly higher for cows fed MOL vs. CM possibly due to enhanced palatability of MOL. Pasture and total DMI were numerically higher for cows fed MOL than those fed CM. Despite enhanced total DMI, no significant differences were observed for milk yield comparing MOL and CM. Likewise, yields and contents of milk components did not differ between MOL and CM. However, cows fed MOL had reduced MUN ($P = 0.03$) and PUN ($P < 0.01$) compared with those fed CM, which may be partially explained by the higher CP of CM vs. MOL. Compared with CM, MOL had no detrimental effect on animal performance and improved N utilization in organic dairy cows. Liquid MOL may be an alternative energy source for CM if economically competitive.

Table 1. Performance and N utilization

	Treatments			
	MOL	CM	SED	$P > F$
Pasture DMI, kg/d	11.5	10.0	-	-
Supplement DMI, kg/d	4.27	3.67	0.13	<0.001
Total DMI, kg/d	15.77	13.67	-	-
Milk yield, kg/d	12.8	11.8	1.53	NS
Milk fat, %	4.82	4.81	0.22	NS
Milk fat, kg/d	0.61	0.56	0.06	NS
Milk protein, %	3.45	3.46	0.15	NS
Milk protein, kg/d	0.43	0.40	0.04	NS
Milk lactose, %	4.70	4.64	0.04	NS
Milk lactose, kg/d	0.60	0.55	0.07	NS
MUN, mg/dL	13.4	14.9	0.59	0.03
PUN, mg/dL	14.8	16.7	0.56	<0.01
BW change, kg/d	0.36	0.22	0.17	NS

SED = standard error of LSM difference; NS = not significant.

Key words: grazing, molasses, organic cows

T150 Sensory properties and abundance of selected volatile compounds in milk from cows fed timothy grass as hay, silage or pasture. M. P. Villeneuve*[1,2], Y. Lebeuf[1,2], R. Gervais[1], G. F. Tremblay[3], J. C. Vuillemard[2,4], and P. Y. Chouinard[1,2], *[1]Département des sciences animales, Université Laval, Québec, QC, Canada, [2]Institute of Nutraceuticals and Functional Foods (INAF), Québec, QC, Canada, [3]Agriculture and Agri-Food Canada, Québec, QC, Canada, [4]Département des sciences des aliments et de nutrition, Université Laval, Québec, QC, Canada.*

To evaluate the effects of feeding different types of forage on milk flavor and volatile compounds, 21 Holstein cows (1st lactation and higher, 209 ± 52 DIM) were blocked according to calving date and randomly assigned to one of three dietary treatments, which consisted of timothy grass (*Phleum pratense*) fed ad libitum as hay (H), silage

(S), or pasture (P) for 27 d. Each cow also received 7 kg/d of concentrates in two equal meals. Cows fed P were grazing on the same parcel where hay and silage were harvested simultaneously at the mid-heading stage, the previous summer. On the last 3 d of the period (d25, d26, and d27), bulk milk from two consecutive milkings was collected separately from each group of cows. The 9 batches of milk thus obtained were standardized to 3.25% fat, homogenized, and pasteurized at 75°C for 16 sec. Samples of each milk produced on d25 were collected and stored at 4°C to be used for sensory evaluation. Additional samples from each batch (d25, d26, d27) were frozen at −20°C for further analysis of volatile compounds using solid- phase microextraction (SPME) and gas chromatography-mass spectrometry. Milk samples from d25 were evaluated in a triangle test by a panel of 30 untrained assessors to compare H vs. P, and H vs. S. Among assessors, 40% were able to distinguish H from S ($P = 0.28$), while 67% perceived a difference between H and P ($P < 0.01$). Milk samples from d25 were also evaluated in a sensory ranking test by a similar panel. Assessors were asked to rank H, S and P milk samples for aroma intensity, as well as sweet and grassy flavors on a scale of 1 to 3 (from less to more intense). For H, S, and P, respectively, sums of rankings were 54, 52, and 74 for aroma intensity, 70, 59, and 51 for sweet flavor, and 53, 54, and 73 for grassy flavor ($P < 0.05$). Chromatographic analyses of free fatty acids, alcohols, aldehydes, ketones, and lactones revealed that all these volatile compound families were present in H, S, and P milk samples. Further investigation is needed to assess the contribution of specific volatile compounds to sensory properties of milk as affected by forage types.

Key words: volatile compounds, milk flavor, SPME

T151 Is horse harvesting and processing plants a horse owner solution to the United States unwanted horse population? S. Lindsey and M. Nicodemus*, *Mississippi State University, Mississippi State.*

Unwanted Horse Coalition did a survey in 2009 to determine activities and perceptions related to the United States unwanted horse population. The survey collected solutions to reducing unwanted horse numbers finding the most favored solution by horse owners was the re-opening of horse harvesting and processing plants. Further questions concerning horse harvesting and processing was unavailable on the 2009 survey, and therefore, study objectives were to determine horse owners understanding and perceptions related to horse harvesting and processing plants. Researcher-developed, 15-item survey instrument focused on horse harvesting and processing plants was given to 89 horse owners. For each question the % of respondents selecting an answer was determined. Ownership of 1–3 horses made up the majority of survey respondents (56%) with the Quarter Horse being the most popular breed owned (48%). Only 46% of respondents supported opening horse harvesting and processing plants in their state, and of those not in support, only 25% would reconsider supporting these plants if restrictions were made against processing horse meat for human consumption. The majority (63%) were in favor of additional restrictions on what horses would be harvested with 75% wanting requirements that the horse should be suffering from a health issue. Awareness concerning horse harvesting and processing was lacking as the majority (79%) were unaware of their local facilities and 35% were unaware of the role of United States Department of Agriculture (USDA) concerning these facilities. For respondents aware of USDA involvement, 51% were unclear of all the USDA regulations associated with these plants. The majority (52%) admitted they were unsure of plant practices and handling methods with 46% getting their information from media. While re-opening of these plants is perceived by horse owners as a solution to the current unwanted horse population, survey respondents reflect the need for investigating additional solutions and the need for more thoroughly educating horse owners concerning these plants so they can make a more informed decision.

Key words: unwanted horses, horse ownership

T152 Selenium status declines in horses fed NRC adequate and low selenium diets. M. Brummer*, S. Hayes, J. E. Earing, S. M. McCown, and L. M. Lawrence, *University of Kentucky, Lexington.*

The NRC recommends a selenium (Se) intake of 1 mg/d for a 500kg horse, based on relatively short-term studies showing no added benefit from dietary Se beyond 1mg/d with regards to glutathione peroxidase activity (GPx). Further, the NRC suggests that 1 mg/d may overestimate the minimum Se requirement of mature horses. This study evaluated changes in whole blood Se (WBSe) and whole blood GPx in mature horses fed adequate (AS) and low (LS) selenium diets for 28 wk. This period was selected to allow for near complete red blood cell turnover. Twenty mares and 8 geldings, blocked by age and gender, were randomly allocated to one of 2 treatments. Horses received pasture (Se < 0.06 ppm DM), hay (Se < 0.05 ppm DM) and cracked corn (Se < 0.04 ppm DM). Horses were also individually fed supplements, so that AS (n = 7) and LS (n = 21) received 140% and 70% of daily recommended Se intake, respectively. More horses were allocated to LS in preparation for a subsequent study. Blood samples were taken before and every 4 wks during the study. Data were analyzed as repeated measures using SAS 9.1 and are reported as LS Means. Initial WBSe was similar ($P > 0.05$) between AS (261.1 ng/mL) and LS (251.2 ng/mL). WBSe decreased in both groups over time ($P < 0.05$), but the decrease was greater in LS (treatment x time; $P < 0.05$). Final WBSe was lower in LS (164.7 ng/mL) than AS (211.1 ng/mL; $P < 0.05$). Final WBSe of AS horses was also lower than their initial WBSe ($P < 0.05$). Whole blood GPx decreased over time in AS and LS. Initial GPx was different for AS and LS (72.5 and 61.11 mU/mg Hb respectively), but later time points were similar until the last 3 time points. Final GPx was higher for AS (55.00 mU /mg Hb) than LS (42.72 mU /mg Hb; $P < 0.05$). Final GPx of AS horses was also lower than their initial GPx ($P < 0.05$). The Se status of LS horses depleted over time as expected, but feeding 140% of recommended Se intake did not maintain WBSe or GPx over the 28 wk period. The current recommendation of 1mg Se/d may be enough to prevent deficiency symptoms, but was not sufficient to maintain WBSe or GPx in adult horses in this longer term study.

Key words: glutathione peroxidase, selenium requirement, equine

T153 Round-bale feeder design affects hay waste and intake during horse feeding. K. Martinson*, K. Cleary, K. Ross, J. Wilson, W. Lazarus, W. Thomas, and M. Hathaway, *University of Minnesota, St. Paul*.

Many horse owners find round bales are more convenient, less laborious and expensive, but report hay waste and horse weight gain compared to feeding other hay types. Objectives were to compare hay waste and intake from nine round- bale feeders and a no-feeder control when round bales were fed to horses. Nine round-bale feeders were tested: Cinch Net, Cone, Covered Cradle, Hayhut, Hay Sleigh, Ring, Tombstone, Tombstone Saver, Waste Less, and no-feeder control. Horse groups of similar age, weight, breed, and gender were formed from 25 Quarter Horse and Thoroughbred geldings and mares. Groups of horses were sequentially assigned to feeders using a 5 × 5 Latin Square. Each feeder was placed on the ground in one of 5 outdoor paddocks (30 × 20 m). Using a crossover design, 5 groups of 5 horses were fed in rotation for 4-d. Every fourth day, groups were rotated among paddocks and a new bale was fed. Five feeders were installed for days 1 through 20, and the remaining 4 feeders and the no-feeder control were installed on days 21 through 40. Hay on the ground surrounding the feeder was considered waste, collected daily, dried and weighed. Hay remaining in the feeder at the end of the 4-d period was removed, dried and weighed. Total 4-d hay waste was reported as percent of weight of the original bale minus the remaining hay. Intake was calculated by subtracting waste and remaining hay from original bale weight and dividing that by average initial pen weight. Feeders were compared using PROC Mixed of SAS. Both carryover and period effects were not significant and groups of horses were considered a random effect. Hay waste differed between round bale feeder designs ($P < 0.01$). Mean percent waste was Waste Less, 5%; Cinch Net, 6%; Hayhut, 9%; Covered Cradle, 11%; Tombstone Saver, 13%; Tombstone, Cone, and Ring, 19%; Hay Sleigh, 33%; and no feeder control, 57%. Feeder design did not affect horse intake; all feeders resulted in daily intake at 2.0 to 2.4% of body weight (BW). The no feeder control resulted in less intake at 1.3% BW ($P = 0.001$). The use of a round bale feeder is necessary to avoid excessive hay waste and reduced intake during horse feeding when compared to the no-feeder control.

Key words: round-bale feeder, waste, intake

T154 Glycemic and insulinemic responses of weanling horses to high and low protein diets. A. L. Wagner*[1], R. N. Digianantonio[1], S. L. Tanner[1], R. B. Ennis[1], P. A. Harris[2], J. T. Sylvester[3], and K. L. Urschel[1], *[1]University of Kentucky, Lexington, [2]WALTHAM Centre For Pet Nutrition, Melton Mowbray, UK, [3]Buckeye Nutrition, Dalton, OH.*

Currently, there is a basic understanding of the requirements of dietary protein to optimize growth in the young horse. However, little is known of the effects of dietary protein on the glycemic and insulinemic responses of weanling horses. Characterization of the insulinemic response is critical because insulin resistance has been linked to various diseases such as osteochondrosis. Thus, the objective of this study was to determine plasma glucose (GLC) and insulin (INS) concentrations in 6-mo-old weanling foals (n = 6) receiving isocaloric concentrates with either high (HP; mean ± SD, as fed; 3.04 ± 0.03 Mcal/kg DE; 18.3 ± 0.2% CP) or low (LP; mean ± SD, as fed; 2.86 ± 0.03 Mcal/kg DE; 9.0 ± 0.1% CP) crude protein content. Either HP or LP meals were offered at 1400 (t = 0 min) following an identical meal at 0700 h. Blood samples were collected every 15 min from t = 0 to 120 min, and then at 240 min. Blood samples were analyzed to determine plasma GLC and INS via the YSI Biochemistry Analyzer and Coat-A-Count®RIA kit, respectively. There was no effect of time or treatment on INS ($P > 0.05$). However, both time and treatment affected ($P < 0.05$) plasma GLC concentrations. There was an increase in plasma GLC in the LP compared with the HP group ($P = 0.04$). Specifically, plasma GLC in the LP group was elevated at 15, 30, and 45 min post-feeding over the HP group. However, regardless of treatment, the plasma GLC concentrations of all the foals did not exhibit the typically expected rise post-feeding followed by a return to baseline within the study period. Instead, a decrease post-feeding until t = 30 min was followed by an increase until t = 120 min. It has been previously shown that both INS and GLC show a greater response to feeding after a morning meal in mature horses. Our atypical glycemic and insulinemic responses therefore may be attributed to time of feeding as a result of circadium rhythms. Additional research is however necessary to confirm whether the differences seen are due to the diets or time of feeding in 6-mo-old weanling foals. Funded by Buckeye Nutrition and the WALTHAM Foundation.

Key words: horse, low protein diet, glycemic response

T155 The development, evaluation and implementation of an online safety course for youth working on equine facilities. E. A. Greene*[1], K. L. Waite[2], G. Heyboer[2], J. Whittle[3], C. D. Skelly[2], and K. Vignare[2], *[1]University of Vermont, Burlington, [2]Michigan State University, East Lansing, [3]University of Kentucky, Lexington.*

The estimated 9.2 million horses in the United States provide a popular recreational, competitive and occupational activity for young people. The labor force on equine facilities is often youth who are unpaid or work in exchange for opportunities to ride horses. In 2005, the US Consumer Product Safety Commission reported that an estimated 23,000 youth under the age of 20 years are annually treated in emergency departments for equestrian related injury. Several reports indicate that 20–30% of equestrian-related injuries occur when the handler is either leading or grooming the horse. There is clearly a gap in youth farm safety education for young people working with horses. To date there is no comprehensive, interactive online course designed to educate youth on best safety practices when working on equine facilities. The purpose of this project is to develop, test and implement an educational, interactive and engaging online safety course for youth working on equine facilities. Instant Survey software (www.instantsurvey.com) was utilized to conduct a national survey of adult volunteer horse leaders to identify interest in youth development focused equine courses and important topics. All methods and survey tools were approved by the Institutional Review Board. Data were analyzed using a binomial test via IBM SPSS Statistics 19 software. Approximately 295 online surveys were completed with 98% showing interest in this type of training. When comparing survey topics that received responses of "Very Interested" against "Not Interested" and "Mildly Interested" responses, there was a significant difference ($P < 0.001$) for all items in General Horse Care. Additionally, several national youth and adult focus groups identified horse health, nutrition, exercising horses, legal issues, and safety as critical components of a course. eXtension and My Horse University have partnered to develop 10 online educational units that are currently in peer review process and will be pre-launched for β testing within the next year. This peer reviewed Youth Equine Safety course will be available on the Internet at no charge to the user.

Key words: youth, online learning, equine safety

T156 Greener pastures, stable footing, and seeking balance: An easy-to-use land stewardship series for all horse owners. E. A. Greene*[1], R. Gilker[1], and K. Martinson[2], *[1]University of Vermont, Burlington, [2]University of Minnesota, St Paul.*

As livestock owners come under scrutiny regarding responsible land stewardship and negative impact on water quality, state agencies are implementing more stringent regulations. Horse facilities are also being monitored for nonpoint source pollution from mud issues, run off, and improper manure storage. Also, as feed/hay prices rise, horse owners are seeking maximum pasture utilization as an affordable component of their horses' diet. This educational series provides easy to understand management options for equine operations. The first ("Greener Pastures: Sacrifice a Little Pasture to Save a Lot!") provides horse owners land stewardship and cost information for renovating high traffic areas through written/pictorial methods. "Stable Footing for Your Horse: Practical Strategies for High Traffic Area Renovation" gives additional details for high traffic paddocks and their use in grazing systems. "Seeking Balance: Elements of a Successful Horse Grazing System" outlines strategies for better utilization of a limited land base to improve pasture quality and reduce feed costs. The overall goal is to motivate horse owners to take action to improve pasture quality and land stewardship. These booklets have been introduced in Pasture Walks, Seminars and Workshops throughout the Northeast and Midwest USA. Participants regularly report that they will apply the tools at their own facilities, demonstrating the national relevance of this information. A recent post-program evaluation at the 2010 Minnesota extension program for improving equine pasture and mud management systems measured the material effectiveness. A Likert scale was used to assess participant (n = 70, 60% response rate) knowledge gain on a scale of 1 (very little) to 5 (very much). Participants reported a knowledge increase from 3.2 to 4.1 on the topic of mud management. Furthermore, 85% of participants thought the information would be useful in the management of their horse operation; 58% planned to implement changes based on the presentation. This text and pictorial format provides an applicable method for equine owners to improve their land stewardship.

Key words: high traffic area, pasture, equine

T157 Genetic evaluation of annual earnings in Quarter Horses. J. A. V. Silva*[1], A. P. A. Silva[1], B. Langlois[2], C. B. Cyrino[1], and M.

D. S. Mota[1], [1]*Faculdade de Medicina Veterinária e Zootecnia, Unesp, Botucatu, São Paulo, Brasil,* [2]*Institut National de la Recherche Agronomique, Jouy en Josas, France.*

The aim of this study was to estimate the heritability of the annual earnings (AE) in Quarter Horse races to provide a reliable and objective tool for horse selection for owners, as a previous genetic evaluation of the breeding animals. Data comprised records from 1978 to 2009 with a total of 22,958 races and 5,218 horses, at the Sorocaba Jockey Club, state of São Paulo, Brazil. All the known ancestors of the recorded horses were included in the pedigree file until the fifth generation. The AE was analyzed for animals of 2 (AE2), 3 (AE3) and 4 (AE4) years old, using a multi-trait animal model based on Gibbs sampling algorithm, considering the effects of sex and year of the race, number of starts (covariate), besides the effects of animal, maternal and residual. The estimates of heritability were 0.26 ± 0.10, 0.12 ± 0.04 and 0.31 ± 0.10, for AE2, AE3 and AE4, respectively, and these values were within the range described in literature. The genetic correlations had moderate magnitude and positive values, varied from 0.19, between AE2 and AE4, to 0.52 between AE3 and AE4, suggesting that selection to improve AE at a specific age would promote, to a greater or lesser extent, a favorable genetic alteration in the remainder. Although considering animals with performance at only one racetrack, these results might be considered for future genetic evaluation including horses with performances at other Brazilian hippodromes.

Key words: equine, genetic correlations, heritability

T158 Genetic correlation between racing performance traits in Quarter Horses. M. D. S. Mota[1], B. Langlois[2], R. A. Curi[1], M. C. L. Dal Coleto[1], and J. A. V. Silva*[1], [1]*Faculdade de Medicina Veterinária e Zootecnia, Unesp, Botucatu, São Paulo, Brasil,* [2]*Institut National de la Recherche Agronomique, Jouy en Josas, France.*

Annual earning, an objective measure of horse racing performance, was recorded in 22,958 races and 5,218 animals, at the Sorocaba Jockey Club, state of São Paulo, Brazil. Annual earning measures were recorded for 3-yr-old animals (AE3) and career earning (CE). AE3 was used because it was the age with the greatest number of records in the database studied. In order to achieve a reasonable approximation to the normal distribution, the traits were transformed by log. The traits were analyzed using a multi-trait animal model based on Gibbs sampling algorithm, considering the effects of sex and year of the race, number of starts (covariate), besides the effects of animal, maternal and residual. The covariate age at last race was included for CE. The heritability estimates for AE3 and CE were 0.18 ± 0.04 and 0.19 ± 0.04, respectively. Genetic correlation across annual earning measurement was 0.97 ± 0.02, indicating a strong underlying genetic basis. The estimates for the simple correlation (Pearson) and for the rank correlation (Spearman) between classifications by breeding values of the top twenty animals considering AE3 were significant ($P < 0.01$) and both with high values (0.80 and 0.84, respectively). Selection based on measures of annual earning at three years old described in this study could be used to predict career performance in the Quarter Horse.

Key words: animal model, career, earning

T159 Genome-wide association of polymorphic gait in the horse. E. A. Staiger*[1], R. R. Bellone[2], N. B. Sutter[3], and S. A. Brooks[1], [1]*Department of Animal Science, Cornell University, Ithaca, NY,* [2]*Department of Biology, University of Tampa, Tampa, FL,* [3]*Department of Clinical Science, College of Veterinary Medicine Cornell University, Ithaca, NY.*

Following domestication, man selected the horse primarily for the purpose of transportation, rather than consumption; thus resulting in the appearance of divergent genetic traits for locomotion. In this regard the horse is a unique model for the study of gait development, as no other mammalian species is known to discretely segregate for preference in cadence and footfall patterns. At intermediate speeds, beyond the flat walk, horses can perform a range of diagonal and lateral, 2-beat or 4-beat, gaits known as trot, pace, foxtrot, rack, and running walk. Although heritability is unknown, a strong role for genetics is supported by the discrete segregation among breeds for the propensity to perform one gait or another indicating that genetic alleles contributing to gait type will be higher in breeds with the ability than those without, regardless of the subsequent influence of training. Our study aims to leverage this genetic trend by identifying loci common in gaited breeds and rare in trotting breeds. To investigate the contribution of genetics to this unique trait, blood or hair samples were collected from each of 3 horses representing 32 diverse breeds. For 3 of these breeds (Paso Fino, Icelandic Horse and American Saddlebred) the ability to perform a lateral 4-beat gait is a key characteristic of the breed. DNA from each these 95 horses were genotyped at 54,602 loci using Illumina Equine SNP50 beadchip at GeneSeek Inc. (Lincoln, NE) or the Genotyping Shared Resource at the Mayo Clinic (Rochester, MN). We used PLINK V1.07 (Purcell, 2007) to simultaneously test the resulting 5 million plus genotypes for significant association within naturally gaited breeds. Allelic association identified 2 independent statistically significant loci at ECA18 and ECA11 for a lateral 4-beat gait (Bonferroni adjusted *P*-values of 2.39E-09, and 7.46E-09). Confirmation of association by genotyping large populations segregating for gait type and sequencing of candidate genes at each of these loci is currently underway.

Key words: association test, horse, gait

T160 Aromatherapy treatment in horses. C. E. Ferguson*, H. Klienman, A. L. Browning, J. Browning, and E. L. Ferguson, *McNeese State University, Lake Charles, LA.*

In the equine industry an acute fear stress response can be deleterious to production. A novel treatment (trt) to reduce the effects of this stress response in excitable horses would benefit the equine industry. The objective of this experiment was to determine if aromatherapy using 100% lavender essential oil would reduce acute stress response in horses. A total of 7 mature horses were used in this experiment following a Latin square design where each horse received each trt 7 d apart. This procedure was performed with groups of 4 horses at a time with 2 receiving the control trt and 2 receiving lavender trt in a barn isolated from other study horses. The heart rate (HR) and respiratory rate (RR) was recorded for each horse at rest in a stall (−1 min) and then an air horn was blown (between 2 adjacent stalls) for 15 s, twice (0 min). The horses were allowed 60 s to calm and then the stressed HR and RR was recorded (1 min). Then control horses were treated with humidified air and aromatherapy horses were treated with humidified air with a 25% mixture of 100% pure lavender essential oil for 15 min. Following the 15 min control or aromatherapy trt the recovery HR and RR was recorded (15 min). The change in HR or RR was calculated by subtracting the recovery HR or RR (15 min) from stressed HR or RR (1 min). All statistical comparisons were performed using SAS Proc GLM. There were no statistical differences ($P > 0.05$) between the control and aromatherapy trt for resting HR 33.7 ± 3.6 vs. 34.0 ±

3.1 bpm (beats per min), stressed HR 38.8 ± 3.9 vs. 45.5 ± 5.3 bpm or recovery HR 39.14 ± 3.3 vs. 36.2 ± 3.8 bpm. However, the change in HR was significantly greater ($P < 0.02$) following aromatherapy −9.25 ± 3.4 bpm compared with the control trt 0.29 ± 1.5 bpm. The RR did not differ statistically ($P > 0.05$) between the control or aromatherapy trt for the resting 21.1 ± 1.4 vs. 21.5 ± 2.6 brpm (breaths per min), stressed 21.1 ± 1.7 vs. 19.6 ± 1.8 brpm and recovery, 20.3 ± 1.5 vs. 16.5 ± 1.2 brpm. These results demonstrate that lavender aromatherapy can significantly decrease heart rate following an acute stress response.

Key words: stress, horses, aromatherapy

T161 L-Arginine supplementation increases ovarian blood flow in postpartum mares. D. E. Kelley*, L. K. Warren, and C. J. Mortensen, *University of Florida, Gainesville.*

L-Arginine (ARG) is a precursor for protein synthesis and other bioactive compounds such as nitric oxide, polyamines, proline, creatine and glutamate. Nitric oxide has potent vasodilative properties and is important in regulating blood flow and angiogenesis. Supplementing diets with ARG has been shown to improve female reproductive performance in other species. The objectives of this study were to evaluate the effects of ARG supplementation on blood flow to the ovary in postpartum mares during the foal heat cycle. Mares were blocked by age, breed and expected foaling date (EFD) and then assigned randomly within block to one of 2 treatments: ARG supplementation (n = 8) or non-supplemented control (n = 8). Treatment mares were supplemented with 100g of ARG once daily mixed into the morning feeding beginning 21 d before the EFD. Mares underwent daily ultrasound examination beginning the day following parturition utilizing a digital color Doppler ultrasound (Micromaxx, Sonosite, Bothell, WA). Spectral-Doppler measurements (pulsatility index) were recorded for both ovarian arteries and calculated by the algorithm package in the Micromaxx ultrasound. Continuous data were analyzed by MIXED procedures of SAS (version 9.2; SAS Institute, Cary, NC) while data from a single day was compared using Student's *t*-test. Results indicated ARG-supplemented mares had improved blood flow to the ovulatory ovary before ovulation ($P \leq 0.05$). There was no difference between groups on arterial blood flow to the nonovulatory ovary. Perfusion to the ovulatory follicle on the day before ovulation tended to be greater in ARG-supplemented mares compared with control (40.6 ± 4.7% versus 28.6 ± 6.9%, respectively; $P = 0.08$). No differences were found between groups in the diameter of the dominant follicle at ovulation. Blood flow plays an important role in ovarian function and follicular perfusion has been correlated to increased pregnancy rates. Additionally, the lower perfusion of the preovulatory follicle in control mares raises the question of whether reduced ovarian blood flow following parturition may contribute to the reduced fertility associated with this period.

Key words: mare, ovary, blood flow

T162 Using glycerol-^{3}H to evaluate equine blastocyst capsule permeability. B. R. Scott*[1], D. B. Carwell[1], R. A. Hill[1], K. R. Bondioli[1,2], R. A. Godke[1,2], and G. T. Gentry[1,2], *[1]School of Animal Sciences, Louisiana State University AgCenter, Baton Rouge, [2]Reproductive Biology Center, Louisiana State University AgCenter, St. Gabriel.*

The limited success of the cryopreservation of equine blastocysts may be due to the presence of the glycoprotein capsule surrounding the early stage equine embryo preventing penetration of cryoprotectants. Currently, equine embryos destined for cryopreservation are collected from mares on d 6 post-ovulation at the morula stage because of higher survival rates following cryopreservation. Therefore, the objective of this study was to verify capsule impermeability by quantifying the amount of tritiated glycerol uptaken by equine blastocysts with intact capsules. Light horse mares of various breeds were used in this study. The mares (n = 14) ranged in age from 3 to 18 yrs and were in good body condition. Estrus detection was performed by chute teasing with a stallion and ovulation was predicted by transrectal ultrasonography followed by artificial insemination and nonsurgical embryo collection on d 7 post-ovulation. Recovered equine blastocysts (n = 30) were randomly assigned to 2 treatment groups. Embryos were incubated in a 500-μL drop of 1.4 *M* or 3.4 *M* tritiated glycerol with a total activity of 20 μCi for 15 min. After incubation embryos were washed 3 times in 500 μL of unlabeled glycerol identical to the treatment concentration. All samples were transferred to 1.5 mL microcentrifuge tubes and incubated overnight in 400 μL of nitric acid at 37°C. After incubation, vials were vortexed for 2 min and 350 μL of the supernatant was transferred to a scintillation vial and mixed with 5 mL scintillation fluor. Samples were then counted on a liquid scintillation counter with 65% efficiency. Results were then converted from disintegrations per minute to percent uptake of labeled glycerol by volume of the individual embryo. There were no differences ($P = 0.32$) in tritiated glycerol uptake between the 1.4 *M* (2.6% ± 1.4%) and 3.4 *M* (1.22% ± 0.53%) treatment groups, however, embryos <400 μm in the 1.4 *M* treatment had a higher glycerol concentration (8-fold increase) compared with embryos >400 μm ($P = 0.002$). This indicates the capsule may not be fully developed in the smaller embryos. These data further suggest that the capsule may be a cryoprotectant permeability barrier.

Key words: equine, cryopreservation, capsule

T163 Effect of centrifugation/freezing extenders and sperm concentrations on post-thaw motility and membrane integrity of frozen-thawed stallion spermatozoa. C. S. Ballard*[1], C. G. Loretan[2], and J. B. Davis[2], *[1]William H. Miner Agricultural Research Institute, Chazy, NY, [2]University of Vermont, Burlington.*

Two experiments were designed to compare combinations of centrifugation and freezing extenders and effect of spermatozoal concentration on post-thaw quality of frozen stallion semen. Three ejaculates from 3 Morgan stallions were collected in June/July, divided equally and assigned to a 2 × 2 factorial arrangement of centrifugation media (Kenneys Modified Tyrodes (KMT) or INRA96) and freezing media (lactose-EDTA-egg yolk containing 20% egg yolk and 5% glycerol (LAC-EDTA) or INRA-Freeze). Centrifugation media was added 1:1 to raw semen, equilibrated at room temperature for 10 min and centrifuged at 500 x g for 20 min. Supernatant was removed and sperm pellet resuspended with respective freezing media to a concentration of 100×10^6 sperm/ml. INRA-Freeze was cooled at 5°C for 75 min and loaded into 0.5 mL straws. Sperm resuspended with LAC-EDTA equilibrated at room temperature for 20 min before loading into 0.5 mL straws. All straws were frozen in vapor phase of liquid nitrogen (LN) for 10 min before immersion in LN. In Experiment 2, 3 ejaculates were collected in Dec/Jan from 2 of the same Morgan stallions and processed using KMT and LAC-EDTA based on the outcome of Exp. 1. After centrifugation, sperm pellets were resuspended with LAC-EDTA to one of 3 spermatozoal concentrations: 100, 250 or 500×10^6 sperm/ml and processed according to procedures described previously. For both studies, post-thaw progressive motility and membrane integrity (hypo osmotic swelling) were assessed and analyzed using the Proc Mixed procedures of SAS. Centrifugation media did not affect sperm

quality post-thaw (P = 0.94). Progressive motility and membrane integrity post-thaw was significantly higher for LAC-EDTA extender (37 vs. 31%, P = 0.03; 15 vs. 11%, $P \leq 0.01$, respectively). Post-thaw quality of sperm was similar for all freezing concentrations ($P \geq 0.10$). Under the conditions of this study, KMT and LAC-EDTA were the best extenders for processing and freezing stallion spermatozoa at concentrations ranging from 100 to 500 × 10^6 sperm/ml.

Key words: equine, spermatozoa, cryopreservation

T164 Evaluation of hCG or Deslorelin for enhancing ovulation and subsequent pregnancy rate in mares in a commercial setting. M. M. Tondre[1], M. M. Vogelsang*[1], C. A. Cavinder[1], C. M. Honnas[2], and S. G. Vogelsang[3], *[1]Texas A&M University, College Station, [2]Texas Equine Hospital, Bryan, TX, [3]Equine Reproductive Consultant, Hearne, TX.*

The variation in length of estrus, time of ovulation during estrus and size of the follicle at ovulation contribute to increased expense and decreased efficiency of breeding mares in today's horse industry. Inefficiency increases when using frozen semen or semen from stallions of marginal fertility. The purpose of this study was to compare efficacy of hCG and Deslorelin (IM) for enhancing ovulation in the mare. Breeding records of 153 mares at a commercial breeding facility were evaluated. The mares were administered either 2500 IU hCG (Chorulon; Intervet Inc., Millsboro, DE) or 1.5 mg/ml Deslorelin (Applied Pharmacy Services, Mobile, Al) after detection of a follicle >35 mm. Thirty-five mares received the hCG injection, 40 mares received the Deslorelin injection and 78 mares did not receive any treatment. Mares were inseminated using fresh, extended semen or cooled transported semen before ovulation. Pregnancy determinations were made using ultrasonography at d 15 and d 30 post-ovulation. Data were analyzed using χ^2 and values were considered significant at $P < 0.01$. Use of hCG (31 of 35; 88.6%) or Deslorelin (36 of 40; 90%) provided similar results for inducing ovulation within 48 h after detection of a 35 mm follicle. However, in untreated mares (17 of 78; 22%) fewer ovulated by 48 h and most took longer to achieve ovulation (15 by 72 h, 30 by 96 h). Pregnancy rate among the 3 groups of mares was not different (hCG, 58%; Deslorelin, 61% and untreated, 69%). In this study, the use of either hCG or Deslorelin for inducing ovulation within 48 h post-treatment yielded similar results. Pregnancy rates between the treatments were similar although not higher than in the mares which were not treated. The use of ovulation-enhancing hormonal stimulation is beneficial in the commercial horse breeding industry. If the time to ovulation can be more precisely controlled, more efficient use of the stallion can be made. Based on this and other studies, the choice of which product to use can rest with the breeding manager without having to be concerned about loss of effectiveness.

Key words: mares, hCG, Deslorelin

T165 Endoscope-guided insemination for off-season mares. G. Rocha-Chavez[1], J. C. Franco[1], E. O. Garcia[2], A. Sepulveda[1], J. G. Gonzalez[1], J. Torres[1], J. M. Tapia[1], and O. Montañez*[1], *[1]CUSUR Univ de Guadalajara, Guadalajara Jalisco Mexico, [2]CUCOSTA SUR, Autlan Jalisco Mexico.*

Although breeding season for equine arrives with the spring, in Mexico mares can be found cycling thorough the entire year and late born foals are always welcomed. The objective of this study was to determine fertility of mares inseminated with frozen/thawed semen during fall using the endoscope as a guide. Twelve mares of known fertility were inseminated deep in the uterine horn with 200 thousand frozen thawed spermatozoa with at least 30% motility. Mares were programmed to be inseminated no more than twice during this season and the estrous cycle was closely monitored via ultrasound to ensure insemination within 4 h post ovulation. Insemination was done with flexible intrauterine pipette guiding a 0.5 mL straw containing the thawed stallion semen that was deposited near the uterotubal junction. Pregnancy diagnosis was made 17 d post ovulation and pregnancy rates (PR) were compared using chi-squared test with same type of insemination made during spring without the aid of endoscope. PR was better for the fall group ($P < 0.05$) as illustrated in Table 1. More research is needed for off-season mares.

Table 1. Pregnancy rates of mares inseminated either on spring or fall

Season	No. of mares	Mares pregnant	Rate
Spring	12	5	41.6[a]
Fall	17	9	52.9[b]

[ab]Differ at $P < 0.05$.

Key words: insemination, mares, off-season

T166 Milk and plasma iodine in Isfahan Holstein dairy cows. A. Nikkhah*[1] and G. Ghorbani[2], *[1]University of Zanjan, Zanjan, Iran, [2]Isfahan University of Technology, Isfahan, Iran.*

Iodine (I) is an essential element for efficient dairy cow metabolism. Iodine status is however not well known on farms. The objective was to measure milk and plasma I concentrations in a selected group of commercial dairy herds in central Iranian province of Isfahan. During summer of 1999 and winter of 2000, 11 dairy farms were randomly chosen and a minimum of 10 cows were sampled from each farm. Tail veins blood and milk samples from a total of 135 lactating Holstein cows in summer and 162 cows in winter were obtained. Totally, 367 blood samples and 297 milk samples were collected. The dairy herds had comparable nutritional (e.g., feed and diet types), reproductive (e.g., artificial insemination), and vaccination programs. Milk was sampled after washing and cleaning teat tips in the milking parlor. Management data including feed ingredients, and average milk properties were recorded. Total plasma and milk I concentrations were assayed using the Sandell-Kolthoff reaction. Data were analyzed as mixed models with acquired fixed effects of season and herd. Correlations among Milk and plasma I with milk production were determined. Iodine in plasma ranged from 9.9 to 46.2 μg/L in winter vs. 17.9–56.2 μg/L in summer. The plasma I in all herds in summer ($P < 0.01$) and in all except one herd in winter ($P < 0.05$) was lower than the minimum critical range in dairy cows (i.e., 50–100 μg/L). Total plasma I was lower in winter than in summer (27.1 ± 12.3 vs. 42.4 ± 16.6 μg/L). Milk I concentrations varied considerably among cows (CV = 14–62%). Across seasons, a negative correlation was found between milk fat % and milk yield ($r = -0.40$, $P < 0.01$), as was a positive correlation between milk and plasma I ($r = 0.22$, $P < 0.01$). In winter but not in summer, milk I concentrations positively correlated with milk fat % ($r = 0.31$, $P < 0.01$). Results indicate prevalent hypo-iodinemia in selected Isfahan dairy herds, suggesting inadequate I supply via feeds and supplements to maintain blood I within normal ranges. It is recommended to provide sufficient edible or non-edible supplemental I to lactating cows in Isfahan.

Key words: iodine, milk, plasma

T167 The effect of stocking rate and calving date on reproductive performance, body state, metabolic, health and welfare parameters of Holstein-Friesian dairy cows. B. McCarthy*[1,2], K. M. Pierce[2], L. Delaby[3], A. Brennan[1], and B. Horan[1], *[1]Animal and Grassland Research and Innovation Centre, Teagasc Moorepark, Fermoy, Co. Cork, Ireland, [2]School of Agriculture, Food Science and Veterinary Medicine, University College Dublin, Belfield, Dublin, Ireland, [3]INRA, AgroCampus Ouest, UMR 1080, Production du Lait, Saint-Gilles, France.*

The objective of this study was to quantify the effect of stocking rate (SR) and calving date (CD) on the reproductive performance, body condition (BCS) (or body state), metabolic and health and welfare of high EBI Holstein-Friesian (HF) dairy cows within systems designed to represent 3 alternative whole farm SRs in a post EU milk quota spring calving pasture-based production system. Two groups of HF dairy cows with differing mean CD were established from within the existing research herd at Moorepark (Teagasc, Ireland). Animals were assigned either to an early calving (EC; mean CD: 12th of February) treatment or a late calving (LC; mean CD: 25th of February) treatment. Animals within each CD treatment were randomly allocated to one of 3 SR (SR) treatments, Low (2.51 cows/ha), Medium (2.92 cows/ha) and High (3.28 cows/ha). A total of 138 and 137 spring-calving dairy cows, comprised of 2 strains of HF (North American HF and New Zealand HF genotypes), were used during 2009 and 2010, respectively. The effects of CD, SR treatment, genotype and their interactions on reproductive performance, body weight (BW), BCS and blood metabolite, hormone and immune profile concentrations and health status were analyzed. Stocking rate and CD had no effect on reproductive performance ($P < 0.05$) except for embryo mortality, with the low SR having greater embryo mortality (9.8%) compared with the medium or high SR (4.4 and 2.2%, respectively). Stocking rate and CD had no effect on immunological profiles or health status. Earlier calving and increased SR resulted in reduced BW, BCS and metabolic status in early lactation. The results show that earlier calving and increased SR can be achieved without adverse effect on overall reproductive performance. The existence of a SR by genotype interaction for several reproductive variables suggests that the smaller New Zealand genotype is better adapted to increased SR systems.

Key words: dairy cow, stocking rate, reproduction

T168 Evolution of raw bovine milk quality: the Hungarian experience (1984-2009). G. Császár[1], A. Unger[1], and L. Varga*[2], *[1]Hungarian Dairy Research Institute, Inc., Mosonmagyarovar, Hungary, [2]Department of Dairy Science, Institute of Food Science, Faculty of Agricultural and Food Sciences, University of West Hungary, Mosonmagyarovar, Hungary.*

First class raw milk is an essential prerequisite for commercial production of high quality dairy foods. The major microbiological, hygienic and physicochemical properties of raw bovine milk produced in Hungary are graded on a regular basis, i.e., 3 times a month or once every 10 d, by the Central Laboratory of the Hungarian Dairy Research Institute. Having been in place for a quarter of a century now, this system has been updated and upgraded several times over the years. The primary purpose of the present study was to give an overview of the history and development of Hungarian raw milk grading and show how this ever-improving system has contributed to the evolution of milk quality in the country. A large pool of data has been accumulated and processed. The results showed that mean total plate counts gradually decreased from 849,000 cfu/ml in 1984 to 36.000 cfu/ml in 2009. As for somatic cell counts, a mean value of 500,000 cells/ml was observed in 1984, whereas only 280,000 cell/ml were measured in 2009. The percentage of samples containing detectable levels of inhibitory substances was as high as 3.7% back in 1984 (and 4.7% in 1985), which has decreased to 0.1% by 2009. The mean concentration of extraneous water in Hungarian raw bovine milk was found to be 0.52% 26 years ago, as opposed to 0.04% in 2009. In conclusion, there has been an enormous improvement in raw milk quality with respect to all the parameters tested. Since 2003 more than 97% of the raw milk produced in Hungary has met the legal requirements in terms of overall quality. However, it should also be noted that somatic cell counts and the percentage of samples positive for residues of inhibitory substances need to be decreased further in the coming years.

Key words: cow′s milk, raw milk quality, grading

T169 Bulk tank somatic cells and its relationship to milk production, milk composition, and revenue in dairy farms located in

central Thailand. D. Jatawa[1], S. Koonawootrittriron[1], M. A. Elzo*[2], and T. Suwanasopee[1], *[1]Kasetsart University, Bangkok, Thailand, [2]University of Florida, Gainesville.*

Quality and quantity of milk are important for price determination and revenue of dairy farmers. Bulk tank somatic cell count (BSC) is used in Thailand as an indicator of milk quality. The objectives of this study were to monitor BSC in Central Thailand and estimate the association between BSC and monthly milk yield per cow (MYC), fat % (FAT), protein % (PRO), lactose % (LAC), solids not fat % (SNF) total solids % (TS), and monthly revenue per cow (MRC). The data set included monthly milk production and composition data collected from 2004 to 2010 (28,580 records) in 811 farms located in Central Thailand (Muaklek, Wang Muang, Phattana Nikhom, and Pak Chong). Seasons were winter (November to February), summer (March to June), and rainy (July to October). Farm sizes were classified by number of milking cows into small (<10 cows), medium (10 to 19 cows), and large (>19 cows). The linear model contained year-season subclasses, farm size-farm location subclasses, and regression BSC as fixed effects, and residual as a random effect. The average BSC in this population was 681,430 ± 641,000 cells/ml. Milk produced in most farms (63%) had BSC values higher than 500,000 cells/ml. The BSC tended to increase over time (11,668 cells/ml/year-season; $R^2 = 0.74$). The BSC was linearly associated with milk production, composition, and revenue. Larger BSC were associated with lower MYC (−1.39 ± 0.12 kg/10^5 cells/ml; $P < 0.0001$), LAC (−0.0074 ± 0.0002%/10^5 cells/ml; $P < 0.0001$), SNF (−0.0022 ± 0.0002%/10^5 cells/ml; $P < 0.0001$), and MRC (−17.51 ± 1.84 Thai baht/10^5 cells/ml; $P < 0.0001$), but with higher FAT (0.0066 ± 0.0004%/10^5 cells/ml; $P < 0.0001$), PRO (0.0055 ± 0.0002%/10^5 cells/ml; $P < 0.0001$), and TS (0.0054 ± 0.0005%/10^5 cells/ml; $P < 0.0001$). These results indicated the need for farmers to implement management practices to reduce BSC to increase milk yield and revenue in central Thailand.

Key words: dairy, somatic cells, tropical

T170 Factors affecting carcass weight, dressing percent, and marbling score of crossbred beef cattle in tropical Thailand. S. Koonawootrittriron[1], M. A. Elzo*[2], C. Kankaew[1], and M. Osothongs[3], *[1]Kasetsart University, Bangkok, Thailand, [2]University of Florida, Gainesville, [3]Pon Yang Khram Livestock Breeding Cooperative NSC Ltd., Sakon Nakhon, Thailand.*

Carcass quantity and quality traits are economically important for the Thai beef cattle industry. Characterization of factors influencing these traits would help beef producers develop appropriate nutrition and management strategies for fattening beef cattle under the tropical conditions in Thailand. The objective of this study was to characterize factors affecting carcass weight (CWT), dressing percent (DP), and marbling score (MBS; 1 = low to 5 = high) of crossbred beef cattle raised under Thai tropical conditions. Data came from 40,107 bulls and heifers, fattened in 3,939 farms, and collected at the slaughter house of the Pon Yang Khram Livestock Breeding Cooperative NSC Ltd. from January 2004 to December 2010. Cattle breeds were classified as 1/2 Charolais 1/2 Brahman (CB), 1/2 Limousin 1/2 Brahman (LB), and 1/2 Simmental 1/2 Brahman (SB). Seasons were winter (November to February), summer (March to June), and rainy (July to October). The model included the fixed subclass effects of year-season, breed group, and sex, covariates for slaughter age and slaughter weight, and a random residual. Least squares means (LSM) for subclass effects were compared using Bonferroni *t*-tests. All subclass effects influenced ($P < 0.05$) CWT, DP, and MBS, except for sex that had no effect on MBS. Crossbred CB and LB animals had similar CWT and DP, but CB had higher ($P < 0.0001$) MBS (3.11 ± 0.01) than LB (3.06 ± 0.01). Crossbred SB had similar MBS to LB, but lower ($P < 0.0001$) CWT (SB: 336.84 ± 0.42 kg; CB: 341.08 ± 0.16 kg; LB: 341.81 ± 0.45 kg) and DP (SB: 55.66 ± 0.07%; CB: 56.32 ± 0.03%; LB: 56.49 ± 0.07%) than CB and LB. Bulls had higher CWT (343.18 ± 0.20 kg vs. 336.64 ± 0.37 kg) and DP (56.74 ± 0.03% vs. 55.57 ± 0.06%) than heifers. Results suggested that CB and LB would be the most advantageous to increase carcass quantity and quality of beef cattle under Thai tropical conditions.

Key words: beef, carcass, tropical

T171 Forage yield and quality of two genetic materials of corn (*Zea mays*) harvested at two different cutting heights in Costa Rica. J. A. Elizondo-Salazar*[1], J. A. Vargas-Elizondo[1], and E. E. Corea-Guillén[2], *[1]Estación Experimental Alfredo Volio Mata, Facultad de Ciencias Agroalimentarias, Universidad de Costa Rica, [2]Departamento de Zootecnia, Facultad de Ciencias Agronómicas, Universidad de El Salvador.*

Corn silage is one of the most popular forages fed to dairy cows in Costa Rica and in many areas of the world due to its good agronomic and ensiling characteristics, high concentration of nutrients, and excellent palatability. It is common to place strong emphasis on total DM yield; however, this measurement alone is a poor indicator of nutritive value. For this reason an experiment was carried out at the Alfredo Volio Mata Experiment Station of the University of Costa Rica, located at an altitude of 1,542 m, with an average annual rainfall of 2,050 mm. The purpose of the study was to determine forage yield and quality of 2 corn cultivars evaluated at the same age and in similar physiological stage. A 2x2 factorial design was used (corn cultivars: hybrid and native, cutting height: 15 and 45 cm). Leaves, stalks, and ears were separated and analyzed for DM, CP, and NDF content. Native corn yielded more DM/ha ($P < 0.05$); however, increasing the height of cutting lowered yields of harvested DM/ha only in the native corn. Cutting height only affected DM content of leaves and ears in the native corn ($P < 0.05$).

Table 1.

	Hybrid 15 cm	Hybrid 45 cm	Native 15 cm	Native 45 cm
Leaves DM, kg/ha	3344.83[b]	3142.29[b]	5175.90[a]	3306.38[b]
Stalks DM, kg/ha	4492.48[c]	4000.43[c]	8622.81[a]	6882.76[b]
Ears DM, kg/ha	3142.19[a]	3280.57[a]	1480.57[b]	195.67[c]
Leaves DM, %	18.38[a]	18.89[a]	17.09[a]	14.84[b]
Stalks DM, %	12.91	14.11	10.12	10.72
Ears DM, %	10.64	10.60	9.47	10.14
Leaves CP, %	17.32	17.30	17.81	17.48
Stalks CP, %	7.30	7.14	7.79	8.04
Ears CP, %	11.91[b]	12.89[b]	16.88[a]	15.21[a]
Leaves NDF, %	68.87	66.89	66.98	66.42
Stalks NDF, %	77.56	77.26	77.13	78.02
Ears NDF, %	70.29[b]	66.37[b]	57.45[a]	56.80[a]

Key words: corn silage, cutting height, forage

T172 Comparison of chemical composition, in situ degradability and in vitro gas production of ensiled and sun-dried mulberry pomaces. Z. Bo*, Q. Meng, L. Ren, F. Shi, and Z. Zhou, *State Key Laboratory of Animal Nutrition, Beef Cattle Research Center, College of Animal Science and Technology, China Agricultural University, Beijing, China.*

The nutritive values of sun-dried (SDMP), naturally ensiled (NEMP) and microbial ensiled mulberry pomace (MEMP) were evaluated using chemical analysis, in situ and in vitro gas production techniques. Compared with SDMP, natural and inoculated ensiling treatment of mulberry pomaces did not change OM, NDF and NDF content ($P > 0.1$), but did decrease ($P < 0.05$) CP content by about 2 percentages, indicating protein degradation occurring during ensiling. Among 2 ensiled mulberry pomaces, treatment with microbial inoculation resulted in reduced pH, increased concentrations of lactate, acetate and propionate, but in unchanged concentration of ammonia in comparison with natural ensiling of mulberry pomaces. These results indicated that microbial inoculation is favorable for improvement of ensiling quality of mulberry pomaces. The in situ effective degradabilities of SDMP were 2.35 and 2.88 percentages higher ($P < 0.01$) for DM, and 10.83 and 7.13 percentages higher ($P < 0.01$) for CP than NEMP and MEMP, respectively, indicating that ensiling treatment of mulberry pomaces can supply more bypass CP and other nutrients to small intestines because of reduced ruminal degradabilities. The in vitro gas production of SDMP was higher ($P < 0.01$) than NEMP and MEMP, while methane proportion of SDMP was highest (63.3%), followed by MEMP (58.7%) and NEMP (48.2%). On the whole, ensiling treatment would be an appropriate way to store mulberry pomaces in terms of their reduced ruminal degradabilities of DM and CP, lower methane production and improved ensiling qualities, compared with sun-drying treatment.

Key words: mulberry pomace, sun-dried, ensiled, in situ, in vitro

T173 Immune status of water buffalo calves allowed to nurse their dams. J. A. Elizondo-Salazar*[1], B. Cáseres-Alvarez[1], and A. J. Heinrichs[2], *[1]Estación Experimental Alfredo Volio Mata, Facultad de Ciencias Agroalimentarias, Universidad de Costa Rica, [2]The Pennsylvania State University, University Park.*

Water buffalo for milk and meat production has increased during the last decade in Costa Rica; however, there is a lack of information on how to improve the productivity and health of these animals. Passive transfer status has been established as a significant source of variation in growth performance of buffalo calves. Measurement of serum total protein (STP) by refractometer as an estimate of serum immunoglobulin concentration is the simplest test to give an indication of adequate passive transfer of immunity. A value of 5.0 g/dL has been established as the cutoff point for assessment of passive transfer status. Since there is no data on the immune status of water buffalo calves in Costa Rica, the objective of this study was to determine STP concentration in neonatal buffalo calves allowed to nurse the dam during the first hours of life. Blood samples were collected between d 1 and 7 of age from 53 heifer and 49 bull calves from one commercial farm in the Northern region of Costa Rica. All blood samples were collected into serum (red top) Vacutainer tubes, refrigerated overnight, centrifuged, and the serum separated from clot within 24 h of collection. A hand-held refractometer (Atago Master-Sur/Nα, Bellevue, WA) was used to measure STP. GLM procedure was used to establish differences between parity and breed of the dams, and sex of the calf. Descriptive statistics were generated to define percentage of failure of passive transfer by sex of the calf and parity of the dam. Overall failure of passive transfer of immunity was not as high as that seen in other species, 7.84% of calves had failure of passive transfer (heifers 9.43%, bulls 6.12%). There was no significant difference between sex of the calves for STP concentration (heifers 6.83 g/dL, bulls 7.01 g/dL). Calves coming from dams of second parity had higher ($P < 0.05$) STP concentration (7.42 ± 0.27 g/dL) than those coming from water buffalo cows with ≥4 calvings (6.55 ± 0.21 g/dL).

Table 1. Failure of passive transfer (%) by parity of dam and sex of neonates

Parity	Heifers	Bulls	Both
1	6.67	0.00	3.33
2	10.00	0.00	5.26
3	7.69	0.00	5.00
≥4	13.33	16.67	15.15

Key words: passive transfer of immunity, serum total protein, water buffalo

T174 Milk composition, blood cellular and chemical components of Saanen and local Lebanese goats. F. T. Sleiman*, H. H. Itani, E. K. Barbour, M. T. Farran, and Z. G. Kassaify, *American University of Beirut, Beirut, Lebanon.*

A study was conducted to determine the effect of prevailing Lebanese management conditions on the performance of imported Saanen goat breed compared with a local breed as reflected in milk and blood components. A total of 30 goats, 15 goats of each breed (5 lactating does, 5 doe kids and 5 bucks), were used and subjected to similar health management and feeding conditions. Daily milk yield, milk mineral and calcium percentages of Saanen goats were significantly higher ($P < 0.05$) than that of the local breed and averaged 5.2 vs. 0.6 L, 0.84 vs. 0.74% and 0.18 vs. 0.14%, respectively. Milk fat, protein and total solids percentages were not significantly different ($P > 0.05$). Does and bucks age (mature vs. kid) had a significant influence ($P < 0.05$) on blood parameters such as eosinophils (1.70 vs. 0.40%), monocytes (6.80 vs. 14.50%), total white blood cell count (12.61 vs. 22.79 × 10^3/mL), packed cell volume (22.90 vs. 33.00%), hemoglobin (7.50 vs. 10.56 g/dL) and plasma glucose level (62.50 vs. 102.90 mg/dL). Other blood components such as basophils, lymphocytes, neutrophils and red blood cells were neither significantly different among breeds nor among genders ($P > 0.05$). Results indicate that Saanen goat breed adapted well to prevailing health and feeding conditions of Lebanon.

Key words: blood components, milk composition, Saanen goat

T175 Assessment nutrient matrix values of three xylanase and β-glucanase on broilers performance fed wheat-based diet. S. A. Moftakharzadeh*, H. Moravej, and M. Shivazad, *Department of Animal Science, Agriculture and Natural Source Pardis, University of Tehran, KarajIran.*

The effect of feeding wheat-based diets supplemented with 3 commercial enzymes containing xylanase and β-glucanase activities based on nutrient matrix values were investigated on the performance, meat yield and jejunal digesta viscosity broiler chicks. A total of 208-d-old male broiler chicks (Ross 308) were allocated to 4 treatment groups, with 4 replicates per treatment group and 13 birds per replicate pen. All data were analyzed in a randomized complete design. Overall, from

0 to 42, only addition of enzyme B to wheat-based diet significantly ($P < 0.05$) increased average daily feed intake (ADFI) and average daily gain (ADG). Moreover, FCR of broilers were significantly ($P < 0.05$) improved when enzyme A added to basal diet. The relative weight of the breast, thigh, liver, and gizzard as percentage of live weight were not affected by enzyme supplementation ($P < 0.05$). The relative weight of the abdominal fat as proportion of live weight was also significantly ($P < 0.05$) increased by addition of enzymes A and B. Enzyme supplementation decreased viscosity of jejunal contents of chicks at d 23, but only enzymes A reduced significantly ($P < 0.05$) the viscosity of jejunum compared with control diet. In conclusion, enzyme A showed the best FCR among enzymes and this enzyme can be preferred choose for adding to wheat-based diets.

Key words: broiler, enzyme, matrix value, performance

T176 Evaluation of nutrient matrix values for different kinds of NSP enzymes on performance, water intake, litter moisture and jejunal digesta viscosity of broilers fed barley-based diet. S. A. Moftakharzadeh*, H. Moravej, and M. Shivazad, *Department of Animal Science, Agriculture and Natural Source Pardis, University of Tehran, KarajIran.*

In this study, we evaluate the effect of using different mixed enzymes on releasing of ME and amino acids (AA) from barley-based diets and compare the results with those fed barley and the corn diets without enzyme. Effects of enzyme on the performance, water intake, litter moisture and jejunal digesta pH and viscosity of chicks were investigated. In entire period, addition of all enzyme to the barley-based diet significantly ($P < 0.05$) increased average daily feed intake (ADFI) and the highest intake was for birds that were fed a diet containing enzyme A ($P < 0.05$). Overall, from 0 to 42 d, average daily gain (ADG) was significantly ($P < 0.05$) increased by enzyme supplementation and the highest body weight belonged to birds that received enzyme A ($P < 0.05$). Generally, from 0 to 42 d of age, feed conversion ratio (FCR) was significantly ($P < 0.05$) improved when diets containing enzyme were compared with barley-based diet without enzyme, but there were no significant differences among diets containing enzymes A and C and the corn-based diet. The carcass weight, and the relative weight of the abdominal fat were significantly ($P < 0.05$) increased by enzyme addition. Enzyme supplementation significantly decreased jejunal viscosity at Day 23 ($P < 0.05$), whereas pH jejunal digesta was not changed ($P > 0.05$). By adding enzymes, water to feed ratio decreased at 15, 25, and 33 d of age and litter quality was significantly improved ($P < 0.05$). In conclusion, considering nutrient matrix values for all used enzymes improved performance of broilers and can be used in formulating diets for decreasing cost of commercial broilers diets based on barley instead of corn.

Key words: broiler, enzyme, nutrient matrix value, performance

T177 The effects of albusin B (bacteriocins) of *Ruminococcus albus* 7 expressed by yeast on the lipid metabolism of mice. Y. H. Hsieh*[1], H. T. Wang[2], J. T. Hsu[1], and C. Y. Chen[1], *[1]National Taiwan University, Taipei, Taiwan, [2]Chinese Culture University, Taipei, Taiwan.*

In the previous study, we successfully isolated albsuin B (bacteriocin) from *Ruminococcus albus* 7 and mass-produced by the *Saccharomyces cerevisiae* expression system. We also found that broilers supplemented with albusin B had a better intestinal absorption of protein and carbohydrate, and caused a greater growth performance. The objective of this study was to elucidate the effect of albusin B on the lipid metabolism in a mouse model. Twenty-four of BALB/c healthy male mice with 6 weeks of age were randomly divided into 3 groups: normal saline (control), yeast (0.125μg /g body weight), yeast with albusin B (0.125 μg/g body weight) were supplemented continuously for 14 d then sacrificed. Compared with the control mice, mice supplemented with albusin B decreased body weight with no effects on feed intake. Neither body weight nor feed intake was changed by the yeast supplementation. In the intestinal morphology, mice with albusin B supplementation had the highest villus height in the jejunum than the other 2 groups ($P < 0.05$). Both yeast and albusin B supplemented mice had a higher mRNA expression of fatty acid binding proteins and acyl-CoA oxidase in the jejunum and liver than the control mice did. Mice with albusin B treatment had a lower mRNA expression of acetyl-CoA carboylase (ACC) and fatty acid synthase (FAS) in the jejunum and liver, while mice with yeast treatment had a higher mRNA expression of ACC and FAS in the jejunum and a lower mRNA expression of ACC and FAS in the liver. Albusin B supplementation caused a lower plasma level of triglyceride and free fatty acids, and a higher plasma level of high density lipoproteins ($P < 0.05$); while yeast supplementation did not modulate the plasma lipid compositions. These results implied that albusin B supplementation modulated the intestinal lipid metabolism, decreased the hepatic fatty acid synthesis, therefore improved the plasma lipid compositions, which might contribute to the lower body weight.

Key words: albusin B, lipid metabolism, mice

T178 Fermentation biomass can replace protein from fish and soybean meals in nursery diets. V. G. Perez*[1], H. Yang[1], T. R. Radke[1], J. Less[2], and D. P. Holzgraefe[1], *[1]ADM Alliance Nutrition Inc., Quincy, IL, [2]ADM Specialty Feed Ingredients, Decatur, IL.*

Fermentation biomass (FBM) is a co-product of threonine production, which contains about 81.5% CP, 5.1% Lys, and 3.9% Thr. A total of 128 pigs (about 21 d of age; 4.9 ± 0.20 kg BW) were used to determine the extent in which FBM can effectively replace fish meal (FM) and soybean meal (SBM) in nursery diets. The experiment was a randomized complete block design; blocks were 2 categories of initial BW. Dietary treatments had a 4 (FBM replacing 0, 25, 50, or 100% of FM) × 2 (FBM replacing 0 or 4% of SBM) factorial arrangement. The FBM replaced FM in feeding phases 1 (7 d) and 2 (12 d), or SBM in feeding phase 3 (10 d). The FM was included at 6, 4, and 0% of the diet in feeding phases 1, 2, and 3, respectively. All diets among treatments were formulated to provide similar ME, CP, and digestible Lys contents within feeding phase. The ME and coefficients of amino acid digestibility used in FBM were generated in broilers, as no swine data were available. Treatments were replicated with 4 pens of 4 pigs per pen. Results are presented by main effects of FM and SBM replaced by FBM because no interactions were detected. Replacing FM or SBM with FBM affected neither growth rate nor feed intake. Overall, pigs fed diets with FBM replacing 0, 25, 50, or 100% of FM had an ADG of 384, 398, 388, and 372 g/d (SEM = 13), respectively. Pigs fed diets with FBM replacing 0 or 4% of SBM had an ADG of 394 vs. 377 g/d (SEM = 9). The G:F was reduced ($P <$ or = 0.05) as more FBM replaced either FM or SBM. At the end of feeding phase 2 (d 19), pigs fed diets with FBM replacing 0, 25, 50, or 100% of FM had a G:F of 926, 886, 868, and 847 g/kg, respectively (FBM linear effect, $P < 0.01$; SEM = 17). Overall, pigs fed diets with FBM replacing 0, 25, 50, or 100% of FM had a G:F of 853, 832, 809, and 798 g/kg, respectively (FBM linear effect, $P = 0.01$; SEM = 14). Pigs fed diets with FBM replacing 0 or 4% of SBM had a G:F of 837 vs. 808 g/kg ($P = 0.05$; SEM = 11). The ME in FBM from broilers probably overestimated ME for swine, which may decreased G:F as more FBM was used. Fermented biomass can replace 100% of FM and up to 4% SBM in nursery diets without affecting growth rate.

Key words: threonine biomass, fish meal, pigs

T179 The digestibility marker used and their inclusion level influence the magnitude of ileal amino acid digestibility response to phytase supplementation of a swine diet. O. A. Olukosi[1], O. Bolarinwa[2], A. J. Cowieson[3], and O. Adeola*[2], *[1]Avian Science Research Centre, Scottish Agricultural College, Ayr, Ayrshire, United Kingdom, [2]Department of Animal Sciences, Purdue University, West Lafayette, IN, [3]Poultry Research Foundation, Faculty of Veterinary Science, The University of Sydney, Camden, Sydney.*

Six barrows fitted with simple T-cannula at the distal ileum were used in an experiment to determine whether the type of digestibility marker (TiO_2 or Cr_2O_3) or its level of inclusion (3 or 5 g/kg diet) affect the magnitude of apparent ileal amino acid digestibility (AIAAD) response to phytase (0 or 1000 FTU/kg diet). The pigs were allocated to 4 diets in a 6 × 4 Youden Square Design and a 2 × 2 factorial arrangement (phytase at 0 or 1000 FTU/kg and combination of digestibility markers TiO_2 and Cr_2O_3 at either 3 or 5 g/kg of diet). Each experimental period lasted 7 d and included a 5-d adjustment period and a 2-d ileal digesta collection. The AIAAD was calculated for each AA using each marker from analyses of diets and ileal digesta for AA, Ti, and Cr. The AIAAD data were analyzed as appropriate for a split-plot design. Phytase or dietary concentration of digestibility marker did not affect AIAAD. The AIAAD values calculated using Ti were greater ($P <$ 0.05) than those calculated using Cr (77.6 vs. 76.8%) but there were no effect of the inclusion level of the marker on AIAAD. By setting the AIAAD values at no phytase supplementation to zero, the magnitude of AIAAD response to phytase supplementation was determined for each AA using each marker. These values as calculated using Ti was greater ($P < 0.05$) than those calculated using Cr (5.03 vs. −0.82) at 3 g/kg. At 5 g/kg marker level, there were no differences in magnitude of AIAAD response as determined with either marker except for Asp and Ser, which had greater ($P < 0.05$) values for Ti than for Cr. At 3 g/kg marker level, Pro and Gly had the greatest magnitude of response to phytase where Glu, Trp, and Met had the least response. The greatest difference in magnitude of AIAAD response to phytase supplementation as measured with either Ti or Cr was for Cys and Thr whereas the least difference was for Arg and Trp. These data show that the type of marker used and the level of inclusion of the marker influence the magnitude of apparent ileal amino acid digestibility response to phytase supplementation.

Key words: amino acid, digestibility marker, phytase

T180 Evaluation of different lysine to threonine ratios on growth performance, relative organ weight, meat quality and blood profiles in broilers. H. W. Cho*, L. Yan, and I. H. Kim, *Dankook University, Cheonan, Choongnam, South Korea.*

A study was conducted to evaluate Lys to Thr ratio on growth performance, relative organ weight, meat quality and blood profiles in broilers. One-d-old ROSS 308 broiler chicks were randomly assigned to 1 of 4 dietary treatments with 10 replicates of 13 chickens each. This experiment lasted for 4 wk. Dietary treatments included: 1) T1: 1.42% Lys: 0.93% Thr, 2)T2: 1.42% Lys: 0.99% Thr, 3)T3: 1.42% Lys: 1.06% Thr, and 4)T4: 1.42% Lys: 1.13% Thr. Growth performance was measured on d 7, 21 and 28 and other response criteria were measured on d 28. During the 1 to 3 wk, broilers fed T3 diet showed a higher ADG than broilers feed T4 diet ($P < 0.05$). Overall experimental period, T2 and T3 diets had a higher ADG than T1 and T4 diets. Moreover, T4 diet had a higher ADG than T1 diet. No changes in ADFI and G:F was observed in response to any of the treatments ($P < 0.05$). On d 28, the T4 treatment had higher blood creatinine level than other treatments ($P < 0.05$). On d 28, the gizzard breast meat, bursa of fabricius, liver, spleen and abdominal fat were removed by trained personel and weighed. Relative organ weight was not significantly different among all treatments. There were no differences in meat quality among all treatments (meat color, drip loss, and water holding capacity). In conclusion, the ratio of 1.42% Lys: 1.06% Thr can improve growth performance of broilers without influence on organ weight and meat quality.

Key words: growth performance, Lys:Thr ratio, broiler

T181 Essential amino acids to crude protein ratio in placenta and uterus during gestation. Y. L. Ma*[1], N. Trottier[2], J. Liesman[2], R. L. Payne[3], and M. D. Lindemann[1], *[1]University of Kentucky, Lexington, [2]Michigan State University, East Lansing, [3]Evonik-Degussa Corp., Kennesaw, GA.*

Because body tissues do not have similar AA profiles, it is necessary to analyze different tissues to accurately model protein accretion. Collected tissues from a separate study were available for analysis of the profiles for placenta and uterus. In that study, crossbred gilts (n = 69) were selected at 183 ± 2.7 d and 137 ± 10 kg BW and allotted to receive Se (0.3 mg/kg diet) as Na selenite or organic Se (Sel-Plex; Alltech Inc., Nicholasville KY). Gilts were then slaughtered at defined time points throughout gestation (d 43, 58, 73, 91, 101, or 108 of gestation; n = 6 to 12 gilts/d) for a variety of fetal and maternal measures. Placenta and uterus samples were each pooled within Se treatment and day of slaughter (n = 4 and 6/d of slaughter for placenta and uterus, respectively) and analyzed to characterize differences in essential AA (EAA) to CP ratio during gestation. There were no consistent effects of Se or day of slaughter on AA profile ($P < 0.05$). The EAA:CP profiles differed between placenta and uterus (Table 1). In general, the means of EAA:CP in uterus were greater than in placenta for lysine, arginine, isoleucine, methionine, and total sulfur AAs and were lower than in placenta for histidine, phenylalanine, tryptophan, and valine and were similar as placenta for leucine and threonine. Total EAA as a percentage of CP was 43.90% for placenta and 44.67% for uterus. The results demonstrate tissue differences in EEAs composition of placenta and uterus.

Table 1. Average of AA to CP ratio (g/16 g N) in placenta and uterus from d 43 to 108 of gestation

Amino acid	Placenta	Uterus	*P*-value	SEM
Lysine	6.36	6.92	< 0.01	0.13
Arginine	6.30	7.12	< 0.01	0.07
Histidine	2.68	2.45	< 0.01	0.07
Isoleucine	3.43	3.60	< 0.01	0.06
Leucine	8.08	8.00	0.33	0.15
Methionine	1.67	1.73	< 0.01	0.03
Total Sulfur	3.29	3.46	< 0.01	0.06
Phenylalanine	4.53	4.39	< 0.01	0.08
Threonine	4.17	4.20	0.65	0.10
Tryptophan	1.22	1.05	< 0.01	0.05
Valine	5.45	5.22	< 0.01	0.10

Key words: essential amino acids, gestation

T182 Estimating fermentative amino acid catabolism in the upper gut of growing pigs. D. Columbus*, J. P. Cant, and C. F. M. de Lange, *Department of Animal and Poultry Science, University of Guelph, Guelph, Ontario, Canada.*

Fermentative catabolism of dietary and endogenous AA in the upper gut of pigs (FAAC) reduces AA available for protein synthesis. Manipulating dietary fiber and protein levels may influence the microbes' preferred N and energy sources and alter FAAC. A 4 d continuous isotope tracer infusion was performed to determine whole body urea flux, upper gut ammonia flux and FAAC, and urea recycling in ileal-cannulated growing pigs individually fed a control diet (C, 20.6% CP; n = 6), a high fiber diet with 12% added pectin (F, 19.5% CP; n = 4) or low protein diet (LP, 14.9% CP; n = 6). ^{15}N-ammonium chloride and ^{13}C-urea were infused intragastrically and intravenously, respectively. Ileal ammonia flow was lower in pigs on LP compared with pigs on F (0.25, 0.47, and 0.13 mmol N/kg BW/d; $P < 0.05$). There was an impact of dietary protein level on urea flux (25.3, 25.7, and 10.3 mmol N/kg BW/d; $P < 0.05$), urea excretion (14.4, 15.0, and 6.2 mmol N/kg BW/d; $P < 0.05$), and urea recycling (12.1, 11.3, and 3.23 mmol N/kg BW/d; $P < 0.05$). ^{15}N enrichments in blood urea [(3.10, 4.46, and 4.89 atoms % excess (APE)] were higher than in ileal ammonia (0.45, 0.23, and 0.95 APE), suggesting rapid absorption of ammonia before the distal ileum and lack of uniformity for enrichment in the digesta ammonia pool. Simple isotope dilution calculations are, therefore, inappropriate for calculating FAAC. Assuming rapid absorption of ammonia and based on tracer kinetics, a 2 compartment model was developed with digesta ammonia and plasma urea as N pools and representing fluxes of FAAC, microbial AA synthesis, absorption and recycling of N, endogenous AA catabolism, and loss of N to the colon and urine, allowing for minimum and maximum estimates of FAAC in the upper gut. Maximum estimated FAAC was lower when dietary protein content was decreased (32.9, 33.5, and 17.4 mmol N/kg BW/d; $P < 0.05$) but there was no impact of dietary fiber on FAAC ($P > 0.05$). There are several challenges associated with quantifying FAAC in the upper gut of pigs. The 2-compartment model presented here allows for estimates of FAAC and further investigation to improve the model and estimates is warranted.

Key words: fermentative catabolism, amino acids, pigs

T183 Serum amino acid concentration and expression of amino acid transporter bo,+ in pigs fed diets with different protein and amino acid levels. H. García[1], A. Morales[1], A. B. Araiza[1], M. Cervantes*[1], J. Yáñez[2], and P. Carrillo[1], *[1]ICA, Universidad Autónoma de Baja California, Mexicali, BC, México, [2]Universidad Autónoma de Tlaxcala, Tlaxcala, Tlax, México.*

Cationic AA are mainly absorbed by the transporter protein bo,+, which exchanges Leu by cationic AA at the apical cell membrane. Lys is the first limiting AA in typical cereal-soybean meal diets that contain excess of Leu and Arg. Low protein diets may reduce the Leu and Arg excesses but become deficient in Lys. An experiment was conducted to analyze the effect of dietary protein level and supplementation of free Lys, Thr, Met, and Leu on the expression of the cationic AA transporter bo,+ and serum concentration (SC) of indispensable AA. Twenty crossbred pigs (BW of 14.9 ± 1.8 kg) were used. Treatments (T) were: T1, basal wheat-based diet; T2, as in T1 plus free 0.70% Lys, 0.27% Thr, and 0.10% Met; T3, as in T2 plus 0.80% Leu; and T4, wheat-soybean meal diet, 20.0% CP, 1.05% Lys, 0.75% Thr, control. At the end of a 28-d trial, all pigs were sacrificed; mucosa from jejunum and blood were collected to analyze expression of bo,+ and SC of AA. Four contrasts were constructed to analyze the effect of the protein level (basal vs. control), AA level (basal vs. free AA), and source of AA (protein-bound in control vs. free AA). Relative expression of bo,+ (arbitrary units, b0,+ mRNA Mol/18S rRNA Mol), was: 4.50, 20.79, 6.06, 0.49 for T1 to T4 respectively. Free AA in T2 increased the expression of bo,+ in jejunum, but Leu in T3 decreased it ($P < 0.05$). Serum AA concentration (μMol/ml) was: Arg, 0.08, 0.10, 0.16, 0.13; Ile, 0.03, 0.04, 0.01, 0.10; Leu, 0.04, 0.06, 0.11, 0.11; Lys, 0.01, 0.21, 0.12, 0.06; Met, 0.03, 0.04, 0.04, 0.08; Phe, 0.03, 0.05, 0.05, 0.06; Thr, 0.07, 0.26, 0.27, 0.12; Val, 0.07, 0.08, 0.09, 0.20, for T1 to T4, respectively. Supplemental Lys increased the SC of Lys; Leu increased the SC of Leu and Arg ($P < 0.05$). SC of Lys was higher ($P < 0.01$) in pigs fed the diet with free Lys than the protein-bound Lys diet. These data indicate that the dietary levels and source of protein and free AA affect the expression of cationic AA transporter and the cellular AA availability in growing pigs.

Key words: swine, amino acids, amino acid transporter

T184 Effect of dietary leucine and isoleucine on productive performance and myosin expression in growing pigs. V. Méndez[1], A. Morales*[1], M. Cervantes[1], B. A. Araiza[1], and M. A. Barrera[2], *[1]ICA, Universidad Autónoma de Baja California, Mexicali, B.C., México, [2]Universidad de Sonora, Hermosillo, Son., México.*

Branched chain AA, especially Leu, are recognized as activators of mTOR, which regulates protein synthesis in muscle cells; myosin is about 40% the total protein content in muscle. But, Leu also competes with Ile for absorption; high Leu in the diet may interfere with Ile for absorption. Thus, an experiment was conducted to evaluate the effect of adding Leu and Ile, above the NRC (1998) requirement, to wheat-based diets on the performance and the expression of myosin (Myo) mRNA in the Longissimus dorsi (LDM) and Semitendinosus (STM) muscles of growing pigs. The response variables were: ADG, ADFI, G:F, and expression of Myo. Twenty-four pigs, initial BW of 15.9 ± 0.6 kg, randomly distributed in 4 dietary treatments according to a randomized complete block design, were used. Treatments (T) were: T1, basal wheat-based diet fortified with 0.69% Lys, 0.27% Thr, 0.10% Met; T2, basal plus 0.50% Leu; T3, basal plus 0.50% Ile; T4, basal plus 0.50% Leu and 0.50% Ile. Pigs were sacrificed at the end of the experiment to collect samples from the LDM and the STM muscles. Performance of pigs, for T1 to T4 was: ADG, 541, 452, 447, 443, g/d; ADFI, 910, 970, 738, 733, g/d; G:F, 0.595, 0.466, 0.606, 0.604, respectively. ADG gain reduced because of the addition of Leu ($P = 0.032$), Ile ($P = 0.025$), or both ($P = 0.020$). ADFI and G:F were not affected by the individual or combined addition of any of these AA ($P > 0.10$). Relative expression values (arbitrary units) of Myo for pigs in T1 to T4 were: LDM, 1.8, 1.3, 6.9, 6.6; in STM, 16.0, 17.3, 2.2, 4.1. Relative expression of Myo in LDM increased because of Ile added alone or in combination with Leu ($P < 0.05$); but reduced in STM ($P < 0.01$). These results show that adding Leu and Ile, alone or in combination, to wheat-based diets, reduce growth rate and differently affect the expression of myosin in LDM and STM.

Key words: pigs, amino acids, myosin

T185 Preference for diets with free L-tryptophan in pigs with different tryptophan status. J. Suárez[1], E. Roura[2,3], I. Ipharraguerre*[2], and D. Torrallardona[1], *[1]IRTA-Mas de Bover, Constantí, Spain, [2]Lucta S.A., Barcelona, Spain, [3]Current address: University of Queensland, Brisbane, Australia.*

The chemosensorial system of pigs may have evolved to identify AA as indicators of protein in the feed, so the use of free AA could affect the palatability of the diet. A double choice test was conducted to determine the preference for diets with different free L-Trp levels in pigs under different Trp status. 108 piglets (18 ± 1.4 kg BW) were divided into 3 groups and adapted (1 wk) to diets that were either deficient (D), adequate (A) or excessive (E) in Trp (1.8, 2.4 or 3.0 g Trp/kg, respectively). After the period of adaptation, the animals were used in pairs to perform a series of double-choice tests (2 d) between diet D (taken as reference) and 3 diets with increasing levels of free L-Trp to provide Trp in excess (E1, E2 and E3; 3.0, 3.6 and 4.2 g Trp/kg, respectively). Diets only differed in their free L-Trp content, which was included at the expense of maize starch in the basal diet. For each double choice comparison and Trp status, a total of 6 observations were obtained. Preference for each tested diet was expressed as its proportional (%) contribution to total feed intake. Preference values were analyzed with ANOVA using the GLM procedure of SAS by considering the main effects of L-Trp level, Trp status, and their interaction. Additionally, each preference mean was compared with the neutral value of 50% (i.e., no difference between the reference and test diets) with the Student's *t*-test. No effects of pig's Trp status ($P = 0.924$), free L-Trp inclusion ($P = 0.995$) or their interaction ($P = 0.614$) on feed preference were observed. Overall, the addition of L-Trp resulted in a preference value of 41 ± 1.8%, which was lower ($P < 0.001$) than the neutral value of 50%. These results indicate that pigs have an aversion for the diets with free L-Trp. In conclusion, the addition of L-Trp decreases feed palatability in pigs, independently of its inclusion level and the Trp status of the animals.

Key words: palatability, double-choice, amino acid

T186 Effects of dietary inclusion of bioactive grape seed extract on protein and amino acid digestibility in broiler chicks. S. Chamorro[1], A. Viveros[2], C. Centeno[1], C. Romero*[3], I. Arija[2], and A. Brenes[1], *[1]Instituto de Ciencia y Tecnología de Alimentos y Nutrición, ICTAN, CSIC, Madrid, Spain, [2]Facultad de Veterinaria, Universidad Complutense de Madrid, Spain, [3]Escuela de Ingenieros Agrónomos, Universidad Politécnica de Madrid, Spain.*

Polyphenols are chemically and biologically active compounds. Grape seed extracts (GSE) have been widely used as a human food supplement for health promotion and disease prevention. However, there was little information regarding its application in animal nutrition. An experiment was conducted to investigate the effect of inclusion of GSE at levels of 0, 0.0025, 0.025, 0.25, and 0.50 g/kg in a wheat soybean basal diet on growth performance and apparent ileal digestibility (AID) of CP and AA at 21 d of age. Each treatment was randomly assigned to 7 replicates (5 birds/replicate). At 21 d-old, 15 birds/treatment were sacrificed, and ileal contents of 3 chicks from the same treatment were pooled (5 samples/treatment) to determine AID of CP and AA. Celite (10 g/kg) was added as an indigestible marker. Performance was not affected by dietary treatments except in the case of birds fed the highest GSE concentration which showed a reduction of body weight and G:F, by 5.7% ($P < 0.05$) and 5.1% ($P < 0.01$) respectively, compared with those fed the basal diet. Animals fed 0.0025 g/kg GSE diets had a higher protein AID than those fed basal diets (86.2 vs. 84.2%, $P < 0.005$). However, a reduction (from 84.2 to 82.2%, $P < 0.005$) in protein AID was observed in chicks fed 0.5 g/kg as compared with those fed the basal diet. Dietary supplementation with GSE increased the AID of arginine and alanine and reduced that of glutamic acid and histidine as compared with the basal diet. The addition of 0.025 g/kg GSE increased the AID of lysine, threonine, cystine, serine, and glycine. A further addition up to 0.5 g/kg GSE reduced the AID of methionine, leucine, isoleucine, valine, aspartic acid, phenylalanine, and proline. The results of this study indicated that dietary GSE addition up to 0.25 g/kg did not impair growth performance nor CP digestibility. Further inclusion worsened growth performance and the AID of CP and that of several AA.

Key words: apparent ileal digestibility, chicks, grape polyphenols

T187 Effect of levels of lysine and ractopamine on the performance of immunocastrated pigs from 97 to 124 kg. D. O. Fontes*[1], B. O. Rosa[1], U. A. D. Orlando[2], M. A. e Silva[1], and P. C. Silva[1], *[1]Department of Animal Science, Veterinary School of UFMG, Brazil, [2]BRF Foods, Brazil.*

This experiment was carried out to evaluate the effect of digestible Lys and ractopamine levels on the performance of immunocastrated pigs. A total of 240 pigs of a commercial line, with an initial BW of 97.72 ± 2.11 kg and final weight of 124.06 ± 4.12 kg were used in

a completely randomized experimental block design with 4 replications and 5 animals per experimental unit. The treatments consisted of a 4x3 factorial scheme, with 4 levels of digestible Lys (0.65, 0.80, 0.95, and 1.10%) and 3 levels of ractopamine (0, 5 and 10 ppm). Significant effect of digestible Lys was evaluated by the regression of the observed variable on digestible Lys level of diet while means of ractopamine supplemented animals were compared by SNK test at 5% probability level. No interaction effects of digestible Lys x ractopamine levels on the recorded variables were observed. The animals fed 10 ppm ractopamine supplemented diets were heavier at the end of the experiment (126.01 kg) than those fed non supplemented (122.25 kg) and 5 ppm supplemented diets (123.93 kg). The animals fed 10 ppm supplemented diets showed higher ($P < 0.05$) ADG (1.35 kg) in comparison to those fed non supplemented diets (1.17 kg) and 5 ppm ractopamine supplemented diets (1.25 kg). Animals fed 10 ppm supplemented diets showed an increase of 180 g in ADG, corresponding to an improvement of 13.33% in comparison to non supplement diet animal. No effects of ractopamine level ($P > 0.05$) on feed intake and on daily digestible Lys consumption were observed. The G:F of animals fed 10 ppm diets (0,384 kg/kg) and 5 ppm diets (0,362 kg/kg) were not different ($P < 0.05$), but bigger ($P < 0.05$) than no supplemented animals (0,331 kg/kg). No effects of digestible Lys ($P > 0.05$) on the performance traits were observed. The results suggest that 0.65% of digestible Lys (23.36 g/d) meets the requirement of immunocastrated pigs from 97 to 124 kg, and 5 and 10 ppm supplemented diets improve feed efficiency of pigs in 9.34 and 16%, respectively, in comparison to non supplemented animals.

Key words: swine, nutrition, additive

T188 Effect of L-tryptophan supplementation on hypothalamic serotonin level and aggression of nursery pigs fed diets varying large neutral amino acid concentrations. Y. B. Shen, G. Voilqué*, and S. W. Kim, *North Carolina State University, Raleigh.*

Cerebral serotonin has been shown as a controlling factor of aggressive behavior of pigs. Serotonin synthesis in the brain largely depends on availability of tryptophan (Trp), which has to compete with large neutral AA (LNAA) for LNAA transporter to cross the blood-brain barrier. The ratio between Trp and LNAA in diets would affect serotonin synthesis in the brain, which may affect aggression through changing Trp availability in brain. Thus, this study evaluated the effect of L-Trp supplementation on serotonin production and aggression of nursery pigs fed diets varying LNAA concentrations. Forty-eight barrows at 6 wk of age were housed individually and randomly allotted to 4 dietary treatments based on a 2x2 factorial arrangement (n = 12). First factor was L-Trp supplementation (0 or 0.6%) and the second factor was LNAA concentrations (4.5 or 3.8%). Pigs were fed the diets for 7 d. On d 4, pigs within a treatment were paired in a pen and their behavior was recorded for 1 d. On d 7, all pigs were euthanized to obtain hypothalamus. Supplementation of 0.6% L-Trp increased ($P < 0.01$) hypothalamic serotonin (99.2 vs. 66.1 ng/mg) and 5-hydroxyindoleacetic acid (896.6 vs. 599.3 ng/mg) in pigs. Supplementation of 0.6% L-Trp reduced the occurrence (1.17 vs. 0.33/hr), total duration (9.83 vs. 1.17 s), and average duration (5.50 vs. 1.17 s) of mutual biting when LNAA concentration was 4.5%. However, there were no changes in aggressive behavior of pigs by L-Trp supplementation when LNAA concentration was 3.8%. Both L-Trp supplementation and dietary LNAA concentrations did not affect the percentage of time that pigs spent on other physical activities such as lying, sitting, standing, eating, and drinking. Overall, L-Trp supplementation increased hypothalamic serotonin synthesis, which may have reduced duration, and the number of occurrence of mutual biting when LNAA concentration was increased from 3.8 to 4.5%.

Key words: pig, tryptophan, serotonin

T189 Importance of sampling diets on the precision of ME studies with swine. G. J. M. M. Lima*, L. C. Ajala, and C. M. Marques, *Embrapa, Brazil.*

Energy balance studies with swine provide data of high variability. The main sources for it are animals and feed. Most studies are done with number of replicates (barrows) per treatment varying from 4 to 12 to improve energy estimate. However, there are no references of how many feed samples should be collected and analyzed. Errors in feed mixing and feed analysis can affect ME estimation. This study was carried out to evaluate the error of determining ingredient ME considering just one feed sample. Therefore, 16 energy balance studies were carried out with 32 ingredients. A total of 384 barrows (50 kg wt, in average) were used. Pigs were kept in individual conventional metabolic cages. Each trial (24 barrows, progeny of the same boar) consisted of one basal diet and 3 test ingredients replacing part of the basal diet. Tested ingredients, number of different batches of each ingredient and inclusion levels in the basal diet were, respectively: poultry viscera and feather meal (VFM), 5 batches, 20%; dry yeast from sugarcane fermentation (DY), 4 batches, 30%; yellow corn (C), 21 batches, 30%; and heated whole soybeans (WSB), 2 batches, 10%. The adaptation period lasted 7 d, followed by 5 d of total collection of urine and feces, separated. Iron oxide was added to feed as marker. Five samples of each test diet were gathered during the collection period. Ingredient ME values were calculated using each individual analyzed feed sample. Based on each sample, estimated ME values for the same batch were different ($P < 0.0001$), regardless the ingredient. Range among batch ME (kcal/kg DM) varied from: 3925 to 4326 for VFM; 3369 to 3572 for DY, 3668 to 4287 for C and 3933 to 4334 for WSB. The difference between the smallest and largest ME estimate (kcal/kg DM), considering individual sampling from a single ingredient batch, reached up to 1811 for VFM, 529 for DY, 236 for C and 1116 for WSB. These results demonstrate the importance of repeating sampling of test diets and use their average value to improve precision of ME estimate of feed ingredients.

Key words: digestibility, feedstuffs, methodology

T190 Influence of dietary net energy concentration provided during the finishing period on carcass, meat and fat characteristics of heavy gilts. M. A. Latorre*[1,2], J. Suárez[1], M. A. Sanz[2], G. Ripoll[2], and M. Joy[2], *[1]Universidad de Zaragoza, Spain, [2]Centro de Investigación y Tecnología Agroalimentaria de Aragón, Zaragoza, Spain.*

A total of 60 Duroc × (Landrace × Large White) gilts were used to study the influence of increasing the energy concentration in diet during the finishing period on carcass, meat and fat characteristics. The experimental diets were based on barley, wheat, corn and soybean meal, contained 13.5% CP and 0.70% lysine and were provided from 100 to 130 kg BW. Pigs were slaughtered at heavy weight because were intended for dry-cured ham industry. There were 3 treatments with 3 NE levels; 2,280, 2,350, and 2,420 kcal NE/kg of feed. Therefore, the NE:lysine ratio was not constant in the experimental diets (CP was 13.5% in all cases and NE was increasing). Each treatment was replicated 4 times and the experimental unit was the pen constituted by 5 pigs allocated together. SAS package was used to analyze data statistically. The model included dietary treatment as main effect and the REG procedure was used on each trait to analyze the responses to diet. The increase of NE in the diet did not modified ($P > 0.05$) pH or carcass or ham size but decreased carcass weight ($P < 0.01$) and carcass yield ($P < 0.05$) and tended to increase ($P < 0.10$) the fat thickness between the third and forth last ribs and at the gluteus medius muscle level. The increase of NE content in diet decreased ($P < 0.01$) the yield of main trimmed lean cuts (shoulder+ham+loin+sirloin) in carcass due to a decrease ($P < 0.01$) of the ham yield. Meat characteristics were not affected by dietary treatment ($P > 0.05$). Also, only some fatty acids were modified ($P < 0.001$) by NE content in diet decreasing as NE increased; C20:0, C21:0, C22:0 and C20:4. We can conclude that the effect of increasing the NE in diet provided during the finishing period on carcass, meat and fat quality of pigs were scarce. However, an increase of NE content from 2,280 to 2,350 kcal/kg might be interesting in the case of pigs intended for dry-cured products when a minimum carcass fat thickness is a criterion to select the carcasses.

Key words: dietary net energy, carcass and meat quality, pigs

T191 Metabolizable energy and digestibility of carbohydrates in cereal grains fed to growing pigs. S. K. Cervantes-Pahm* and H. H. Stein, *University of Illinois, Urbana.*

The objective of the experiment was to measure the ME and the apparent ileal (AID) and the apparent total tract (ATTD) digestibility of carbohydrates (CHO) and total dietary fiber (TDF) in 8 cereal grains. The 8 cereal grains were yellow dent corn (YD), NutriDense corn (ND), de-hulled barley, de-hulled oats, polished rice, rye, sorghum, and wheat. Each cereal grain was included in 1 diet and titanium dioxide (0.5% was included in each diet as an indigestible marker. Twenty-four ileally cannulated pigs (BW = 30.7 ± 3.2 kg) were randomly allotted to the 8 diets in a completely randomized design. Pigs were fed experimental diets during 3 14-d periods. In each period, 3 pigs were fed each diet for a total of 9 observations per diet and no pig was fed any diet more than once. Pigs were placed in metabolism cages and fecal samples were collected quantitatively from d 6 to 11 and ileal samples were collected on d 13 and 14 of each period. Results of the experiment indicated that ME in de-hulled oats was greater ($P < 0.01$) than in ND, barley, and rice. The ME in sorghum was not different from the ME in YD and rye. The AID of CHO was greatest ($P < 0.01$) in polished rice and least ($P < 0.01$) in sorghum. The ATTD of CHO in rice was greater ($P < 0.01$) than in all other grains and the ATTD of CHO in wheat was least ($P < 0.01$) among the grains. The AID of TDF in YD, ND, de-hulled barley, and rye were not different, but were greater ($P < 0.01$) than in de-hulled oats and rice. The AID of TDF in de-hulled barley was also greater ($P < 0.01$) than in sorghum and wheat. The ATTD of TDF was less ($P < 0.01$) in polished rice than in all other cereal grains, but no differences among the other grains were observed. In conclusion, rice had the greatest ATTD of CHO, but de-hulled oats had the greatest ME among all cereal grains.

Table 1. ME and digestibility of carbohydrates in cereal grains

Item	ME, kcal/kg	AID CHO	AID, TDF	ATTD, CHO	ATTD, TDF
YD	3,443^{bc}	81.4^{cd}	12.1^{ab}	95.3^{bc}	54.7^{a}
ND	3,507^{b}	88.0^{b}	10.4^{ab}	94.5^{c}	50.4^{a}
Barley, DH	3,504^{b}	80.3^{cd}	24.0^{a}	95.6^{bc}	44.6^{a}
Oats, DH	3,661^{a}	83.6^{c}	−70.5^{e}	96.8^{b}	13.3^{a}
Rice	3,513^{b}	96.8^{a}	−6.3^{d}	98.4^{a}	−55.8^{b}
Rye	3,327^{d}	75.8^{e}	10.8^{abc}	94.8^{c}	62.8^{a}
Sorghum	3,388^{cd}	66.5^{f}	5.8^{bcd}	91.8^{d}	33.0^{a}
Wheat	3,471^{b}	78.8^{de}	−5.0^{cd}	89.8^{e}	27.3^{a}
SEM	31	1.2	4.9	0.6	25.6
P-value	0.001	0.001	0.001	0.001	0.01

CHO was calculated as DM − (CP + crude fat + ash).

Key words: carbohydrates, cereal grains, energy

T192 Nutritional value of acerola meal for broiler chickens. L. H. Zanetti*[1], V. C. da Cruz[1], G. do Valle Polycarpo[2], A. C. Pezzato[2], J. R. Sartori[2], V. B. Fascina[2], R. F. de Oliveira[1], A. L. C. Brichi[1], M. L. Poiatti[1], O. J. Sabbag[1], F. Vercese[2], and F. B. de Carvalho[2], *[1]São Paulo State University, Dracena Campus, Dracena, São Paulo, Brazil, [2]São Paulo State University, Botucatu Campus, Botucatu, São Paulo, Brazil.*

This study was carried out at the experimental aviary of the Sao Paulo State University, Botucatu Campus, Brazil. A metabolism assay with 100 8- to 16-d-old male Cobb broiler chicks was carried out using the method of total excreta collection. The birds were stored in 20 cages that were previously adapted with plastic covered trays to collect excreta. The experimental design was entirely random with 4 treatments and 5 replications of 5 birds per experimental unit. Acerola meal (AM) was substituted at 10, 15 and 20% of reference feed formulated with corn and soybean meal. The GE values were obtained using a colorimetric pump of 4.143 kcal/kg, and from these results the apparent ME (AME) was calculated and apparent corrected by the nitrogen balance (AMEn) of AM. The bromatological analyses determined the DM, CP, ether extract (EE), mineral matter (MM), crude fiber (CF), NDF, and ADF. The values of AME and AMEn decreased linearly ($P < 0.05$) as AM addition to the diet increased (AME = 1,215.88 – 24.37x; $R^2 = 0.33$ and AMEn = 1,313.72 – 31.86x; $R^2 = 0.35$). The recommended value of AME and AMEn for the use of AM in the nutritional matrix of broiler chickens′ feed was the one of the treatment with 20% AM addition, corroborating the literature where the greater the feed ratio in the reference feed, the more precise its determination is. The values of AME and AMEn decrease as the AM additions increase. It can be inferred that the values of AME and AMEn for AM are 754 kcal/kg and 756 kcal/kg, respectively. The results of the chemical and bromatological composition of AM used in the experiment for the other analyses were: 89.15% (DM), 8.36% (CP), 4.57% (EE), 3.19% (MM), 46.27% (CF), 50.86% (NDF), and 41.33% (ADF).

Key words: bromatological composition, industrial by-product, metabolism

T193 Concentration of DE and ME in fermented soybean meal, conventional soybean meal, and fish meal fed to weanling pigs. O. J. Rojas* and H. H. Stein, *University of Illinois, Urbana.*

An experiment was conducted to measure the concentration of DE and ME in US-produced fermented soybean meal (FSBM), conventional soybean meal (SBM-CV), and fish meal fed to weanling pigs. A corn-based diet consisting of 96.4% corn was formulated. Three additional diets were formulated containing corn and each of the experimental ingredients (FSBM, SBM-CV, and fish meal, respectively.) Thirty-six growing barrows (initial BW: 22.0 ± 3.85 kg) were placed in metabolism cages and allotted to a randomized complete block design with 4 diets and 9 pigs per diet. Feces and urine were collected for 5 d after a 5 d adaptation period. The ATTD and concentrations of DE and ME were calculated in fish meal and the 2 soybean meals using the difference procedure. Results indicated that the ATTD of energy in SBM-CV was 91.1% which was greater ($P < 0.001$) than in corn (88.0%) and fish meal (84.1%), and the ATTD of energy in FSBM (89.4%) was greater ($P < 0.001$) than in fish meal. The concentrations of DE and ME in SBM-CV were 4,608 and 4,144 kcal/kg DM, which was greater ($P < 0.001$) than the DE and ME in FSBM (4,223 and 3,678 kcal/kg DM, respectively), corn (3,921 and 3,768 kcal/kg DM, respectively), and fish meal (3,819 and 3,361 kcal/kg DM, respectively). However, FSBM contained more ($P < 0.001$) DE than corn and fish meal and more ($P < 0.001$) ME than fish meal. In conclusion, the concentration of DE and ME are less in FSBM than in SBM-CV. However, DE and ME are greater in FSBM than in fish meal.

Key words: energy, fermented soybean meal, soybean meal

T194 The effect of n-3 fatty acid supplementation on growth performance, nutrient digestibility, blood profiles, meat quality and lean and adipose tissue fatty acid profiles in finishing pigs. J. P. Wang*, B. U. Yang, and I. H. Kim, *Dankook University, Cheonan, Choongnam, South Korea.*

This study was conducted to evaluate the effect of dietary n-3 fatty acid supplementation on growth performance, nutrient digestibility, blood profiles, meat quality and fatty acid profiles of lean and adipose tissue in finishing pigs. A total of 150 crossbred barrows (initial BW = 55.7 ± 1.4 kg) were randomly allotted into 1 of 3 treatments by their BW and litters (10 replicate pens per treatment, 5 pigs per pen). The 3 treatments were corn-soybean diet with 0% (CON), 1.5% (T1), and 3% (T2) of unrefined tuna oil at the cost of corn, and the diet were isolysinic and isocaloric by manipulation of soybean meal and fat source (soy oil). The trial lasted 12-wk, and the pigs were killed to measure the carcass characteristics at the end of experiment. Data were subjected to the GLM procedure of SAS. During the entire experiment, none of the tuna oil treatments had effects on growth performance and apparent total tract nutrient digestibility (ATTD) of DM, nitrogen and energy. No differences were shown on the blood total cholesterol, high density lipoprotein cholesterol (HDL), low density lipoprotein cholesterol (LDL), and triglycerides among treatments in this experiment. The pigs in T2 treatment had lower loin muscle area than CON treatment (45.91 vs. 51.46 cm^2, $P < 0.05$). Water holding capacity (WHC), ultimate (24 h) pH value, as well as backfat thickness were not different between treatments. There was a decrease ($P < 0.05$) in palmitric acid (T1:24.99, T2:25.27 vs. CON:26.26%) in lean tissue, whereas n-6 fatty acids (T1:2.73, T2:3.03 vs. CON:3.15%) largely decreased ($P < 0.05$). Dietary supplementation of tuna oil (at 3%) feeding resulted in a lower docosahexaenoic acid concentration, and total n-3 fatty acid contents in adipose tissue ($P < 0.05$). These results show that the inclusion of tuna oil (rich in n-3 fatty acids) had no negative effects on growth performance and the n-3 fatty acids ingested can be deposited in lean and adipose tissue in fattening pigs.

Key words: finishing pig, meat quality, n-3 fatty acid

T195 The granulated barley provided during growing or finishing period improves the major fatty acid composition in the intramuscular fat of longissimus dorsi muscle and of dry-cured ham from 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 BW were used to study the effect of diet on fatty acid profile of intramuscular fat (IMF) of longissimus dorsi muscle (LD) and of dry-cured ham after 18 mo of ripening. Experimental diets were provided ad libitum according to the following treatments: i) control diet with 3,210 kcal ME/kg, 13.7% CP and 0.62% digestible Lys from 45.6 to 127.8 kg BW (group C), ii) 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 control diet from 93.1 to 135.1 kg BW (group GB+C). Each treatment was replicated 8 times with 2 gilts per replicate. Data were analyzed by ANOVA using SAS. The model included dietary treatment as main effect. The LD from C+GB gilts had 18% higher ($P < 0.05$) C18:1n-9 and MUFA than that from C gilts, whereas the C18:2n-6 and PUFA were lower in the LD from C+GB gilts than in that from C or GB+C gilts (8.2 vs 12.7 and 10.2; 9.7 vs 15.0 and 9.7; $P < 0.05$). The C16:0 was lower in LD from GB+C gilts than in that from C+GB (4%) or C (5%) gilts, and SFA was 4.7% lower ($P < 0.05$) in BG+C than in C gilts. A relation adjusted to a quadratic function between IMF percentage and C18:1n-9 proportion in LD was observed: C18:1n-9 = 25.75 + 6.64 IMF – 0.56 x IMF^2 ($R^2 = 0.78$, RSD = 1.24, $P < 0.001$). The diet had no effect ($P > 0.05$) on C16:0, C18:0 and SFA of IMF from hams. However, hams from C+GB and GB+C gilts had ($P < 0.05$) higher C18:1n-9 (37.9, 40.9 and 40.0%) and lower C18:2n-6 (13.2, 10.8 and 10.8%) and PUFA (17.1, 14.4 and 14.1) than those from C gilts. The MUFA was 8.4% higher in hams from C+GB gilts than in those from C gilts, but no differences were detected ($P > 0.05$) when hams from C and GB+C and from C+GB and GB+C gilts were compared. It is concluded that granulated barley given during growing or finishing periods to heavy gilts improved the major fatty acids profile in the IMF of LD and of dry-cured ham of heavy pigs.

Key words: barley, fatty acid composition, heavy pigs

T196 Sulfur addition in corn-soybean meal diets reduced nursery pig performance. V. G. Perez*, H. Yang, T. R. Radke, and D. P. Holzgraefe, *ADM Alliance Nutrition Inc., Quincy, IL.*

Dietary sulfur (S) from distillers dried grains has been suggested to be detrimental for pig growth. The objective of this study was to determine the effect of increasing concentrations of dietary S on pig performance. Corn-soybean meal-based diets were used to differentiate any S effect from distillers dried grains. The experiment was a randomized complete block design; blocks were 4 categories of initial BW. Treatments were the inclusion of dietary S at 0.0, 0.2, 0.4, or 0.6% of the diet. Each treatment was replicated with 8 pens of 4 pigs per pen. Polynomial contrasts were used to determine linear and quadratic effects of dietary S addition. Sources of added S were sodium bisulfate ($NaHSO_4$) and calcium sulfate ($CaSO_4 \cdot 2H_2O$); both were provided in equal amounts. The Na and Ca from these compounds replaced dietary salt and limestone, respectively. All diets were formulated to provide similar amounts of ME, CP, Ca, available P, and digestible Lys within feeding phase. Two feeding phases were used for 14 and 21 d, respectively. Pigs were weaned at about 21 d of age and the experiment started 2 wk after weaning. The treatment with 0.0% added S had the lowest concentration of analyzed dietary S, with 0.25 and 0.24% S in feeding phases 1 and 2, respectively. Pig growth and feed efficiency were reduced ($P < 0.05$) proportionally to the inclusion of dietary S (Table 1). Feed intake followed a similar pattern of response to dietary S on the overall period. The larger reduction in ADG was observed between treatments with 0.0 vs. 0.2% added S, which can explain the quadratic effect observed in G:F. Increasing concentrations of added S up to 0.6% of the diet, proportionally decreased pig performance.

Table 1. Dietary sulfur addition and pig performance

Item	0.0% S	0.2% S	0.4% S	0.6% S	SEM
Initial BW, kg	9.63	9.65	9.65	9.66	0.03
Days 1-14					
ADG, g/d[a]	593	564	538	536	15
ADFI, g/d	771	762	751	745	20
G:F, g/kg[a,b]	770	741	716	722	8
Days 1-35					
ADG, g/d[a]	759	733	716	697	11
ADFI, g/d[c]	1,170	1,163	1,147	1,118	17
G:F, g/kg[a]	649	631	626	624	6

[a]Sulfur linear, $P < 0.01$; [b]Sulfur quadratic, $P < 0.05$; [c]Sulfur linear, $P < 0.05$.

Key words: sulfur, nursery, pigs

T197 The effect of Kapok seed meal supplementation on growth performance, nutrient digestibility, blood characteristics, meat quality, and fatty acids profile in finishing pigs. H. J. Kim*, T. X. Zhou, and I. H. Kim, *Dankook University, Cheonan, Choongnam, South Korea.*

This study was conducted to evaluate the effect of Kapok seed meal supplementation on growth performance, nutrient digestibility, blood characteristics, meat quality, and fatty acids profile in finishing pigs. A total of 96 finishing pigs [(Landrace × Yorkshire) × Duroc] with an average initial BW of 67.0 ± 1.5 kg were used in a 10 wk trial. Pigs were allotted to 1 of 3 dietary treatments with 8 replicate pens per treatment and 4 pigs per pen. The treatments included: 1) CON (basal diet), 2) K1.5 (basal diet + 1.5% Kapok) and 3) K3.0 (basal diet + 3.0% Kapok). Data were subjected to the GLM procedure of SAS. Differences among treatments were evaluated by Duncan multiple test. Growth performance was unaffected. Apparent total tract digestibility (ATTD) of DM and N was lower (74.15 vs. 77.68, 73.76 vs. 78.71%; $P < 0.05$) in K3.0 treatment than in CON treatment. At the end of the experiment, K1.5 and K3.0 diets had higher low density lipoprotein (LDL) cholesterol concentrations than CON diet (53.25 vs. 42.50; $P < 0.05$). Redness (a*) of pigs fed K3.0 diet was greater than that of CON diet (18.85 vs. 17.82; $P < 0.05$). Marbling score was higher in K3.0 treatment than that in CON treatment (2.2 vs. 1.9; $P < 0.05$). Total SFA of pigs fed K3.0 diets were greater than those of pigs fed CON diet (57.37 vs. 38.01%; $P < 0.05$) in adipose tissue. Palmitoleic acid, and oleic acid in K1.5 and K3.0 treatments were lower than CON treatment (1.49 vs. 2.35%; $P < 0.05$) in adipose tissue and lean. Stearic acid in K1.5 and K3.0 diets was increased compared with CON diet (24.67 vs. 13.24%; $P < 0.05$). In lean, pigs fed K3.0 diets had a greater stearic acid than that of pigs fed CON and K1.5 diets (22.34 vs. 14.25, 16.63%; $P < 0.05$). However, no significant differences were

observed on myristic acid, palmitic acid, linoleic acid, linolenic acid, SFA, PUFA, and SFA/PUFA in this study. In conclusion, kapok seed meal can improve meat quality but decrease nutrient digestibility and unsaturated fatty acid (UFA) in adipose tissue of finishing pigs.

Key words: fatty acids, finishing pigs, Kapok

T198 Performance of 1-d-old to 42-d-old broiler chicks fed with increasing levels of acerola meal replacing corn in diet. V. C. da Cruz*[1], L. H. Zanetti[1], G. do Valle Polycarpo[2], R. F. de Oliveira[1], A. L. C. Brichi[1], D. D. Millen[1], L. C. Carvalho[1], D. O. dos Santos Gomes[1], O. J. Sabbag[1], and M. L. Poiatti[1], *[1]São Paulo State University, Dracena Campus, Dracena, São Paulo, Brazil, [2]São Paulo State University, Botucatu Campus, Botucatu, São Paulo, Brazil.*

This study, carried out at the São Paulo State University, Campus of Dracena, Brazil, aimed to evaluate the performance of 1 to 42-d-old broilers fed with different additions of acerola meal (AM) replacing corn (C) in the diet. Nine hundred eighty 1-d-old male Cobb chicks were housed with an initial density of 14 chickens/m^2. The experiment had a completely randomized design, 4 treatments: T0- basal diet - without addition of AM, T5- addition of 5% AM replacing C, T10- addition of 10% AM replacing C, T15- addition of 15% AM replacing C, and 7 replications with 35 birds each. At 42 d, a significant difference ($P < 0.05$) was observed in the final BW, ADG and G:F of chickens by regression analysis. Final BW and ADG decreased linearly with the addition of AM in diet (BW = - 8.7780x+2210.78; ADG = −0.2090x+51.5772). The G:F of birds, obtained from the gain-to-feed ratio, increased linearly with the addition of AM percentage in diets (G:F = 0.0038x +1.6784). Therefore, the AM effects on the body weight of the birds influenced the G:F. This situation was more evident in treatments with greater amounts of AM, which resulted in worse G:F. The ADFI was not influenced by the treatments ($P > 0.05$), corroborating previous research that evaluated byproducts in broilers' diets. Since the diets were isocaloric, it can be inferred that ADFI was not affected by the AM addition, because birds primarily satisfy their energy needs, except when there is a limitation in the capacity of digestive tract. This seems to have been primordial in the initial phase, but it could not be applied to the entire breeding period due to the development of the birds′ digestive tract. In this period, no difference ($P > 0.05$) among the treatments was observed for the production efficiency index (PEI). The AM addition becomes interesting at 5% without affecting the broilers′ performance. When analyzing the PEI, addition of 15% is still advantageous because it allows a smaller addition of corn.

Key words: poultry, residue byproducts

T199 Inclusion of acerola meal replacing corn in the diet of broilers of 1-d-old to 21-d-old. L. H. Zanetti*[1], V. C. da Cruz[1], G. do Valle Polycarpo[2], R. F. de Oliveira[1], A. L. C. Brichi[1], D. D. Millen[1], V. B. Fascina[2], M. L. Poiatti[1], and O. J. Sabbag[1], *[1]São Paulo State University, Dracena Campus, Dracena, São Paulo, Brazil, [2]São Paulo State University, Botucatu Campus, Botucatu, São Paulo, Brazil.*

This work, carried out at the São Paulo State University, Dracena Campus, Brazil, aimed to evaluate different levels of inclusion of acerola meal (AM) replacing corn (C) on the performance of broiler chickens during the initial phase (1 to 21-d-old). 980 1-d-old male Cobb chicks were housed with an initial density of 14 chickens/m^2. The experiment had completely randomized design, 4 treatments: T0- basal diet - without addition of AM, T5- addition of 5% AM replacing C, T10- addition of 10% AM replacing C, T15- addition of 15% AM replacing C, and 7 replications with 35 birds each. Throughout the experimental period, water and feed were provided ad libitum. The statistical analysis of data was done by ANOVA, and when the treatment effect was positive, it was unfolded by polynomial regression analysis. At 21 d old, the chickens were weighed to evaluate performance. It was observed that the addition of AM replacing C in the diets influenced ($P < 0.05$) G:F and ADFI, the latter having a linear reduction (ADFI = 3.1811x + 1091.19, $P < 0.01$) with the inclusion of AM in diet, which may be justified by the crude fiber level (43.34%) in this byproduct, which can decrease the density of the diet. The inclusion of AM exerted a quadratic effect on G:F (G:$F = 0.0004x^2 - 0.0082x + 1.4061$, $P < 0.05$), demonstrating that this variable was more efficient in the treatment with 5% of MA replacing C in diet, and from this point, G:F of chickens tends to worsen, showing undesirable results with higher inclusions. Otherwise, final BW, ADG and viability were not affected by the addition of AM ($P > 0.05$). For the phase (1–21-d), the different levels of AM inclusion replacing C does not interfere on broiler performance, which shows that the AM inclusion can be made up to 15% without causing damage to group.

Key words: animal feeding, industrial by-product, poultry

T200 Fatty acid content and sensory evaluation of trimmed loins as influenced by timing of feeding flaxseed or fish oil to pigs. H. R. Martínez-Ramírez*[1], L. M. Pivotto[1], I. B. Mandell[1], J. K. G. Kramer[2], and C. F. M. de Lange[1], *[1]Centre for Nutritional Modelling, Department of Animal and Poultry Science, University of Guelph, Guelph, ON, Canada, [2]Agriculture and Agri-Food Canada, Guelph, ON, Canada.*

Pork containing n-3 fatty acids (FA) can provide health benefits to consumers. The effect of timing of feeding n-3 FA from ground flaxseed (FS) or fish oil (FO) to pigs on the FA content and sensory evaluation of trimmed loins (Loin) was investigated. Either FS or FO was included in corn based diets and fed continuously (treatments FSC and FOC, 25 to 120 kg BW), only during the growing phase (FSG and FOG, 25 to 65 kg BW), or only during the finishing phase (FSF and FOF, 85 to 120 kg BW). The 7th treatment, a diet free of FS and FO served as control (CON). At 25 kg BW, 4 barrows and 4 gilts (Landrace × Yorkshire × Duroc) were assigned to treatments. Pigs were fed ad libitum and feed intake was recorded per pig. Cumulative intake of FS was similar for FSG, FSF, and FSC ($P > 0.10$; 6.8, 7.2, 7.2 kg/pig, respectively), whereas intake of FO was similar for FOG, FOF, and FOC ($P > 0.10$; 2.0, 2.0, 2.2 kg/pig, respectively). Growth performance and measures of Loin meat quality (color, drip loss, 24 h pH) were not influenced by dietary treatments ($P > 0.10$). In terms of FA content (mg/100 g fresh Loin), α-linolenic acid (ALA) was independent of FS feeding regimen ($P > 0.10$; 274, 237, 187 for FSG, FSF, and FSC, respectively), and higher ($P < 0.01$) than the other treatments (40.1, 38.6, 63.0, and 30.5 for FOG, FOF, FOC and CON, respectively). Content of highly unsaturated n-3 FA (sum of n-3 FA minus ALA) was independent of FO feeding regimen ($P > 0.10$; 122, 138, and 129 for FOG, FOF, and FOC, respectively), higher ($P < 0.01$) than FS (102, 66.8 and 77.4, for FSG, FSF and FSC, respectively); and lowest for CON (32.2; $P < 0.05$). Based on a trained taste panel analysis, off-flavor ratings were higher for FOF than FSC ($P < 0.05$; 1.47 vs. 0.54); whereas ratings were similar for FSG, FSF, FOG, FOC, and CON ($P > 0.10$; 1.10, 0.95, 1.27, 1.30, and 0.91). These results indicate that enrichment of n-3 FA in Loin appears independent of timing of when n-3 FA containing diets are fed during pig development, and that feeding FO in the pre-slaughter diet may reduce consumer acceptance of pork.

Key words: pig growth, n-3 fatty acid, pigs

Nonruminant Nutrition: Gastrointestinal Physiology

T201 Intestinal short-chain fatty acid sensors, FFA2 and FFA3, and control of food intake. M. Al-Rammahi*, K. Daly, A. Moran, and S. Shirazi-Beechey, *University of Liverpool, Liverpool, UK.*

Dietary fiber and resistant starch are fermented by colonic microbiota to short-chain fatty acids (SCFA), acetate, propionate and butyrate. SCFA are known to have variety of physiological effects on gastrointestinal function. However, until recently little was known about the mechanism by which lumenal SCFA are sensed by colonic epithelial cells. Two orphan human G protein-coupled receptors, free fatty acid receptor 3 (FFA3; formerly GPR41) and free fatty acid receptor 2 (FFA2; formerly GPR43), have been cloned and demonstrated to be sensors for SCFA. It has been reported that, in response to dietary fiber, the large intestine secretes gut hormones such as glucagon-like peptide 1 (GLP-1) and peptide YY (PYY), which control appetite and food intake, and SCFA have been implicated in this effect. Here we report, using qPCR, that FFA3 and FFA2 are expressed in human and pig colon with FFA2 having higher expression. Using immunohistochemistry, we show that FFA2 and FFA3 proteins are solely expressed in enteroendocrine L- and enterochromaffin cells of pig and human colon and not on the luminal membrane of colonic absorptive epithelial cells or intra-cellularly as shown by Karaki et al. (2006, 2008). Furthermore we show that FFA2 and FFA3 are co-expressed in endocrine cells containing, GLP1, PYY and serotonin. In addition, using GluTag cells, a murine enteroendocrine L-cell model, we show that these cells express FFA2 and FFA3 and that they secrete GLP-1 in response to either 10 mM butyrate or 10 μM chloro-α-(1-methylethyl)-N-2-thiazolylbenzeneacetamide (4-CMTB), a specific activator of FFA2.

Key words: dietary fiber, food intake, nutrient sensing

T202 Gene expression of the L-amino acid–sensing receptor T1R1/T1R3 changes in gut tissues of pigs in response to dietary protein. G. Tedo[1], E. Roura[1,3], I. Ipharraguerre*[1], and X. Manteca[2], *[1]Lucta SA, Feed Additives Division, Montornes del Vallés, Barcelona, Spain, [2]Autonomous University of Barcelona, Bellaterra, Barcelona, Spain, [3]Current address: University of Queensland, Brisbane, Australia.*

We have shown that the porcine umami taste receptor T1R1/T1R3 is present in pig′s gut and its mRNA abundance increases in the small intestine after weaning. The aim of this study was to determine if the expression of the pT1r1/pT1r3 genes in taste and gut tissues changes in response to variation in the content of dietary CP and essential AA (EAA). Forty-eight Pietrain x Landrace piglets were used from weaning (26 d of age) to 20 d after weaning. Piglets were allotted to 3 dietary treatments (16 piglets/treatment): high CP diet (HCP, 24%CP, 15 g/kg of Lys), low CP diet (LCP, 17%CP, 9 g/kg of Lys) and LCP diet supplemented with all EAA (SAA, 17%CP, 15 g/kg of Lys). Four animals per treatment were sacrificed on d 20 after weaning to collect tissue samples of fungiform and circumvallate papillae (TC), stomach (S), liver (L), duodenum (D) and ileum (I). Remaining piglets (12 pigs/treament) were used to monitor animal performance. The relative abundance of mRNA of the pT1r1 and pT1r3 genes was quantified via real-time PCR using the tata box binding protein as housekeeping gene. Real-time data were analyzed using the GEE model with an exchangeable correlation structure and the GENMOD procedure of SAS. Fold change estimations were performed for sex, diet, tissue and their interaction relative to liver and the HCP group. The expression of the pT1r1 gene was upregulated ($P < 0.05$) in S (3-fold), D (22.6-fold) and I (7.9-fold) of the LCP group, whereas the expression of the pT1r3 gene was upregulated ($P < 0.05$) in TC (1.7-fold), S (2.8-fold) and D (1.6-fold) of the SAA group and tended ($P < 0.06$) to increase in D (2-fold) and I (3.2-fold) of the LCP group. In summary, the expression of the porcine umami taste receptor genes mainly responded to changes in CP intake. Interestingly, supplementing the LCP diet with essential AA to meet piglet′s requirement tended to prevent such a response in the pT1r1 gene. Taken together, these observations suggest that the porcine umami taste receptor plays a role in sensing the enteral supply of protein.

Key words: gut sensing, amino acids, umami taste receptors

T203 Gene expression of the porcine sweet taste receptor in tongue and gut tissues changes after weaning. G. Tedo[1], X. Manteca[2], I. Ipharraguerre*[1], M. Reina[3], D. Torrallardona[4], and E. Roura[1,5], *[1]Lucta SA, Feed Additives Division, Montornes del Valles, Barcelona, Spain, [2]Autonomous University of Barcelona, Veterinary School, Bellaterra, Barcelona, Spain, [3]University of Barcelona Cell Biology Dpt., Celltec-UB, Barcelona, Spain, [4]IRTA -Mas de Bover, Constanti, Tarragona, Spain, [5]Current address: University of Queensland, Brisbane, Australia.*

Sugars and artificial sweeteners are sensed by the sweet taste receptor T1R2/T1R3 present in taste buds. Recent studies in rodents showed that this receptor is also present in the gut forming part of the mucosal chemosensing system by which luminal glucose and other chemicals are sensed to trigger gut physiological responses. The aim of this study was to investigate the expression and changes during development of the porcine T1r2 and T1r3 genes in taste and gastrointestinal tissues of pigs. Fifty-six Pietrain x Landrace piglets were selected at birth and fed standard diets from weaning until 46 d of age. On d 0 (birth), 26 (weaning), 28 (48h after weaning), and 46 from birth, 4 piglets (2 of each sex) were sacrificed to collect tissue samples of fungiform and circumvallate papillae (TC), stomach (S), liver (L), duodenum (D), jejunum (J), and ileum (I). Remaining piglets (40) were used to monitor animal performance. The relative abundance of mRNA of the pT1r2 and pT1r3 genes was quantified via real-time PCR using the tata box binding protein as housekeeping gene. Real–time data (Ct values) were analyzed using the GEE model with an exchangeable correlation structure and the GENMOD procedure of SAS. Fold change estimations ($2^{-\Delta\Delta Ct}$) were performed for sex, age, tissue and their interaction relative to liver and the weaning group (d 26). Both genes were expressed ($P < 0.05$) in all tissues at all ages and the interaction between age and tissue for the expression of the pT1r2 gene tended to be significant ($P < 0.07$). On d 46, the expression of pT1r2 was upregulated ($P < 0.05$) in TC (4.7-fold), D (11.1-fold), and I (17.4-fold), but downregulated in L (0.14-fold). In conclusion, the receptor T1R2/T1R3 is present in taste buds and gastrointestinal tract of pigs and its expression changes remarkably after weaning.

Key words: sweet taste receptor, pig, weaning

T204 Evaluation of seaweed-derived polysaccharides on indices of gastrointestinal fermentation and selected populations of microbiota in newly weaned pigs challenged with *Salmonella* Typhimurium. S. Dillon[1], J. Fanning[2], T. Sweeney[1], J. Egan[2], C. J. O'Shea[1], M. Gutierrez[2], C. Mannion[2], F. Leonard[1], and J. V. O'Doherty*[1], *[1]University College Dublin, Dublin, Ireland, [2]Cen-*

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Growing pigs encounter multiple stressors in the immediate post-weaning period, and become vulnerable to infection by microbial pathogens such as *Salmonella*. An experiment was conducted to investigate the effects of offering diets containing seaweed-derived laminarin or fucoidan on numbers of *Salmonella* Typhimurium in the distal gastrointestinal tract (GIT), in select tissue locations, and in fecal matter of pigs experimentally challenged with *Salmonella* Typhimurium. Twenty-four individually penned entire male pigs (n = 6), weaned at 24 d (7.9 kg) were assigned (d 0 to 32) to 1 of 4 dietary treatments: T1) basal diet (control); T2) basal diet + a commercial admixture containing organic acids and herbs (positive control; 3.6g/kg); T3) basal diet + laminarin (300 mg/kg); (T4) basal diet + fucoidan (240 mg/kg). Sampling of fecal matter was carried out periodically during the experiment and GIT contents and tissue samples were collected post-sacrifice (d 32). Consumption of diets containing fucoidan increased counts of lactobacilli in the cecum ($P < 0.05$) and the molar proportion of butyric acid in the cecum ($P < 0.05$) and colon ($P < 0.05$) and decreased the molar proportion of valeric acid in the cecum ($P < 0.05$) and colon ($P < 0.01$). However, fecal counts of *Salmonella* Typhimurium increased on d 2 ($P < 0.05$) and d 14 ($P < 0.05$) post-challenge (PC) of pigs offered fucoidan, and on d 14 ($P < 0.05$) and d 20 ($P < 0.05$) PC of pigs offered laminarin ($P < 0.05$) compared with the control. Diets containing the commercial admixture increased lactobacilli ($P < 0.05$) and butyric acid ($P < 0.05$) in the cecum and decreased counts of *Salmonella* Typhimurium ($P < 0.001$) in tonsil tissue. In conclusion, consumption of diets containing fucoidan induced increases in lactobacilli in the cecum, and butyric acid in the cecum and colon, however both laminarin and fucoidan increased shedding of fecal *Salmonella* Typhimurium at select sampling periods of the experimental study.

Key words: *Salmonella*, pig

T205 Fermentation activity of colonic microbiota from piglets fed diets including alfalfa, citrus pulp or inulin. S. Brambillasca*[1], M. Hernández[1], A. Britos[1], L. Reyes[1], P. Zunino[2], and C. Cajarville[1], *[1]Departamento de Nutrición Animal, Facultad de Veterinaria, UdelaR, Montevideo, Montevideo, Uruguay, [2]Departamento de Microbiología, Instituto de Investigaciones Biológicas Clemente Estable, MEC, Montevideo, Montevideo, Uruguay.*

The effect of including alfalfa, citrus pulp or inulin in diets for piglets on the fermentation activity of the colonic microbiota was studied. Twenty 4 cross breed piglets (12.1 ± 1.7kg BW) in a randomized complete block design were housed in metabolic cages and assigned to one of 4 diets for 23d: 100% corn and soybean meal based diet (CO), 97% CO+3% inulin (IN), 95.5% CO+4.5% fresh alfalfa (AL) and 95.5% CO+4.5% fresh citrus pulp (CP) in DM basis. The last day of the experiment all animals were euthanized and colonic digesta was individually sampled. In vitro gas production was performed using individual diluted colonic digesta as inoculum and pre-digested (pepsin+pancreatin) CO as substrate (6 flasks/animal, n = 144). Gas volume was recorded between 2 and 90h post inoculation. Asymptotic gas production (A, mL/g OM), time to reach 50% of the asymptote (B, h), maximal rate of gas production (Rmax, mL/h) and time of occurrence of Rmax (Tmax, h) were determined. DM disappearance (DMD) and organic matter disappearance (OMD) were determined by drying and ashing the fermentation residues respectively. Data were analyzed by PROC MIXED considering treatment effect, and means were separated by orthogonal contrasts. Rmax was the unique parameter affected by treatments and was highest for IN ($P = 0.003$). Gas production tended to be higher with fiber inclusion and AL tended to produce a higher B and Tmax than CP, whereas DMD for CP tended to be higher than AL. Piglets receiving IN presented a microbiota adapted to ferment substrates faster than the other treatments. Acknowledgments: ANII for scholarship of the first author.

Table 1. In vitro fermentation parameters for different treatments

	A (mL/g OM)	B (h)	Rmax (mL/h)	Tmax (h)	DMD (%)	OMD (%)
CO	146.3	1.77	23.0	1.71	37.0	40.3
IN	153.3	1.75	24.8	1.62	37.7	41.1
AL	148.6	1.78	22.2	2.06	35.8	42.3
CP	153.9	1.67	22.5	1.60	40.3	39.3
SEM	8.42	0.06	1.24	0.23	1.72	2.17
P						
CO vs ADDIT	0.09	ns	ns	ns	ns	ns
IN vs AL+CP	ns	ns	0.003	ns	ns	ns
AL vs CP	ns	0.07	ns	0.06	0.06	ns

ADDIT: additives; SEM: standard error of means; P: probability of contrasts ($P \leq 0.05$).

Key words: fiber, hindgut fermentation, swine

Physiology and Endocrinology II

T206 Quantitative bioluminescence imaging of functional estrogen receptor activity within intact porcine ovarian follicles in vitro. S. Jung* and S. T. Willard, *Mississippi State University, Mississippi State.*

Activated estrogen receptors (ER) in response to estrogen bind to specific sequences (estrogen response elements; ERE) to induce transcription. The objective of this study was to evaluate whether the estrogen induced ER binding activity in granulosa cells of antral ovarian follicles can be detected by bioluminescence imaging in vitro, and correlated to estrogen concentrations in follicular fluid. In this study, we used lipid–mediated gene transfer and an ERE–luc reporter gene (which consisted of 3 tandem repeats of EREs upstream from the luciferase gene) to transfect granulosa cells within intact follicles. When the endogenous functional and activated ERs bind to the ERE–luc sequences within the transfected granulosa cells, the expression of luciferase is enacted for detection. A total of n = 58 follicles between 4.2 to 9.4 mm in diameter were dissected from the ovaries. DNA–lipid complexes were formed at a DNA (μg): lipid (μl) ratio of 1:3, by adding FuGene 6 in PBS to 3 μg of ERE–luc DNA and injected into each follicle using a microinjector. The follicles were cultured individually with αMEM and 45% O_2; 50% N_2; 5% CO_2 at 39°C. After 20 h post–transfection, the luminescence from each follicle was detected using an IVIS 100 imaging system. Each follicle was imaged with 10 min exposure and signal intensity was reported (and normalized) as mean ± SEM of photons per second (p/s). Estradiol concentrations of follicular fluid were measured by radioimmunoassay in each follicle. Regression coefficients were determined, and a *P*–value of <0.05 was considered significant. Concentrations of estradiol in follicular fluid significantly increased as follicle size increased (r = 0.607; $P < 0.05$). Estradiol total content in each follicle was positively correlated with ERE-driven luciferase expression level of follicles (r = 0.39; $P < 0.05$). These results demonstrate the initial development of a new methodology for measuring functional and ligand activated estrogen receptor activity within intact porcine ovarian follicles in vitro using bioluminescence imaging methodologies.

Key words: bioluminescence imaging, estrogen receptor, porcine ovarian follicles

T207 Propionate increases mitochondrial phosphoenolpyruvate carboxykinase mRNA in Madin-Darby bovine kidney epithelial cells. S. I. Tindell*, S. L. Koser, and S. S. Donkin, *Purdue University, West Lafayette, IN.*

Phosphoenolpyruvate carboxykinase (PEPCK) is a rate determining enzyme for gluconeogenesis that is present in both a cytosolic (PEPCK-C) and a mitochondrial (PEPCK-M) form in bovine liver. Considerable research has documented the importance and control of PEPCK-C however there is little information available on hormonal and nutritional control of bovine PEPCK-M. The objectives of this study were to clone the promoter region of bovine PEPCK-M, to determine the transcription factor binding sites within the proximal promoter region, and determine the response of bovine PEPCK–M to nutrients and hormones. Genomic DNA isolated from liver of lactating dairy cows was used to clone a 906 nucleotide (nt) sequence that includes promoter specific elements and the first few bases of the coding sequence for bovine PEPCK–M promoter. Computer assisted analysis of this sequence revealed that all the elements necessary for promoter activity are contained within 896 nt relative to the transcription start site and there is no sequence similarity between bovine PEPCK-M and PEPCK-C promoters. The direct individual effects of 1 μ*M* dexamethasone, 10 μ*M* Wy14643, 100 n*M* insulin, 4.5 n*M* somatotropin, 1 μ*M* cAMP, 2 m*M* propionate, 2 m*M* acetate, 2 m*M* butyrate, or 2 m*M* lactate for 24 h on bovine PEPCK-M mRNA were determined in Madin-Darby bovine kidney epithelial (MDBK) cells. The data indicate that expression of PEPCK-M mRNA is increased ($P < 0.05$) by propionate (1.62 vs. 2.94 ± 0.19; control vs. propionate, respectively) but there were no effects ($P > 0.05$) of the other hormones and metabolites tested. The data would suggest that PEPCK-M may be regulated by propionate supply which may serve to enhance the capacity for mitochondrial phosphoenolpyruvate flux and gluconeogenesis.

Key words: PEPCK, gluconeogenesis, gene

T208 Staining bovine sperm for sex-sorting: Concentration effects of seminal plasma, sperm and Hoechst 33342. C. A. Burroughs*[1], J. K. Graham[1], R. W. Lenz[2], and G. E. Seidel[1], *[1]Colorado State University, Fort Collins, [2]Sexing Technologies Inc., Navasota, TX.*

We investigated various combinations of sperm, seminal plasma, and Hoechst 33342 (H33342) concentrations during staining of bull sperm to improve sex-sorting of sperm. Ejaculates from 11 bulls with at least 60% motile and 70% morphologically normal sperm were collected by artificial vagina on 2 different days. Semen was centrifuged at 1,000 × *g* for 15 min to separate sperm from seminal plasma, which was then clarified by additional centrifugation (2,000 × g for 10 min). Sperm were resuspended in TALP (pH 7.4) at 160 × 10^6 or 240 × 10^6 sperm per ml with 0 or 10% seminal plasma. H33342 was added (final concentrations of 49, 65 or 81 μ*M*) followed by incubation for 45 min at 34.5°C. An equal volume of TALP (pH 5.5) containing red food dye was added; sperm were sorted using a MoFlo SX (Dako, Denmark) flow cytometer and analyzed for % live-oriented cells, X sort rate, % dead (sperm membrane permeable to red dye), and splitability (peaks to valley ratio - degree of separation of X and Y populations). Overall, staining with 0% seminal plasma resulted in higher % live-oriented cells (57.4% vs. 53.7%) and a faster sort rate (3.60 × 10^3sperm per s vs. 3.28 × 10^3sperm per s) compared with 10% seminal plasma (both $P < 0.01$). There was an interaction between sperm concentration and H33342 concentration for ability to separate X and Y populations and for sort rate (Table 1). Using 65 μ*M* H33342 was sufficient to optimally stain 160 × 10^6 sperm per ml, while 240 × 10^6 sperm required 81 μ*M* H33342 to reach similar splitability and sort rates. The optimal combination for staining bull sperm was 0% seminal plasma, 160 × 10^6 sperm per ml, and 65 μ*M* H33342.

Table 1. Sperm and H33342 concentration responses averaged over 0 and 10% seminal plasma

Sorting Parameter	Sperm Conc (10^6)	49μM H33342	65μM H33342	81μM H33342
% live-oriented cells	160	55.0^{ab}	57.1^{b}	56.8^{b}
% live-oriented cells	240	52.2^{a}	55.5^{ab}	56.9^{b}
X Sort Rate (10^3 sperm/sec)	160	3.41^{bc}	3.82^{d}	3.76^{cd}
X Sort Rate (10^3 sperm/sec	240	2.67^{a}	3.32^{b}	3.66^{bcd}
Splitability %	160	29.2^{c}	39.6^{d}	37.7^{cd}
Splitability %	240	5.0^{a}	16.7^{b}	37.2^{cd}

Means without common superscripts differ ($P < 0.05$).

Key words: sex-sorting, sperm, bull

T209 Effect of feed restriction on reproductive and metabolic hormones in dairy cows. H. Gencoglu[1,2], A. Nascimento[1], K. Hackbart[1], L. F. Ferraretto*[1], F. Dalla Costa[1], J. Guenther[1], R. Meyer[1], R. D. Shaver[1], and M. C. Wiltbank[1], *[1]Department of Dairy Science, University of Wisconsin-Madison, Madison, [2]Department of Animal Nutrition and Nutritional Diseases, Faculty of Veterinary Medicine, University of Uludag, Bursa, Turkey.*

The objective of this trial was to evaluate the effects of feed restriction (FR) on serum concentrations of glucose, nonesterified fatty acids (NEFA), progesterone (P4), insulin and follicle-stimulating hormone (FSH), and milk production in dairy cows. Eight pregnant multiparous Holstein cows, 114 ± 14 d in milk and 685 ± 39 kg body weight (BW) at trial initiation were randomly assigned to a replicated 4 × 4 Latin Square design with 14-d periods. During the first 8 d of each period, all cows were fed for ad libitum feed intake. On d 9 through d 12 of each period, the feed restricted groups were fed 25 and 50% of the average daily dry matter intake (DMI) based on previous 8-d ad libitum feeding. The 4 dietary treatments were: ad libitum (AL), 25% feed restriction (25FR), 50% feed restriction (50FR), and 50% feed restriction produced by adding 50% wheat straw to diet (50FRS). Blood samples were collected before feeding from jugular vein at 0700, 1500, and 2300h on d 8 and continuing through d 14 of each period. On d 12 of each period, blood samples were collected before and at 60, 120, 180, 240, 300, 360, 420, and 480 min after morning feeding. The conventional TMR compared with the TMR with straw was higher in crude protein (15.1 vs. 10.8%) and starch (26.8 vs. 17.0%) and lower in NDF (32.1 vs. 50.5%) concentrations. Cows fed AL had 6.7, 12.7, and 11.3 kg/d greater DMI than cows fed 25FR, 50FR, and 50FRS, respectively ($P < 0.0001$). Likewise milk production and glucose concentration followed the same linear decrease ($P < 0.0001$). Serum concentrations of insulin (μIU/mL) were lower ($P < 0.0001$) for cows fed 50FR (8.27) and 50FRS (6.24) than cows fed AL (16.65) and 25FR (11.16). Furthermore, plasma NEFA concentrations increased linearly ($P < 0.0001$) followed by linear BW ($P < 0.0003$) and BCS ($P < 0.02$) loss. In addition, serum P4 concentrations were lower for cows fed AL than cows fed 50FRS and 25FR ($P < 0.01$). FSH concentrations did not differ among treatments ($P > 0.10$). The current trial suggests that, FR results in lower glucose and insulin levels, fat mobilization, BW and BCS loss, and increased circulating P4 concentration.

Key words: feed restriction, reproductive hormones, dairy cows

T210 Fetal growth and maternal body condition following melatonin supplementation in adequately fed or nutrient restricted ewes. C. O. Lemley*, A. M. Meyer, L. E. Camacho, T. L. Neville, D. J. Newman, J. S. Caton, and K. A. Vonnahme, *North Dakota State University, Fargo.*

Low birth weight offspring often exhibit poor growth performance and lower daily rates of gross energy accretion. Using a maternal nutrient restriction model, we examined fetal growth following melatonin supplementation as a 2 × 2 factorial design. At d 50 of gestation 16 primiparous ewes were allocated to receive 100% (adequate; ADQ) or 60% (restricted; RES) of nutrient requirements and were supplemented daily with 5 mg of melatonin (MEL) or no melatonin (CON) until d 90. All ewes were exposed to a 12:12 light dark cycle with lights on at 0700 h and off at 1900 h. Ewes were fed a pelleted ration with or without melatonin 5 h before the end of the photophase (1400 h). Serum melatonin was determined over a 24 h period using an ELISA kit. Maternal BCS, back fat, and loin muscle area were examined at 50 and 90 d of gestation, while fetal growth was measured at d 48, 50, 60, 70, 80 and 90 of gestation using ultrasonography. The melatonin feeding schedule resulted in a melatonin treatment by h interaction ($P < 0.01$), where serum melatonin concentrations peaked at 1500 h in MEL. Melatonin concentrations remained elevated in MEL versus CON until the scotophase (1900 h). A gestational d by nutritional plane interaction ($P < 0.01$) was observed for maternal BCS, which was similar at d 50 and decreased in RES vs. ADQ at d 90. Moreover, a nutritional plane by melatonin interaction ($P < 0.05$) was observed for maternal BCS, where MEL-ADQ had a greater BCS vs. CON-ADQ and MEL-RES had a lower BCS vs. CON-RES. Maternal back fat tended ($P < 0.1$) to decrease while loin muscle area increased ($P < 0.05$) from d 50 to 90. All fetal growth parameters listed below increased ($P < 0.01$) with gestational day. Biparietal distance was similar between treatments ($P > 0.3$), while abdominal diameter tended ($P < 0.1$) to be larger in MEL vs. CON fetuses. Fetal kidney length and width were increased ($P < 0.05$) in MEL vs. CON. In conclusion, dietary melatonin appears to increase fetal kidney development, which may have direct implications in improving offspring performance.

Key words: fetal growth, melatonin, pregnancy

T211 Effects of realimentation after nutrient restriction during early to mid-gestation on uterine blood flow in pregnant beef cows. L. E. Camacho*[1,2], C. O. Lemley[1,2], B. W. Neville[1,2], C. R. Dahlen[1,2], G. P. Lardy[1,2], and K. A. Vonnahme[1,2], *[1]Center for Nutrition and Pregnancy; Department of Animal Sciences, Fargo, ND, [2]North Dakota State University, Fargo.*

During pregnancy, dramatic changes occur in the maternal cardiovascular system alongside prominent growth and development of the uteroplacental vascular bed. Pregnancy is associated with increases in cardiac output and uterine blood flow and a fall in systemic vascular resistance. We hypothesized the duration of nutrient restriction would impact uterine blood flow and vascular resistance. Moreover, we further hypothesized that upon realimentation, blood flow would ultimately surpass blood flow in control animals. Our objectives were to examine the effects of maternal realimentation after nutrient restriction during early to mid-gestation on uterine blood flow. Multiparous beef cows (n = 17) were assigned randomly to one of 3 treatments: 1) 100% NRC requirements from d 30 to 226 of gestation (CCC; n = 6); 2) 60% NRC from d 30 to 85, thereafter being re-alimented to 100% NRC to d 226 (RCC; n = 5); 3) or receive 60% NRC from d 30 to 140, thereafter being re-alimented to 100% NRC to d 226 (RRC; n = 6). Cows were individually fed once daily in a Calan gate system at 1500 h. Baseline measurements were obtained via Doppler ultrasonography at 0700 h on d 30 and every 14 d thereafter until d 226. Measurements include maternal heart rate (HR), uterine blood flow (BF), pulsatility index (PI), and resistance index (RI). Percentage change of each measurement from the initial measurement on d 30 was calculated. There was a treatment by day interaction ($P = 0.01$) for HR percentage change, where RCC reached a greater HR at d 156 compared with CCC and RRC was intermediate. Uterine BF percentage change was not affected by treatment ($P > 0.72$). However, there were treatment by day interactions ($P \leq 0.02$) for PI and RI where RRC cows had a greater reduction in resistance than CCC cows after d 140. In summary, although maternal realimentation after nutrient restriction did not affect uterine BF percentage change, maternal diet affected PI and RI percentage change. Further investigations in uterine and placental vascular reactivity may help explain the differences observed in resistance indices.

Key words: nutrient restriction, pregnancy, uterine blood flow

T212 Effects of propiogenic supplements on serum concentration of insulin and progesterone in nonlactating cows: I. Monensin. T. Leiva[1], M. Barbosa[1], R. O. Rodrigues[1], R. F. Cooke[2], and J. L. M. Vasconcelos*[1], *[1]UNESP – Faculdade de Medicina Veterinária e Zootecnia, Botucatu, SP, Brazil, [2]Oregon State University – Eastern Oregon Agricultural Research Center, Burns.*

Insulin has been shown to increase circulating progesterone (P4) concentrations by stimulating ovarian steroid synthesis and alleviating hepatic steroid catabolism. Therefore, the objective was to determine if monensin is a nutritional alternative to increase circulating concentrations of insulin and consequently P4 in forage-fed cows. Fifteen nonlactating ovariectomized Gir × Holstein cows were ranked by BW and BCS and randomly assigned to receive, in a crossover design, 0.1 kg/d of corn in addition to 2 g/d of kaolin (control) or 0.2 g/d of monensin Na (MO). During the study, cows were maintained in *Brachiaria brizantha* pastures, and received treatments individually in a feed bunk every morning. Each period contained 21 d, where the initial 5 d served as adaptation when MO and control cows received 0.1 kg/d of corn in addition to, respectively, 0.1 g of monensin or 1 g of kaolin. Within each period, cows received a previously used intravaginal P4 device (CIDR, originally containing 1.9 g of P4) on d 0, which was replaced by a new CIDR at the end of the adaptation period (d 5). Blood samples were collected on d 12, 13, 19, and 20 immediately before (0 h) and 6, 12, 18, and 24 h relative to treatment feeding. On d 12 and 19 cows had access to pastures between samplings, whereas on d 13 and 20 cows were maintained in the working facility without access to forage. Blood samples were analyzed for serum concentrations of insulin and P4. Within samples collected when cows had no access to pastures, a treatment × time interaction was detected ($P = 0.05$) for P4 and insulin. Cows receiving MON had greater ($P < 0.01$) P4 concentrations compared with control at h 18 (2.6 vs. 2.1 ng/mL, respectively) but reduced insulin concentrations at h 0 (4.9 vs. 6.9 μIU/mL, respectively; $P < 0.01$) and h 6 (3.3 vs. 4.7 μIU/mL, respectively; $P = 0.07$). No treatment differences were detected for insulin and P4 concentrations when cows had access to pastures. In conclusion, supplemental monensin reduced serum insulin concentration but increased, by alternative physiological mechanisms, serum P4 concentrations in feed restricted cows.

Key words: monensin, progesterone, insulin

T213 Effects of propiogenic supplements on serum concentration of insulin and progesterone in nonlactating cows: II. Propylene glycol. A. M. L. Madureira[1], M. A. S. Borges[1], R. O. Rodrigues[1], R. F. Cooke[2], and J. L. M. Vasconcelos*[1], *[1]UNESP – Faculdade de Medicina Veterinária e Zootecnia, Botucatu, SP, Brazil, [2]Oregon State University – Eastern Oregon Agricultural Research Center, Burns, OR, USA.*

Insulin can increase circulating progesterone (P4) concentrations by stimulating ovarian synthesis and alleviating hepatic catabolism. Therefore, the objective was to determine if propylene glycol (PPG) supplementation increases circulating concentrations of insulin and thus P4 in forage-fed cows under negative or positive nutritional balance. From d −7 to d 14, 15 nonlactating ovariectomized Gir × Holstein cows were maintained in a *Brachiaria brizantha* pasture with proper forage availability and received 2 kg of concentrate/d. From d 15 to d 42, cows were move to a *B. brizantha* pasture with reduced forage availability without supplementation. Cows were inserted with an intravaginal device containing 1.9 g of P4 on d −7, which was replaced every 14 d during the study. Mean cow ADG was 0.57 ± 0.1 kg/d from d −7 to d 14, and −0.37 ± 0.1 kg/d from d 15 to 28. On d 6 of the study, cows were ranked by BW and BCS and assigned to receive a drench with PPG or water (control) at 2.5 mL/kg of $BW^{0.75}$. Blood was collected, relative to treatment application (h 0), at −0.5, 0, 0.5, 1, 2, 3, 4, 5, 6, and 7 h for determination of serum insulin and P4 concentrations. Cows received concentrate and returned to pastures in-between samplings. On d 7, cows received the converse treatment in a crossover design and were sampled similarly as in d 6. On d 13 and 14, 20 and 21, and 27 and 28, cows were again assigned to the same crossover and sampling schedule, but were not fed during the collection period. When cows were on adequate nutritional status, independently if feed restricted or not, PPG cows had greater ($P < 0.01$) insulin but reduced ($P < 0.01$) P4 concentrations compared with control cows (8.5 vs. 4.3 μIU/mL of insulin and 1.89 vs. 2.04 ng/mL of P4, respectively). However, when cows were on negative nutritional balance, PPG cows had greater ($P < 0.01$) insulin and P4 concentrations compared with control cows (7.0 vs. 3.4 μIU/mL of insulin and 2.16 vs. 2.03 ng/mL of P4, respectively). In conclusion, PPG supplementation increased circulating insulin and P4 concentrations only in cows under negative nutritional balance.

Key words: propylene glycol, insulin, progesterone

T214 Follicular fluid composition in cyclic Hereford cows supplemented with rice bran in grazing conditions. L. Veloz[1,2], M. E. Trobo[1,2], C. García Pintos[1,2], C. Viñoles[2], and M. Carriquiry*[1], *[1]School of Agronomy, UdelaR, Montevideo, Uruguay, [2]National Research Institute for Agriculture, Tracuarembó, Uruguay.*

The aim of this study was to evaluate the effect of short-term supplementation with rice bran before initiation of the breeding period on follicular fluid composition of beef cows grazing native pastures. Fifteen non-pregnant nonlactating Hereford cows (492 ± 6 kg BW and 5.6 ± 0.1 BCS, scale 1–8) were randomly allocated to 2 groups: control, non-supplemented (CON, n = 7) and supplemented (SUP, n = 8). The supplement (2.5 kg/cow of whole rice bran; 90.3%DM, 10%CP, 9%EE, 14%NDF) was fed daily for 23 d. All cows grazed on native pasture. Cows were synchronized with 3 prostaglandin (PG) injections 11 d apart. Thirty-six hours after the last PG injection, cows were castrated and all follicles ≥5mm were dissected and follicular fluid was aspirated for metabolite and hormone analyses. Means from a mixed analyses were considered to differ when $P < 0.05$. Follicular size did not differ between cow groups and averaged 10.2 ± 1.0 mm. Estrogen (19750 vs. 10009 ± 16570 pmol/L) and progesterone (135.7 vs. 108.5 ± 29.9 ng/mL) concentrations as well as estrogen/progesterone ratio (229.9 vs 273.2 ± 188.1) in follicular fluid were not different between SUP and CON cows. Similarly, glucose, nonesterified fatty acids, and cholesterol concentrations in follicular fluid (74.3 vs. 81.1 ± 8.5 mg/dL, 0.87 vs. 0.82 ± 0.05 mmol/L, 111.0 vs. 95.3 ± 10.1 mg/dL, SUP vs. CON, respectively) were not affected by nutritional treatment. Glucose concentrations increased and cholesterol concentrations tended ($P = 0.09$) to increase with follicle size (3.8 ± 0.9 mmol/L and 2.9 ± 1.6 mmol/L for each mm of increase in follicle size, respectively). Results susggest that short-term supplementation did not affect follicular fluid composition in cyclic beef cows in good BCS on grazing conditions

Key words: cattle, nutrition, ovary

T215 Capability of a new or once-used CIDR to develop persistent follicles and the capability of additional progesterone for persistent follicle turnover in replacement beef heifers. G. H. L.

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Two experiments evaluated the capability of new or once-used (for 7 d) CIDR to develop a persistent follicle and we hypothesized that high concentrations of progesterone with an additional CIDR would induce turnover of the persistent follicle. In Exp. 1, 59 crossbred heifers received a new (n = 29) or once-used (n = 30) CIDR from d 0 to 11. On d 8 heifers assigned randomly to receive either an injection of saline (n = 19), a second new CIDR from d 8 to 11 (n = 20), or follicular aspiration of all follicles ≥ 5mm (n = 20) resulting in a 2 × 3 arrangement of treatments. Transrectal ultrasonography was used daily to monitor follicular development and follicle turnover. When the dominant follicle had failed to turnover by d 8 the follicle was deemed to be persistent. Follicle turnover was defined as a dominant follicle that was present on d 8 that had disappeared by d 11. Heifers receiving the once-used CIDR (83%) tended ($P = 0.10$) to develop more persistent follicles than those receiving the new CIDR (64%). For treatments on d 8, 100% of heifers receiving follicular aspiration had follicle disappearance by d 11 which was greater ($P < 0.05$) than those receiving a second new CIDR (69%) which was greater ($P < 0.05$) than those receiving saline (32%). In Exp. 2, 41 heifers received a once-used CIDR from d 0 to 13 and all follicles ≥ 5mm were aspirated on d 0. On d 10 heifers were assigned randomly to one of 2 treatments: 1) injection of saline (Sal; n = 21); or 2) new additional CIDR insert for 3 d (CIDR; n = 20). Blood samples and ultrasonography were performed daily from d −10 to 16 to evaluate concentrations of progesterone (P4) and monitor follicle development and turnover. Concentrations of P4 were greater ($P < 0.01$) for CIDR than Sal at 4, 8, and 72 h after treatment on d 10. However, the ability of the CIDR (58%) and Sal (64%) treatments were similar. We conclude that a once-used CIDR develops more persistent follicles than new CIDR, whereas follicular aspiration was more effective at follicle turnover than an additional CIDR or saline treatments.

Key words: persistent follicle, beef heifer, progesterone

T216 Influence of CIDR-based protocols associated with supplementation of calcium soap on reproductive performance of Nellore cows. M. V. Biehl*[1], A. V. Pires[1,2], I. Susin[2], D. D. Nepomuceno[2], J. R. S. Gonçalves[4], L. H. Cruppe[3], F. M. Da Rocha[1], and M. L. Day[3], *[1]University of Sao Paulo, Pirassununga, SP, Brazil, [2]University of Sao Paulo, Piracicaba, SP, Brazil, [3]Ohio State University, Columbus, [4]Experimental Station Georgina Hildegard von Pritzelwitz, Londrina, PR, Brazil.*

The aim of this study was to compare reproductive performance of lactating Nellore cows (n = 264) submitted to estrus synchronization using either 7 or 9 d CIDR+Estradiol Benzoate (EB) program and 3 mineral supplements. Cows were blocked according to BW (428.5 ± 50.4 kg) and BCS (2.84 ± 0.23, 1 to 5) in a 2x3 (2 protocols and 3 supplements) factorial arrangement. The supplement treatments were mineral mixture (MM); MM+Megalac E+Citrus Pulp (CP) (MEG); MM+Kaolim+CP (KAO). At the beginning of the experiment, cows were 55 ± 0.36 d postpartum. Supplementation treatments began 30 d before the initiation of the synchronization program and were terminated 30 d after timed AI. Blood samples for progesterone analysis were collected 10 d before and at CIDR insertion to classify cows as cyclic. The CIDR was inserted with a 2 mg injection of EB and it was removed either 7 or 9 d later. All cows received 25 mg PGF2α (Lutalyse) 48 h before CIDR withdrawal and 300 IU eCG (Novormon) and 0.6 mg estradiol cipionate (ECP) at CIDR removal. Treatments were defined as follow: 7dMM (n = 42; e.g., 7d CIDR and MM supplementation), 7dKAO (n = 46), 7dMEG (n = 47), 9dMM (n = 40), 9dKAO (n = 46), and 9dMEG (n = 43). Estrus was detected for 5 d after CIDR removal and timed AI was performed 50 h after CIDR withdrawal. Second estrus detection was performed 16 d after timed AI for 6 d and AI submitted. Pregnancy diagnosis was performed by US 60 d after timed AI and at the end of the breeding season. At CIDR insertion, 85% (224/263) of cows were in anestrus. Estrus was detected in 52.8% (139/263) of the cows and time to estrus (43.5 ± 5.7 h after CIDR removal) did not differ among treatments. Timed AI pregnancy rates did not differ between supplements MM, 51; KAO, 69.5; MEG, 54.7% or with 7 d, 57.1, 58.7 and 52.5%, 9 d of CIDR treatment. Pregnancy rates were not different at the end of the breeding season. In conclusion, supplementation with Megalac E or Kaolin, did not improve reproductive performance in this study. In addition, timed AI pregnancy rates did not differ between CIDR treatments of 7 or 9 d in the CIDR-EB program used in the present study.

Key words: Megalac E, estrus, cows

T217 Effect of dietary conjugated linoleic acid on reproduction and tissue responses in dairy cows. G. Esposito*[1,2], A. Schneider[3], V. A. Absalón Medina[2], S. H. Pelton[2], and W. R. Butler[2], *[1]University of Naples Federico II, Naples, Italy, [2]Cornell University, Ithaca, NY, [3]Universidade Federal de Pelotas, Pelotas, RS, Brazil.*

Feeding rumen-protected isomers of conjugated linoleic acid (CLA) to early lactation dairy cows reportedly improves fertility by reducing the postpartum interval to first ovulation and enhancing circulating IGF-I levels. CLA supplementation increases high density lipoprotein (HDL) cholesterol in mice. Also, in vitro studies with bovine granulosa and luteal cells have shown that HDL and LDL promoted granulosa cell viability and stimulated IGF-I production. The objectives of this study were to examine ovarian follicles, corpora lutea, and liver tissues for effects induced by dietary CLA supplementation (top-dressed once daily from 15 d before expected calving to 65 DIM). Twenty-four lactating Holstein cows were assigned to 2 treatments: control and CLA diet. Milk production and DMI were recorded daily and milk components every 10 d. At 26 DIM ovulation was synchronized with a vaginal controlled internal drug-releasing device and injection of GnRH followed by an injection of PGF2α after one week. Blood samples were collected every 4 d. Follicular fluids, from follicles larger than 9mm, were collected every 8 d from 34 DIM. Plasma and follicular fluid samples were analyzed for estradiol (E2), progesterone, IGF-I, cholesterol, LDL, and HDL. At 56 DIM ovulations were synchronized in all cows. The resulting CL and the liver were biopsied at 64 and 65 DIM, respectively. Tissues were analyzed for gene expression of IGF-I, GHR, VEGFA and ANGPT2 or for PPARα, IGF-I, GHR, PC and PECK, respectively. In the CLA treated cows milk fat production was lower ($P < 0.05$) and energy balance was improved ($P < 0.05$). No differences between the 2 groups were observed for milk production. CLA-supplemented cows tended to have higher plasma concentrations of E2 and LDL ($P < 0.1$) and plasma concentrations of IGF-I were higher ($P < 0.001$). No differences were observed for the mRNA expression in tissues. This study confirms the improvement of plasma IGF-I levels, but dietary CLA did not alter plasma lipoprotein concentrations in cows as had been shown in mice. Moreover, CLA supplementation failed to alter gene expression in the tissues examined.

Key words: CLA, ovarian follicles, corpus luteum, liver

T219 Endocrine and ovarian parameters associated with increased fertility after resynchronized timed artificial inseminations in lactating dairy cows. J. O. Giordano*, M.C. Wiltbank, and P. M. Fricke, *Department of Dairy Science, University of Wisconsin, Madison.*

Lactating dairy cows failing to conceive to a previous timed AI (TAI) were resynchronized to receive TAI either using Double-Ovsynch (DO, Pre-Resynch, GnRH–7 d–PGF–3 d–GnRH, 7 d later Breeding-Resynch, GnRH–7 d–PGF–56 h–GnRH–16 h–TAI) or Ovsynch initiated 32 d after TAI (D32, GnRH–7 d–PGF–56 h–GnRH–16 h–TAI). All DO cows received the first GnRH injection of Pre–Resynch 22 d after TAI, and cows (n = 981) diagnosed not pregnant using ultrasonography (US) 29 d after TAI continued the protocol. All D32 cows received GnRH 32 d after TAI, and cows (n = 956) diagnosed not pregnant using transrectal palpation 39 d after TAI continued the protocol. In subgroups of DO and D32 cows, the proportion of cows with a functional corpus luteum (CL) at the first GnRH of Breeding-Resynch and D32 protocols (G1), CL regression after PGF, and ovulation to the last GnRH (G2) of both protocols was determined using US and serum progesterone (P4). Pregnancy diagnosis was performed 29 d after TAI using US. Overall, P/AI was greater ($P < 0.01$) for DO vs. D32 cows (38.7 vs. 30.0%). The proportion of cows with high (HP4) vs. low P4 (LP4; cutoff 0.5 ng/mL) at G1 was greater ($P < 0.01$) for DO vs. D32 cows [86.7 (368) vs. 62.5% (375)]. At 29 d after TAI, cows with HP4 at G1 had greater ($P < 0.01$) P/AI than LP4 cows [33.9 (554) vs. 19.5% (190)], and cows that ovulated to G1 had greater ($P < 0.01$) P/AI than cows that did not [32.6 (285) vs. 28.3% (466)]. Synchronization rate (HP4 at PGF, LP4 at G2, and ovulation to G2) was greater ($P < 0.01$) for DO vs. D32 cows [71.8 (223) vs. 50.5% (210)]. At 29 d, P/AI were similar between treatments for synchronized [D32 = 43.4 (106) vs. DO = 43.1% (160)] and non-synchronized [D32 = 9.6 (104) vs. DO = 4.8% (63)] cows. Similarly, synchronization rate was greater ($P < 0.01$) for cows with HP4 at G1 [69.2 (321) vs. 37.1% (105)] and for cows that ovulated to G1 [65.6 (151) vs. 58.9% (275)]. We conclude that resynchronized lactating cows that had high P4 at G1 and that ovulated after G1 had an increased synchronization rate resulting in increased fertility to TAI. Supported by Hatch project WIS01171

Key words: double-Ovsynch, resynchronization

T220 Use of the CIDR+EB synchronization program in prepubertal Nellore heifers. M. V. Biehl*[1], A. V. Pires[1,2], I. Susin[2], L. H. Cruppe[3], D. D. Nepomuceno[2], J. R. S. Gonçalves[4], F. M. Da Rocha[1], and M. L. Day[3], *[1]University of Sao Paulo, Pirassununga, SP, Brazil, [2]University of Sao Paulo, Piracicaba, SP, Brazil, [3]Ohio State University, Columbus, [4]Experimental Station Georgina Hildegard von Pritzelwitz, Londrina, PR, Brazil.*

The objective of this study was to compare reproductive performance of prepuberal Nellore heifers (n = 407) using either a 5, 7, 9 or 11 d CIDR treatment with an estradiol benzoate (EB)-based synchronization program. Heifers were blocked to treatments based on body weight (282 ± 18 Kg) and body condition score (2.63 ± 0.21, scale of 1 to 5) in a 4 × 2 factorial arrangement. All animals received 2 mg EB at time of CIDR insertion, and after either 5, 7, 9 or 11d the CIDR was removed and all heifers received 25mg PGF2α (Lutalyse) and 300 IU of eCG (Novormon). Approximately half of the heifers in each treatment were administered 1mg EB at 48 h after CIDR withdrawal. Therefore, experimental treatments were designated as 5d-EB (n = 61; e.g., 5 d of CIDR with 1mg EB 48 after CIDR removal), 5d (n = 51; e.g., 5 d of CIDR without EB after CIDR removal), 7d-EB (n = 51), 7d (n = 47), 9d-EB (n = 49), 9d (n = 50), 11d-EB (n = 52) and 11d (n = 46). Estrus detection was performed for 5 d after CIDR removal and artificial insemination (AI) was performed according to the AM/PM protocol. Detection for return to estrus and AI, in heifers not conceiving to the initial AI, began 16 d after CIDR withdrawal and continued for 6 d. Pregnancy was diagnosed by ultrasonography 60 d after the first AI. Binominal data were analyzed using GLIMMIX procedures of SAS. During the synchronization period (5 d after CIDR withdrawal), a greater ($P < 0.05$) proportion (87.3%) of heifers that received EB presented estrus as compared with the proportion (54.6%) of heifers with no second EB treatment in estrus. Timing (68.1 ± 17.3 h after CIDR removal) and distribution of estrus did not differ among treatments. The additional EB did not increase conception rate, but tended ($P = 0.06$) to improve pregnancy at first AI (with EB, 21.6; without EB, 14.9%). Final pregnancy rates did not differ among treatments. Effects of the duration of CIDR treatment were not detected. In prepubertal Nellore heifers, inclusion of EB treatment at 48h after CIDR removal improved estrus response, did not influence conception rate, but tended to improve pregnancy rate following treatment with CIDR.

Key words: prepuberal, heifers, estradiol benzoate

T221 Effects of ethanol and acetic acid fed to high-producing dairy cows on blood parameters. J. L. P. Daniel*, L. G. Nussio, R. C. Amaral, E. H. C. Garcia, A. W. Bispo, F. C. L. Oliveira, I. F. Silva, and M. Zopollatto, *University of Sao Paulo, College of Agriculture "Luiz de Queiroz", Piracicaba, SP, Brazil.*

Ethanol and acetic acid are common end products from silages, especially from tropical forages. The objective of this study was to determine whether ethanol and acetic acid affect plasmatic glucose, insulin, ethanol, and gamma-glutamyl transferase (GGT) at peripheral blood. Hypothetically, ethanol present in the diet could reach portal blood, damage liver and increase GGT activity. Thirty lactating Holstein cows averaging 40 kg/d of milk at beginning of trial were grouped in 10 blocks and fed either: Control (33% Bermuda hay + 67% concentrates); Ethanol (control diet + 5% ethanol on DM basis); or Acetic acid (control diet + 5% acetic acid on DM basis) diets. Ethanol and acetic acid were diluted in water (1:2) and sprayed onto total mixed ration twice daily before feeding. The same amount of solution was replaced with water in the control diet. During the 1st week of trial the cows received half-dose of these chemical compounds. Blood was collected from coccyges vessels into evacuated tubes containing sodium heparin, 6 h after morning feeding on d 7, 14 and 42. Tubes were immediately centrifuged and plasma was frozen for a 28d period. Plasmatic concentration of ethanol was lower than 0.1 g/L in all cows. Diets did not affect ($P = 0.95$) plasmatic GGT (26.2, 27.0, and 26.6 U/L, respectively for control, ethanol and acetic acid diets). Insulin concentration was unaffected ($P = 0.96$) across diets (0.28, 0.27, and 0.29 mU/L, respectively). However, blood from cows supplemented with acetic acid showed lower ($P = 0.04$) glucose concentration (58.3 mg/dL) than those fed ethanol containing diets (62.7 mg/dL). It might be due to the lower dry matter intake observed, during 2nd and 3rd experimental weeks, from cows fed acetic acid (not showed). Control diet presented an intermediary blood sugar level (61.0 mg/dL). In conclusion, blood parameters were not altered by feeding ethanol to high producing dairy cows, up to studied level. The conversion of ethanol to acetate into the rumen might be a plausible explanation to understand the ordinary blood parameters to the alcohol containing diet.

Key words: GGT, insulin, glucose

T222 Estrous response in yearling and multiparous ewes during reduction on the synchronized luteal phase and eCG injection. J. L. Cordero[1], T. Sánchez[1], P. Molina[2], R. Nieto[1], J. Peralta[2], O. Mejía[3], L. Olivares[4], E. García*[5], and J. L. Figueroa[1], *[1]Colegio de Postgraduados, Texcoco, Estado de México, [2]Universidad Autónoma del Estado de Hidalgo, Tulancingo, Hidalgo, México, [3]FMVZ, Universidad Autónoma de México, Tres Marías, México, [4]Universidad Autónoma del Estado de México, Toluca, Estado de México, [5]CUCSUR, Universidad Autónoma de Guadalajara, Jalisco, México.*

The aim of the experiment was to evaluate the effect of reducing the synchronized luteal phase and eCG injection in yearling and multiparous ewes and their response on estrous and pregnancy rate. Seventy-nine ewes were divided according to their reproductive status in yearling (n = 36) and multiparous (n = 43), which were then randomly subdivided into groups for the assignment of hormonal treatments. Ewes were pre-synchronized with 2 doses of prostaglandin F2α (cloprostenol, 65 mg) 8 d apart, before sponge insertion. Yearling ewes (P) were synchronized with cronolone sponges (20 mg) for a 12 d period (P12+0, n = 8) without and with 100 IU of eCG injection (P12+eCG, n = 9); and for a 6 d period without (P6+0, n = 9) and with 100 IU of eCG injection (P6+eCG, n = 10), both eCG injections were given at sponge removal. Multiparous ewes (M) were synchronized by the same protocol (M12+0, n = 12; M12+eCG, n = 11; M6+0, n = 9 and M6+eCG, n = 11, respectively). All ewes (P and M) showed estrous response (100%) after sponge removal. There were no differences ($P \geq 0.05$) for reduction of the synchronized luteal phase and eCG injection in beginning and estrous duration in yearling ewes. However in multiparous ewes estrous duration was affected ($P \leq 0.05$) by reduction of the luteal phase (M12, 37.04 ± 1.9 vs M6, 45.2 ± 2.1) and eCG injection (M+0, 36.2 ± 1.5 vs M+eCG, 32.8 ± 1.1). There was no difference ($P \geq 0.05$) in gestation rate between groups (P = 86 and M = 81%). It is concluded that reducing the period of synchronization or eCG injection does not alter the response, onset and duration of estrous in yearling ewes, but it does alter estrous duration in multiparous ewes, so it should be considered when performing AI at fixed time or when yearling and multiparous are synchronized together.

Key words: *Ovis aries*, estrus synchronization, progestogen

T223 Fertility following fixed-time AI in infertile CIDR-treated dairy cows given rbST throughout extended (>500 d) lactations. A. Zúñiga-Serrano*, F. G. Véliz-Deras, J. Méndez-Lara, L. M. Tejada-Ugarte, and M. Mellado-Bosque, *Universidad Autónoma Agraria Antonio Narro, Torreón, Coahuila, México.*

With extended lactations (beyond 17 mo) due to the use of rbST throughout lactation, attempts to fecundate subfertile cows around 300 d in milk (DIM) can be commercially viable. Thus, the purpose of this study was to determine, using multiple logistic models, factors affecting pregnancy rates (PR) following fixed-time AI (FTAI) in subfertile (up to 12 services) cows treated with rbST throughout lactation. Four hundred ninety-eight Holstein cows of all parities, unable to become pregnant when approaching 300 d in milk received a CIDR device and 100 mg of GnRH on Day 0. CIDR removal and PGF2α (25 mg) treatment were done concurrently on Days 7. Estradiol benzoate (2 mg) was injected on d 8 and GnRH on d 9; cows were inseminated 16–20 h later. Cows that produced <15000 kg of milk in their previous lactation had only half the chance ($P < 0.05$) to become pregnant compared with cows with total lactations of > 15000 kg. Cows with an average milk fat <3% in their previous lactation were 43% more likely ($P < 0.05$) to become pregnant at FTAI than cows with milk fat >3%. Cows with <5 services had significantly increased chances of becoming pregnant than cows with >5 services at FTAI (PR 36 vs. 27%; $P < 0.05$). Cows with less than 2 lactations were 1.7 times more likely ($P < 0.05$) to become pregnant than older cows. Cows with >350 DIM were less likely to become pregnant (PR 27 vs. 35%; $P < 0.05$) than cows subjected to FTAI with <350 DIM. Cows with peak milk yields lower than 55 kg were 1.5 times more likely to conceived than cows with peak milk yields greater than 55 kg (PR 28 vs. 37%; $P < 0.05$). Cows subjected to FTAI with a temperature-humidity index (THI) <73 were 45% more likely ($P < 0.05$) to become pregnant than cows inseminated with a THA >73. It was concluded that an acceptable percentage of subfertile cows can become pregnant with the protocol used in the present study, and this practice seems to be biological feasibility and economically justifiable in dairy operations with 3X milking and the use of rbST throughout lactations, which would assure lactations >500 d.

Key words: reproductive performance, estrus synchronization, Holstein cows

T224 Adiponectin system and peroxisome proliferator-activated receptor gamma2 (PPARγ2) mRNA abundance in different bovine fat depots considering conjugated linoleic acids (CLA) or lactation stage related changes. B. Saremi*[1], H. Sauerwein[1], D. von Soosten[2], S. Dänicke[2], and M. Mielenz[1], *[1]Institute of Animal Science, Physiology and Hygiene Unit, University of Bonn, Bonn, North Rhine-Westphalia, Germany, [2]Institute of Animal Nutrition, Friedrich-Loeffler-Institute (FLI), Federal Research Institute for Animal Health, Braunschweig, Lower Saxony, Germany.*

Adiponectin (Ad) is secreted from adipose tissue (AT) and exerts insulin sensitizing effects via Ad receptor 1 and 2 (AdR1/2) in humans. PPARγ2 increases plasma Ad concentrations and thus improves insulin sensitivity in monogastrics. We hypothesized that the CLA-induced reduction of milk fat might improve energy balance and insulin sensitivity in dairy cows. From 25 heifers, 5 were slaughtered on d 1 postpartum. Remaining heifers were randomly allocated to CLA (Lutrell pure, BASF, Germany, n = 10) or control fat supplementation (Silafat, BASF, n = 10) each at 100 g/d. Five animals per group were slaughtered at d 42 or 105. Subcutaneous (Sc) (chest, wither and tail head) and visceral (Vc) AT (mesenterial, omental and retroperitoneal) samples were collected. Ad, AdR1/2 and PPARγ2 mRNA abundance (Ab) was quantified by qPCR. Pearson correlation, GLM or non parametric tests were used for statistical analysis (SPSS 17; $P < 0.05$). Ad, AdR1 and PPARγ2 Ab increased from d 1 and 42 to d 105 in most VcATs. AdR1 Ab was highest at d 105 in all ATs except omental fat. In the merged data from VcATs, Ad and AdR2 were reduced in CLA-treated heifers at d 105. Comparing individual AT depots, Ad and AdR2 Ab was reduced in omental and retroperitoneal AT from CLA-treated animals. PPARγ2 was increased by CLA in Vc depots regardless of time. In general, the different depots had different Ab values, e.g., retroperitoneal AT displayed higher Ad, AdR1 and AdR2 Ab than mesenterial AT. Ad Ab was correlated to AdR1/2 and PPARγ2 (r = 0.5, 0.8, and 0.5, respectively). In conclusion, the observed CLA effects on Ad and AdR2 as well as the timely changes of Ad, AdR1 and PPARγ2 Ab were fat depot dependent. The increase in Ad and AdR1 Ab at d 105 (post peak lactation) is possibly regulated by PPARγ2, and might improve insulin sensitivity as compared with pre-peak lactation (d 42). As to whether the effects of CLA on the Ad system and PPAR expression will affect insulin sensitivity in the different depots and in the entire organism remains to be clarified.

Key words: adipose tissue, adiponectin, PPARγ2

T225 Relationship between follicular and ovulatory responses with embryo production during superovulatory treatment in cattle. H. Kohram[1,2] and M. Poorhamdollah*[1], [1]*Department of Animal Science, Faculty College of Agriculture and Natural Resources, University of Tehran, Karaj, Iran,* [2]*Department of Clinical Sciences, Faculty of Veterinary Medicine, Shahid Chamran University, Ahvaz, Iran.*

The efficiency of embryo transfer technology is still limited because of high variability and unpredictability of superovulatory responses of the donor cows. The aim of this study was to investigate relationship between follicular and ovulatory responses with embryo production during superovulatory treatment in cattle. The experiment was carried out in one to 4 random cycles of superovulation in 47 Holstein cows, for a total of 88 superovulatory cycles. Animal were superstimulated between d 8 and 12 of estrous cycle with 400 mg Folltropin-v given in decreasing doses: 3.5; 3, 3; 2.5, 2.5; 2, 2; 1.5 mg (a.m. and p.m.) over 4 d and luteolysis was induced with 2 mg intramuscularly injection of Cloprostenol with the 7 injection of folltropin-v. The ovaries of all cows were examined by ultrasonography on the day of estrus following superovulatory treatment and on the day of embryonic collection (7 d after estrus). Ova and embryos were collected by a nonsurgical procedure, evaluated and classified as quality I (freezable), quality II (transferable) and degenerated embryos. Criteria used to classify each type of superovulatory responses as low, medium or high. For each type of the superovulatory responses, data were analyzed by means of the GLM procedure of the SAS. The results showed in Table 1. In conclusion the high follicular or ovulatory responses are not necessarily coupled with a high yield of embryos.

Table 1. Percent of superovulation cycles with various types of responses

	Class		
Type of response	Low (%)	Medium (%)	High (%)
Follicle ≥ 7 mm at estrus	10	21	69
Ovulations	23	24	53
Quality I embryos	59	22	19
Quality II embryos	77	18	5
Quality I+ II embryos	52	24	24
Degenerated embryos	80.6	17.1	2.3

Key words: embryo, superovulation, Folltropin-v

T226 Differentiation of estrus versus nonestrus cow cervix morphology: Verification of a cost-effective methodology. A. Nikkhah*, M. A. Sirjani, A. A. Assadzadeh, and H. Amanloo, *University of Zanjan, Zanjan, Iran.*

The increasing trend in milk solids secretion over the last few decades has noticeably depressed cow fertility. Accurate estrus detection has been a major challenge to achieve. Our objective was to quantify dairy cow cervix morphology during standing-estrus (SE) and nonestrus (NE) days of the estrus cycle. Four multiparous Holstein cows (50 ± 14 d in milk, 31 ± 3.6 kg milk yield, 643 ± 66 kg BW, 3.0 ± 0.18 BCS) were monitored daily for cervical region morphologies for an entire 21-d estrus cycle. The cervix was videotaped using a recording on-farm apparatus to score tissue morphology as affected by estrus. The apparatus had 45 cm length and 2.7 cm diameter, internal electrical settings, external polyvinyl coat, lights on the front, wires at its terminal, and a connection to a laptop computer with an image processing software. Cervix was scored for distinctness from surrounding vaginal tissues, central positioning, motility, and secretions on a 5-scale basis. The score of 1 described cervices with quite distinct, central, stable, and mucosal manifestation, and the score of 5 represented quite nonseparate, noncentral, moving, and dry appearance. Data were analyzed as a mixed model with fixed day effect and random effects of cow within day plus residuals. Findings demonstrated that cervix area was markedly ($P < 0.01$) more distinct (1.0 vs. 3.0), more central (1.1 vs. 3.6), more stable (1.5 vs. 2.8), and more mucosal (1.1 vs. 3.7) during SE than NE days. As such, on SE days, the cervix was rigidly observable in the central end of vaginal tract, whereas NE cervices were hardly separable from the surrounding tissues. The data verify our earlier results and establish the on-farm feasibility of using the new inexpensive technique (e.g., <US$200) to differentiate SE and NE cervices.

Key words: cervix, morphology, estrus

T227 Metabolic characteristics of pregnant gilts fed low and excess protein diets associated to intrauterine growth retardation (IUGR). C. C. Metges*[1], I. S. Lang[1], U. Hennig[1], M. Peters[1], K.-P. Brüssow[1], E. Kanitz[1], M. Tuchscherer[1], F. Schneider[1], J. Weitzel[1], A. Ooster[2], H. Sauerwein[2], G. Nürnberg[1], C. Rehfeldt[1], and W. Otten[1], [1]*Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany,* [2]*Institute of Animal Science, Rheinische Friedrich-Wilhelms-Universität, Bonn, Germany.*

Limited and excess dietary protein in pregnant gilts lead to IUGR (Rehfeldt et al. 2011, J. Anim. Sci.). To explore metabolic reasons, gilts' plasma metabolite and hormone concentrations were analyzed. Low (6.5%, LP), adequate (12%, AP), and high (30%, HP) protein diets were fed to 16, 17, and 15 pregnant gilts, respectively. At d −5, 24, 66, and 108 of pregnancy fasted blood was collected. Concentrations of glucose (Glc), triglyceride (TG), nonesterified fatty acids (NEFA), cholesterol (C), low density lipoprotein cholesterol (LDLC), high density lipoprotein cholesterol (HDLC), insulin, glucagon (Gg), leptin, insulin-like growth factor-1 (IGF1), cortisol and progesterone (P_4) were analyzed in plasma; urea (U) and protein were analyzed in serum. At d 92, in 9 gilts/group diurnal blood samples were analyzed for Glc, NEFA, TG, C, and U metabolic profiles. Diet effects were evaluated with repeated measure ANOVA. Concentrations of HDLC were reduced in HP compared with AP gilts ($P < 0.01$). In LP gilts LDLC was lowest ($P < 0.01$). Highest and lowest U were observed in HP and LP ($P < 0.001$). Serum protein was lowest in LP gilts ($P < 0.05$). In the HP group Gg was higher than in LP and AP, whereas IGF1 was lower in LP than in AP gilts at d 24 and 66 ($P < 0.05$). Plasma P_4 was higher in HP than in LP and intermediate in AP ($P < 0.05$). In HP gilts cortisol levels were lower than in AP gilts ($P < 0.05$). Metabolic profiles indicated that plasma Glc was lower in HP ($P = 0.04$) and LP ($P = 0.09$) gilts. In HP U was 3 times the values observed in AP whereas in LP U reached only 60% of AP ($P < 0.001$). Plasma TG levels tended to be lower in LP than in AP ($P = 0.09$) and HP ($P = 0.07$). In HP diurnal NEFA levels were higher compared with AP and LP ($P < 0.01$). In LP gilts C was higher than in AP and HP ($P < 0.01$). In conclusion, HP gilts have a low glucose and energy status as reflected in higher NEFA and lower body fat. In LP gilts, deficiency of essential amino acids altered lipoprotein and C metabolism and favored lipid disposal. Both conditions are related to IUGR. Supported by Deutsche Forschungsgemeinschaft ME1420/8-1 and OT 137/3-1 (PAK 24)

Key words: high protein, metabolites, pregnancy

T228 Induction of luteal tissue in PGF_{2a}-treated sows. D. Gandy*, A. L. Greathouse, H. Klienman, F. M. LeMieux, and C. E. Ferguson, *McNeese State University, Lake Charles, LA.*

In the sow, corpora lutea must be present the entire length of gestation in order for the pregnancy to result in normal parturition at ~114 d post-mating. The objective of this experiment was to determine if induced luteal tissue following PGF_{2a} treatment could support pregnancy in the sow. A total of 12 cross-bred mature sows between the ages of 2 and 5 years were mated with a boar and evaluated for pregnancy at 30 to 60 d post-mating via ultrasonography. Pregnant sows were then allotted to 1 of 2 treatments, control or induction of luteal tissue. Sows randomly selected for the control treatment (n = 5) received 15 mg of PGF_{2a} 12 h apart and were then administered 30.8 mg of matrix at time of PGF_{2a} treatment. Then the matrix dose (daily) was reduced in a declining manner from to 22 mg, 15.4 mg, 6.6 mg and 0 mg matrix in 7 d intervals. Treatment sows (randomly selected for ovulation induction) were maintained on the same matrix schedule however, they received 750 IU of eCG 7 d post-PGF_{2a} and 500 IU hCG 48 h post-eCG. Blood samples were collected on all sows at 0, 4, 8, 12 and 24 h post-PGF_{2a} and 48 h post-hCG. There were no differences in the number of sows aborting in the control group (5/5, 100%) and the treatment group (7/7, 100%). The time from the start of 0 mg matrix to abortion was not different between the control group (1.8 ± 0.3 d) and the treatment group (5.0 ± 2.8 d). Among treatment sows, 2/7 (29%) developed luteal tissue (≥2 ng/mL P_4 48 h post-hCG) in response to eCG and hCG treatment while 5/7 (71%) did not (≤2 ng/mL P_4 48 h post-hCG) and success of induced luteal tissue may have affected the length of pregnancy maintenance. The length of time from 0 mg of matrix to abortion for sows with induced luteal tissue was 13 ± 7.5 d compared with 5.0 ± 2.8 d for sows with no induced luteal tissue. There was a high positive correlation $r^2 = 0.90$ between P_4 levels 48 h post-hCG and days to abortion post-hCG. These results indicate that pregnancy can be maintained in a PGF_{2a}-treated sow and induced luteal tissue can extend gestation in the absence of supplemental P_4.

Key words: abortion, pregnancy, luteal

T229 Effects of increased GnRH dose post–TAI in Brahman influenced cattle. B. Pousson*[1], D. J. Kesler[2], M. Poole[1], W. Storer[1], and C. E. Ferguson[1], *[1]McNeese State University, Lake Charles, LA, [2]University of Illinois, Urbana-Champaign.*

Brahman cattle have a history of lower pregnancy rates following artificial insemination (AI) compared with European cattle. The decrease in pregnancy rates among Brahmans has been linked to the higher excitability in stressful situations in which an increase in cortisol can result in delaying or blocking ovulation. This experiment was designed to determine if an increased GnRH dose at AI would improve pregnancy rate in Brahman and Brahman–type cattle. From 6 different location in Texas and Louisiana a total of n = 50 heifers, n = 123, cross–bred Angus heifers (no Brahman influence), n = 83 lactating cross-bred Brahman cows were bred using conventional semen following a CO-Synch+CIDR schedule with timed artificial insemination (TAI) at 48 to 58 h. Additionally, n = 32 Brahman dry cows were bred using sex–sorted Brahman semen (sorted for Y–chromosome) and the same synchronization schedule and TAI. All females were randomly selected to receive either 100 μg (n = 84) or 200 μg (n = 81) of GnRH at TAI and ultrasound for pregnancy ~30 d post-TAI. The administration of 200 μg GnRH at TAI resulted in a significantly higher ($P < 0.004$) pregnancy rate (0.43 ± 0.05) compared with 100 μg GnRH (0.21 ± 0.04). This pattern existed in heifers receiving 200 μg of GnRH (0.63 ± 0.10) vs. 100 μg GnRH, (0.29 ± 0.09), cows receiving conventional semen and 200 μg (0.40 ± 0.08) vs. 100 μg (0.23 ± 0.67) and cows receiving sex–sorted semen and 200 μg (0.21 ± 0.11) vs. 100 μg (0.06 ± 0.06). Among non-Brahman heifers increasing the dose of GnRH at TAI did not affect pregnancy rates 200 μg (0.49 ± 0.06) compared with 100 μg (0.55 ± 0.06). These results indicate that increasing the dose of GnRH at time of AI can result in an increase in the pregnancy rate in Brahman and cross-bred Brahman cattle, however there was no effect on pregnancy rate among non-Brahman heifers.

Key words: Brahman, ovulation, stress

T230 Dynamics of fat cell turnover in visceral and subcutaneous fat tissue in dairy cows. S. Häussler*[1], S. Dänicke[2], K. Friedauer[1], D. Germeroth[1], D. von Soosten[2], and H. Sauerwein[1], *[1]University of Bonn, Germany, [2]Federal Research Institute, Braunschweig, Germany.*

Adipose tissue can expand either by cell proliferation, cell enlargement or both. The number of adipocytes seems constant in mature humans; in cattle, in particular dairy cows, dynamics of fat cell turnover were unknown. To characterize lactation-induced changes in fat cell number, we targeted cell proliferation (marker Ki67) and preadipocyte differentiation (marker Pref-1) using immunohistochemistry, and apoptosis via the TUNEL method in both a visceral (retroperitoneal (RP)) and a subcutaneous (tailhead (SC)) depot obtained from 25 Holstein heifers. The heifers were divided in a control (CTR) and a CLA group; from d 1 of lactation until sample collection, animals from the CLA group were fed with 100 g CLA (Lutrell Pure, BASF, Germany) per day. On d 1, 42 and 105 postpartum, 5 animals of CTR were slaughtered; from CLA, 5 cows were slaughtered each on d 42 and 105. For the detection of apoptosis and Pref-1, deparaffinized sections (12 μm), for Ki67 frozen sections (14 μm) were used. Bovine lymph nodes (apoptosis), placenta (Pref-1) and liver (Ki67) served as controls. The portion (%) of positive cell was defined as mean number of positive stained cells/mean number of total cells x 100 and analyzed using the general linear model and the Student's *t*-test (SPSS). An apoptosis-proliferation index (A:P index) was calculated from the portions of apoptotic and proliferating cells. The A:P index was lower in RP than in SC due to a higher apoptotic rate in SC ($P \leq 0.001$) and concomitantly very low cell proliferation rates, irrespective of time and treatment. The same applied for preadipocyte portions being similar in both RP and SC, with mean values of 1.17 ± 0.33% for RP and 1.76 ± 0.65% for SC, respectively. In addition to decreasing fat cell size demonstrated in our group recently, the reduction of fat mass in early lactation seems to be dominated by apoptosis. Further dynamics of fat cell turnover are more likely defined by activation of preadipocytes than by cell proliferation.

Key words: bovine adipocyte, cell turnover, CLA

T231 Insulin sensitivity in obese (Iberian) and lean (Landrace) 50-kg barrows. I. Fernandez-Figares*, L. Gonzalez-Valero, J. M. Rodriguez-Lopez, and M. Lachica, *EEZ-CSIC, Granada, Spain.*

The Iberian pig is a slow growing obese breed with a distinct serum hormone and metabolite profile compared with lean (Landrace) pigs (Fernandez-Figares et al., 2007 Livest. Sci.110:73-81). The objective of the present work was to explore the possibility that Iberian pigs show peripheral insulin resistance. An intravenous glucose tolerance test was performed using Iberian (n=4) and Landrace barrows (n=5), 50 kg average BW, fitted with permanent carotid artery catheters. After surgery recovery, they were injected intravenously 500 mg glucose/kg

BW and blood samples collected at −10, 0, 5, 10, 15, 20, 25, 30, 45, 60, 90, 120, 150 and 180 minutes. Plasma samples were frozen in aliquots until analysis for glucose and insulin. Glucose was determined using Precision PCx Blood Glucose Test Strips. Insulin was determined using a Linco porcine insulin RIA kit and human insulin was used as standard. Responses of plasma glucose and insulin to the intravenous glucose challenge test was evaluated by computing areas under the response curves (AUC) for the 3-hour period following glucose administration determined using trapezoidal geometry. Insulin/glucose ratios were used as an index of insulin resistance. Area under the curves were analyzed using the GLM procedure of SAS. Insulin/Glucose ratios were evaluated using a mixed ANOVA with repeated measures with breed, time of sampling and their interaction in the model statement. Concentration at time zero of the analyte was included as a covariate in the statistical analysis. Significant differences among treatments were assessed using Bonferroni's multiple-range test. Iberian pigs had increased plasma insulin AUC (67.9%, $P < 0.01$) and insulin/glucose ratio (78.8%, $P < 0.001$) although no statistical difference in plasma glucose AUC was found ($P = 0.18$) compared to Landrace pigs. In conclusion, Iberian pigs showed lower insulin sensitivity of peripheral tissues evaluated using an intravenous glucose tolerance test.

Key words: insulin sensitivity, Iberian pig, glucose tolerance

T232 Reproductive performance of replacement beef heifers when estrus was synchronized with progesterone (CIDR) for 5 or 7 d, GnRH, and $PGF_{2\alpha}$. K. M. Bischoff*[1], T. E. Black[1], R. D. Estermann[2], G. A. Bridges[3], G. C. Lamb[1], and J. V. Yelich[2], *[1]North Florida Research and Education Center, University of Florida, Marianna, [2]Depertment of Animal Sciences, University of Florida, Gainesville, [3]North Central Research and Outreach Center, University of Minnesota, Grand Rapids.*

We determined if reproductive performance differed in replacement *Bos indicus* × *Bos taurus* beef heifers when estrus was synchronized with one of 3 protocols that included CIDR, GnRH, and $PGF_{2\alpha}$ (PG). Reproductive tract scores (RTS; scale 1 to 5 with 1 = immature and 5 = estrous cycling) were determined on d −7 and used to stratify heifers to one of 3 treatments: 1) GnRH (100 μg) and a CIDR insert d −7 and PG (25 mg) and CIDR removal on d 0 (7dCIDR; n = 113); 2) GnRH and CIDR insert on d −5 and CIDR removal and PG on d 0 (5dCIDR; n = 113); 3) PG and CIDR on d −7, GnRH on d −5, and CIDR removal and PG on d 0 (7dMOD; n = 117). All heifers received a second PG (25 mg) 8 h after CIDR removal. Estrus was detected for 60 h after CIDR removal, with heifers detected in estrus inseminated using the AM/PM rule. Heifers not detected in estrus received TAI 72 h after CIDR removal coincident with GnRH (100 μg). Bulls were inserted 10 d following TAI for a 103 d breeding season. Transrectal ultrasonography was used to diagnose pregnancy 55 d after TAI and 30 d following bull removal. Estrous response was reduced ($P < 0.05$) in the 5dCIDR (21%) treatment compared to the 7dMOD (43%) and 7dCIDR (35%) treatments. A. greater ($P < 0.05$) percentage of heifers with RTS of 3 (40%), 4 (49%), and 5 (46%) exhibited estrus than those with a RTS of 1 (14%) or 2 (11%). Conception rates of heifers exhibiting estrus were greater ($P < 0.05$) for the 7dMOD (62%; 31/50) than the 5dCIDR (33%; 8/24) and 7dCIDR (39%; 15/39) treatments. For heifers failing to exhibit estrus, TAI pregnancy rates (16%) did not differ between treatments. Synchronized AI pregnancy rates were greater ($P < 0.05$) in the 7dMOD (38%) treatment than the 5dCIDR (20%), and 7dCIDR (23%) treatments. Synchronized pregnancy rates for heifers with RTS of 1 (10%) and 2 (16%) were less ($P < 0.05$) than those with RTS 3 (34%), 4 (36%), and 5 (32%). Breeding season pregnancy rates did not differ between treatments (81%). In summary, synchronized AI pregnancy rates were greatest with the 7dMOD protocol and RTS affected reproductive performance.

Key words: estrus synchronization, beef heifer, CIDR

T233 Fat mobilization during early lactation: Effects on milk performance, feed intake, body condition and metabolic changes in dairy cows. C. Weber*[1], F. Becker[1], C. Hametner[1], B. Losand[2], R. M. Bruckmaier[3], W. Kanitz[1], and H. M. Hammon[1], *[1]Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany, [2]State Institute for Agriculture and Fishery, Dummerstorf, Germany, [3]Veterinary Physiology, Vetsuisse Faculty, Bern, Switzerland.*

Dairy cows mobilize body fat during early lactation to provide energy for milk production due to insufficient feed intake. However, there is huge individual variation in postnatal fat mobilization among cows indicated by a broad range of postnatal NEFA changes in blood plasma and liver fat concentration (LFC). The objective of the present study was to investigate feed intake, milk performance, and metabolic and endocrine changes in German Holstein cows (>11,000 kg milk/305 d in 2nd lactation) grouped according to different mean LFC on d 1, 14, and 28 after calving: L (<200 mg total fat/g DM; n = 10), M (200 – 300 mg total fat/g DM; n = 10), and H (>300 mg total fat/g DM; n = 7). Cows were studied from dry off up to 63 DIM in their 3rd lactation and were fed TMR ad libitum. DMI and milk yield were recorded daily, BW, BCS, and milk composition were measured weekly. Plasma concentrations of NEFA, BHBA, glucose, and insulin were measured in blood taken at 56, 28, 15, 5 d before expected calving and once weekly up to 63 DIM. Liver biopsies were taken at 1, 14, 28 DIM to measure total fat content. Data were analyzed by the Mixed Model of SAS with LFC and time as fixed effects. Mean hepatic fat concentration for H, M, and L were different ($P < 0.05$) among groups: 351 ± 14, 250 ± 10 and 159 ± 9 mg/g liver DM, for H, M, and L, respectively. DMI was lowest ($P < 0.05$) before calving in H, increased ($P < 0.01$) after calving in all groups, but was highest ($P < 0.05$) in L. Milk yield was not affected by LFC, but energy balance was least negative ($P < 0.01$) in L. BCS were highest ($P < 0.05$) before calving in H and the postnatal decrease was higher ($P < 0.05$) in H and M than in L. Plasma concentrations of NEFA and BHB increased more around calving ($P < 0.05$) in H than M and L, but plasma glucose was lowest in H. Plasma insulin concentrations after calving were highest in L. Greater fat mobilization in cows with elevated BCS before calving was associated with reduced DMI and a more severe negative energy balance, did not affect milk production, but influenced postnatal glucose and insulin status in cows.

Key words: dairy cow, fat mobilization, energy metabolism

T234 Fat mobilization around calving in high-yielding dairy cows affects hepatic gene expression of gluconeogenic enzymes but not enzymes involved in fatty acid oxidation. H. M. Hammon*[1], C. Weber[1], F. Becker[1], C. Hametner[1], B. Losand[2], and W. Kanitz[1], *[1]Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany, [2]State Institute for Agriculture and Fishery, Dummerstorf, Germany.*

Energy demands largely increase after calving in dairy cows and hepatic energy metabolism is affected by elevated glucose output due to milk production. As cows differ in fat mobilization around calving the objective of the study was to investigate hepatic gene expression of key-enzymes involved in gluconeogenesis, fatty acid oxidation, and ketone body formation in cows with variable liver fat concentration

(LFC) after calving. German Holstein cows were grouped according to mean LFC (as indicator of fat mobilization) on d 1, 14 and 28 after calving in low (L) (<200 mg total fat/g DM; n = 10), middle (M) (200 – 300 mg total fat/g DM; n = 10), and high (H) (>300 mg total fat/g DM; n = 7). Cows were fed TMR ad libitum. Liver biopsies were taken at 56 and 15 d before calving and at 1, 14, 28, and 49 DIM to measure LFC, glycogen, and mRNA concentrations of pyruvate carboxylase (PC), cytosolic phosphoenolpyruvate carboxykinase, glucose-6-phosphatase, propionyl-CoA-carboxylase (PCCA), carnitine palmitoyl-transferase 1A, acyl-CoA-synthetase long chain, acyl-CoA-dehydrogenase very long chain, hydroxy methyl glutaryl-CoA-synthetase 2, and peroxisome proliferator-activated factor (PPAR)α. Data were analyzed by the Mixed Model of SAS with LFC and time as fixed effects. Mean hepatic fat concentration for H, M, and L differed ($P < 0.05$) among groups: 351 ± 14, 250 ± 10 and 159 ± 9 mg/g DM, for H, M, and L, respectively. Glycogen concentrations decreased after calving in all groups, but were lowest in H ($P < 0.05$). All measured enzymes changed with time during the experimental period. PC mRNA concentrations increased immediately after calving highest ($P < 0.05$) in H and M. PCCA and PPARα tended to be lowest in H. Elevated fat mobilization indicated by LFC during early lactation affected hepatic glycogen and gene expression involved in glucose production and nuclear energy sensing, but not gene expression referred to hepatic fatty acid oxidation and ketone body formation.

Key words: dairy cow, fat mobilization, hepatic energy metabolism

T235 Ovarian characteristics, serum estradiol and progesterone concentrations, and fertility in lactating dairy cows in response to equine chorionic gonadotropin (eCG). S. L. Pulley*, L. D. Wallace, H. I. Mellieon, and J. S. Stevenson, *Kansas State University, Manhattan.*

Numbers of FSH receptors are greatest in maturing follicles on d 4 of the first follicular wave of the estrous cycle when LH receptors are first detected in granulosa cells of the dominant follicle. After having acquired LH receptors dominant follicles respond to both LH and FSH or eCG. Because the potential for eCG to influence follicle size and estradiol secretion, objectives were to evaluate the effects of eCG on serum ovarian steroids, corpus luteum (CL) diameter, estrual activity, and timed AI pregnancy rates. Cows (n = 121) in a single herd were enrolled in a Presynch-Ovsynch program. Cows received 2 injections of prostaglandin F2α (PG) 14 d apart (Presynch), with the second injection given 11 d before the onset of the Ovsynch protocol (GnRH injection 7 d before [GnRH-1] and 56 h after PG [GnRH-2], with AI administered 14 to 18 h after GnRH-2). Cows randomly received either saline or 400 IU eCG concurrent with the PG injection of the Ovsynch protocol (d 0). Blood samples were collected to monitor serum progesterone (d −7, 0, 2, 4, 9, 16, and 33) and serum estradiol (d 0, 1, 2, and 3). Serum estradiol did not differ between treatments from d 0 to 3. Estrual activity also was not affected by treatment. Overall expression of estrus was poor (eCG: 15.4%; 10/65 vs. saline: 16.4%; 9/55). Treatment with eCG improved neither ovulation response (96.9% vs. 100%; $P = 0.15$) nor multiple ovulation rates (20.3% vs. 18.2%) after GnRH-2 injection. Administration of eCG tended to increase the number of CL and on d 9 ($P = 0.08$) and d 16 ($P = 0.09$) after PG. Volume of luteal tissue was increased ($P = 0.04$) only on d 16 in response to eCG. Pregnancy diagnosis was determined by transrectal ultrasonography on d 33. Timed AI pregnancy rates did not differ between eCG (36.9%) and saline-treated cows (41.8%) cows. We concluded that administration of eCG at the time of PG provided no profertility advantages to dairy cattle when programmed for a timed insemination at first service.

Key words: eCG, fertility, Ovsynch

T236 A mechanistic metabolic model of regulation of reproductive processes in dairy cattle. J. P. McNamara[1], S. L. Shields*[1], and I. Lean[2], *[1]Washington State University, Pullman, [2]University of Sydney, Camden, NSW, Australia.*

The objective was to expand and continue evaluation of a deterministic, mechanistic, dynamic model of reproductive processes in the dairy cow. This research model will 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 in the literature (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 explicit. The physiological processes are integrated at the pathway level into one system to link genetic elements, nutrient use and reproductive processes. For example, equations link glucose, IGF-I and growth hormone to rates of follicle stimulating hormone, luteinizing hormone, and follicular growth. The days in milk at which cycling commences is directly related to amount of body fat (days at start cycling = 37.41 DIM − 0.1489 × body fat kg; $r^2 = 0.979$), which is an integral function of the sum of nutritional pathways. Degradation of estrogen and progesterone by the liver is a function of metabolic rate, as described by total ATP demand, so that for example, peak progesterone and estrogen in the first cycle are reduced by 10.9% and 6.3% as milk yield increases from 34 to 50 kg/d for the first 90 DIM. Related to feed intake, progesterone and estrogen first peak are reduced 15.2 and 8.1% as DMI increases from 19.6 to 27.0 kg/d. Progesterone directly affects early embryonic growth (energy used in embryonic growth (kcal/d) = 13.59 + 1.923 × (progesterone, ng/ml); $r^2 = 0.946$) and must be maintained at a pre-set level to allow embryonic growth to continue after 21 to 45 d after conception. The model behavior (pattern and direction of response) is consistent with literature values. This research model should be useful to frame specific hypotheses on control of reproductive processes by genetic and nutritional driven mechanisms.

Key words: reproduction model, nutrition, genetics

T237 Effect of prostaglandin $F_{2\alpha}$ on growth of *Escherichia coli* and *Streptococcus uberis* associated with bovine mastitis. C. Autran*[1], B. Shafii[2], M. McGuire[1], J. Dalton[3], and A. Ahmadzadeh[1], *[1]University of Idaho, Moscow, [2]Statistical Programs, College of Ag & Life Sci, Moscow, ID, [3]Caldwell R & E Center, Caldwell, ID.*

Certain fatty acids have been shown to inhibit the growth of mastitis pathogens. Moreover, prostaglandin $F_{2\alpha}$ ($PGF_{2\alpha}$: dinoprost tromethamine) inhibits the growth of *Staph. aureus* in vitro. The objective was to determine the bacteriostatic effects of $PGF_{2\alpha}$ on growth of *E. coli* and *Strep. uberis* in vitro. In Exp. 1, flasks containing tryptic soy broth were inoculated with *E. coli*, and subsequently treated with $PGF_{2\alpha}$ at concentrations of 0, 1.2, 2.4, 4.8 and 9.6 mg/mL. Cultures were sampled every 4 h over 24 h to determine bacterial growth (log cfu). The experiment was repeated 3 times. In Exp. 2, *Strep. uberis* was treated with $PGF_{2\alpha}$ (0, 0.6, 1.2, 2.4 and 4.8 mg/mL). The procedures were identical to Exp. 1. Data were analyzed using ANOVA, and regression procedures. In Exp. 1 there was an effect of treatment by time interaction on mean log cfu ($P < 0.05$) for *E. coli*. Only the mean log cfu values of the 9.6 mg/mL $PGF_{2\alpha}$ were different ($P < 0.05$) at 12 h from

the control. The regression models showed that the pattern of bacterial growth over time for 4.8 mg/mL ($P = 0.05$) and 9.6 mg/mL $PGF_{2\alpha}$ ($P < 0.05$) were different from the control. Moreover, 9.6 mg/mL of $PGF_{2\alpha}$ was the most effective dose inhibiting *E. coli* growth. In Exp. 2, there was an effect of treatment and treatment by time interaction on mean log cfu for *Strep. uberis* ($P < 0.05$). At 12 and 24 h of growth, mean log cfu for all $PGF_{2\alpha}$ concentrations differed ($P < 0.05$) from the control, in a dose-dependent manner. Regression results revealed that the growth curve pattern of *Strep. uberis* over 24 h for each treatment was different compared with the control ($P < 0.05$), and the increase in growth rate over time for treatments 2.4 and 4.8 mg/mL was different from the control ($P < 0.05$). These results provide evidence for the first time that $PGF_{2\alpha}$ has inhibitory effects on growth of *Strep. uberis* in vitro; however, growth inhibition of *E. coli* was only achieved with the greatest concentration of $PGF_{2\alpha}$. Gram-positive mastitis causing bacteria (*Strep. uberis*) appear to be more susceptible to $PGF_{2\alpha}$ than gram-negative bacteria (*E. coli*).

Key words: prostaglandin $F_{2\alpha}$, *E. coli*, *Strep. uberis*

T238 Effects of sequential injections of GnRH at 17 and 24 d after AI on progesterone concentration and pregnancy losses. A. L. A. Scanavez*[1], J. G. N. Moraes[1], R. G. Bruno[2,3], K. J. Lager[2,3], J. A. H. Rivera[2], P. R. B. Silva[1], L. G. D. Mendonça[1], T. R. Bilby[2], and R. C. Chebel[1], *[1]Department of Veterinary Population Medicine, University of Minnesota, St. Paul, [2]Texas AgriLife Research and Extension Service, Texas A&M System, Stephenville, [3]Department of Agricultural Science, West Texas A&M University, Canyon.*

Objectives of the current study were to determine whether sequential injections of GnRH at 17 ± 3 and 24 ± 3 d after pre-enrollment artificial insemination (AI), would reduce pregnancy losses between 31 ± 3 and 66 ± 3 d after AI by increasing progesterone concentrations (P4) at 24 ± 3 and 31 ± 3 d after AI. Lactating cows from 2 dairies (MN-Jersey cows and TX-Holstein cows) were enrolled in the study at 17 ± 3 d after pre-enrollment AI. At enrollment cows were grouped by parity and number of AI and assigned to 1 of 3 treatments in a ratio of 1:2:1. Cows assigned to the 2GnRH treatment received 100 µg of GnRH at 17 ± 3 and 24 ± 3 d after pre-enrollment AI; cows assigned to the 1GnRH treatment received 100 µg of GnRH at 24 ± 3 d after pre-enrollment AI; and, control cows received no GnRH. All cows were examined by ultrasound at 31 ± 3 d after pre-enrollment AI and those diagnosed pregnant were re-examined at 66 ± 3 d after pre-enrollment AI. Blood samples were collected from a subgroup of cows at 24 ± 3 (MN-123 cows and TX-160 cows) and 31 ± 3 (MN-142 cows) d after pre-enrollment AI for determination of P4. There were 514 2GnRH, 1099 1GnRH, and 648 control cows pregnant at 31 d after AI and re-examined at 66 d. At 24 d after pre-enrollment AI P4 was not ($P = 0.70$) affected by treatment (7.5 ± 0.2ng/mL). At 31 d after pre-enrollment AI P4 was greatest ($P < 0.01$) for 2GnRH cows (8.5 ± 0.4ng/mL), but was not ($P = 0.16$) different between 1GnRH (6.2 ± 0.4 ng/mL) and control (7.0 ± 0.5ng/mL) cows. Treatment ($P = 0.99$) and site ($P = 0.81$) did not affect pregnancy loss, but the interaction between treatment and site affected ($P = 0.04$) pregnancy loss. In the MN-dairy 2GnRH (7.5%) cows had fewer pregnancy losses than 1GnRH (11.8%) and control (10.4%) cows and in the TX-dairy 2GnRH (11.9%) had more pregnancy losses than 1GnRH (7.9%) and control (8.8%) cows. There was a quadratic correlation between P4 at 31 d after AI and pregnancy loss [pregnancy loss = 87.4 − (26.5xP4)+(2.1xP42); r2 = 99.7%]. Jersey cows treated with GnRH at 17 and 24 d after AI had greater P4 at 31 d after AI and reduced pregnancy losses, but Holstein cows did not benefit from GnRH treatment after AI.

Key words: dairy cow, pregnancy loss, GnRH

T239 Effect of GnRH treatment at critical stages of estrous cycle following artificial insemination on pregnancy rate in lactating Holstein dairy cows. Z. Hakimi, A. Z. Shahne, H. M. Yegane, and R. Masoumi*, *University of Tehran, Karaj, Karaj, Iran.*

Embryonic mortality is regarded as one of the major causes of reproductive failure in cattle resulting in reduced pregnancy rates, slower genetic improvement and substantial financial losses to dairy operations. Progesterone hormone deficiency after insemination has an important place among the causes of early embryonic death. Even though average fertilization rates of heifer and cows are between 88 and 90, 20% or more of the embryos are lost after insemination before 21th days. GnRH injections are applied from 4 to 15 d after insemination for the prevention of early embryonic death which is attached to inadequate progesterone hormone in cattle. The aim of present field study was to determine the effect of GnRH treatment on pregnancy rate of lactating Holstein dairy cows in critical stages of estrous cycle following AI. A total of 174 Holstein cows were randomly assigned into one of 5 following treatment groups: Cows in group A (n = 35) were not treated and served as control group. Cows in group B (n = 35) were treated intramuscularly with a GnRH analog (Gonadorelin acetate; 25 µg) on d 0 (at the time of AI). Cows in group C (n = 39) were treated with GnRH on d 0 and 5. Cows in group D (n = 36) were treated with GnRH on d 0 and 11. Cows in group E (n = 29) were treated with GnRH on d 0, 5 and 11. Pregnancy was diagnosed by rectal palpation 45–50 d after insemination. Dichotomous data were analyzed using PROC LOGISTIC of SAS. Pregnancy rate for treatment groups were 42.2, 60, 51.8, 63.9, 55.1%, respectively. Although, there was a notable difference between control and treatment groups in PR, but the differences were not statistically significant ($P < 0.05$). Therefore, GnRH administration to stimulate CL function using single or multiple doses of GnRH during the luteal phase could not increase pregnancy rate in present study.

Key words: GnRH, pregnancy rate, dairy cattle

T240 Effect of insemination timing on conception rates of dairy cows having high activity as identified by the Select Detect activity monitor. R. L. Nebel*[1], J. M. DeJarnette[1], and E. Harty[2], *[1]Select Sires Inc., Plain City, OH, [2]Dairymaster, Causeway, Co. Kerry, Ireland.*

The primary objective of this field trial was to determine the effects of interval to AI on conception rates of dairy cows identified as high activity using the Select Detect activity system. The Select Detect system uses neck-mounted sensors to scrutinize acceleration and intensity of movement with continuous 24-h surveillance of estrous related activity. Farm personnel inseminated cows at random intervals after onset of HA according to standard procedures, which in most herds was a once daily AI program. The hour activity exceeded the HA threshold was used to determine interval from onset to AI. Conception rates from 4,126 services were recovered from 19 herds located in 8 states. The mean duration of HA was 10.5 ± 0.1 h with a median of 10.0 h indicating a slightly skewed distribution. The distribution of duration of HA was as follows: ≤4 h, 15.8%; 5 to 8 h, 17.2%; 9 to 16 h, 46.2% and ≥16 h, 21.3%. The parity by AI interval interaction significantly influenced conception rates. Among primiparous cows, a curvilinear relationship was apparent with optimum conception occurring at AI intervals of 13 to 16 h after HA and trended lower for both earlier and later AI intervals. Among multiparous cows, conception rates at intervals ≤12 h were different that those >16 h with 13 to 16 h being intermediate. Specifically, conception rates for primiparous and multiparous cows respectively were 36 and 32.4% (0 to 4 h), 37.5 and 32.2% (5 to 8 h), 41.2 and 32.9% (9 to 12 h), 45 and 28.9% (13 to 16 h), and 37.7 to 23.3% (17 to 26 h). In conclusion, these results are consistent with similar studies based on observed mounting activity wherein optimum conception rates are obtained at AI intervals proximal to 12 h after detected estrus (HA) with shorter intervals appearing to be less compromising to conception rates that are longer intervals. The Select Detect system allows conception rates to be optimized because of 24-h surveillance and precision of determining activity related to estrus.

Key words: timing of AI, Select Detect, MooMonitor

T241 Reproductive performance in Mexican Holstein dairies by geographic region. H. Lopez*, F. Cavazos, A. Gonzalez, L. Ruiz, and C. Vergara, *ABS Global Inc.*

Our objectives were to compare reproductive indicators from Holstein dairies in 5 regions of Mexico and establish benchmarks for the 20% most efficient herds. Data from 119,097 cows and 377,025 inseminations were evaluated from January to December 2010 form 54 dairies in Region 1 (R1[BCN, BCS; n = 10 herds]), Region 2 (R2[CHH; n = 5 herds]), Region 3 (R3[AGU, JAL; n = 14]), Region 4 (R4[QUE; n = 6]), and Region 5 (R5[COA, DUR; n = 19]). Analyses were conducted with the MIXED procedure using herd as the experimental unit. Mean herd size was greater ($P < 0.05$) for R2 (4,178 ± 3,702) and R5 (3,308 ± 2,573) than R1 (735 ± 225), R3 (1,484 ± 866), and R4 (1,202 ± 735). Days for waiting period (R1 = 51 ± 4; R2 = 51 ± 2; R3 = 50 ± 4; R4 = 53 ± 9; R5 = 47 ± 6), pregnancy diagnosis (R1 = 41 ± 4; R2 = 37 ± 1; R3 = 40 ± 4; R4 = 42 ± 4; R5 = 40 ± 1), and reconfirmation (R1 = 120 ± 42; R2 = 94 ± 21; R3 = 114 ± 37; R4 = 105 ± 35; R5 = 91 ± 6) did not differ among regions. Insemination risk was greater ($P < 0.05$) for R2 (62%) and R5 (65%) than R1 (58%), and R3 and R4 (56%). Percentage of cows bred at estrus was greater ($P < 0.05$) for R3 (83%) and R4 (85%), intermediate for R2 (79%) and R5 (77%), and lower for R1 (71%). Conception rate for cows bred at estrus was greater ($P < 0.05$) for R1 and R2 (36%), intermediate for R3 and R4 (33%), and lower for R5 (29%). The % of cows bred after synchronization was greater ($P < 0.05$) for R1 (29%), intermediate for R2 (21%) and R5 (23%), and lower for R3 (17%) and R4 (15%). Conception rate for TAI cows was greater ($P < 0.05$) for R1 (34%), intermediate for R2 and R3 (29%), and R4 (31%), and lower for R5 (26%). Pregnancy rate was greater ($P < 0.05$) for R1 (20%) and R2 (22%) than R3 and R4 (18%), and R5 (17%). Percentage of cows pregnant by 100 DIM was greater ($P < 0.05$) for R1 (52%) and R2 (55%) than R3 and R4 (48%), and R5 (44%). The 20% most efficient operations had mean pregnancy rate of 23%, waiting period of 54 ± 3 d, insemination risk of 63%, conception rates to estrus of 38%, TAI of 35%, and percentage of cows pregnant by 100 DIM of 58%. Regional differences existed in reproductive parameters in Mexican dairies, which may be attributed to program compliance and differences in herd size.

Key words: fertility, reproduction, estrus

T242 Effects of 2.1 and 10 x 10^6 dosages of sex-sorted or conventionally processed sperm on conception rates of Holstein heifers. J. M. DeJarnette*[1], M. A. Leach[1], R. L. Nebel[1], C. E. Marshall[1], C. R. McCleary[2], and J. F. Moreno[3], *[1]Select Sires Inc., Plain City, OH, [2]Sexing Technologies Inc., Plain City, OH, [3]Sexing Technologies Inc., Navasota, TX.*

The conception rates of Holstein heifers after AI with 2.1 or 10 × 10^6 sperm dosages of sex-sorted or conventionally processed sperm were compared. Ejaculates collected by artificial vagina from 8 Holstein sires were cryopreserved at either 2.1 or 10 × 10^6 sperm per dose with or without sorting to 90% purity for X-chromosome bearing spermatozoa using flow cytometry. All treatments were processed in an egg-yolk (20%), TRIS, glycerol (7%) extender and packaged in color-coded 0.25-mL French straws. Straws (n = 350 straws/treatment per sire) were packaged and distributed in aliquots of 12 (3 straws of each treatment) to 51 herds of Holstein heifers. Straw color was recorded in the on-farm record keeping system at the time of AI and retrieved by electronic download. A total of 9,172 services were recovered providing a mean sample size of 287 ± 3.5 services/sperm dose per semen type within sire (range: 248 to 318). Conception rates (LSM) were influenced (Tukey test) by the main effects of herd, sire, semen type, sperm dosage, and service number. The herd by sperm dosage interaction was significant and implied some herds (technicians) are more proficient than others at maintaining high levels of conception with reduced sperm dosages. Across herds and sires, the conception rates of each semen type by sperm dosage combinations were as follows: 2.1 × 10^6 sex-sorted, 38%, n = 2,319; 10 × 10^6 sex-sorted, 44%, n = 2,279; 2.1 × 10^6 conventional, 55%, n = 2,282; 10 × 10^6 conventional, 60%, n = 2,292. The observation that conception rates of sex-sorted semen were improved by the 10 × 10^6 sperm dosage is encouraging toward the prospectus of development of a commercially available sex-sorted product with improved conception potential over existing technology. However, the failure of the 10 × 10^6 sex-sorted sperm dosage to achieve conception rates comparable to either dosage of conventional semen is somewhat discouraging toward the plausibility of comparable conception rates to conventional semen in the absence of major technological advances in efficiency of sperm sorting or cryopreservation.

Key words: sex-sorted semen, sperm dosage, flow cytometry

T243 IGF-I increases in vitro embryo production and protects against deleterious effects of heat stress in Nelore (*Bos indicus*) and Holstein (*Bos taurus*) breeds. R. A. Satrapa, E. M. Razza, C. F. Silva, T. Nabhan, R. A. L. Simoes, and C. M. Barros*, *Department of Pharmacology - IBB, University of São Paulo State, Botucatu, Sao Paulo, Brazil.*

In the present study the beneficial effect of IGF-I during in vitro culture of embryos was tested comparatively between a more tolerant (Nelore = N) versus a less thermo tolerant breed (Holstein = H). Oocytes, obtained in a local abattoir, from N and H females were matured and fertilized with semen from N (n = 6) and H (n = 6) sires, respectively. Embryos cultured was performed at 39°C, 90% N_2, 5% CO_2, and 5% O_2 in SOFaaci medium. In experiment 1 and 2, embryos from both breeds with ≥16 cells were randomly allocated in 4 groups: Control (maintained at 39°C all the time) HS (96 h after fertilization the embryos were subject to heat shock of 41°C for 9h and then returned to a temperature of 39°C), IGF (cultured in the presence of IGF, 100 ng/ml), and IGF-HS (IGF and HS). In experiment 1 cleavage, morula, and blastocyst rates were evaluated; whereas in experiment 2 apoptosis was determined by TUNEL, in both breeds simultaneously. The results were analyzed by logistic regression using the Proc GENMOD (SAS). In experiment 1, HS significantly decreased blastocyst rates in N (29.6 vs. 24.1%, control vs. HS, respectively) and H (20.1 vs. 15.5%). Adding IGF-I to the culture medium increased significantly blastocyst rates in both breeds N (23.3% vs. 29.9%, -IGF vs. +IGF, respectively) and H (15.7 vs. 21.4%). In experiment 2, HS increased ($P < 0.05$) apoptosis rates both in N (3.3 ± 0.2 vs. 4.1 ± 0.3) and H (4.8 ± 0.3 vs. 6.0 ± 0.4). It is concluded that adding IGF to the culture medium of embryos of both breeds increases blastocyst rate and decreases apoptosis. Additionally, Holstein were more sensitive to the deleterious effects of HS than Nelore embryos, since there was a higher decrease in blastocyst rate of heat stressed embryos from Holstein than from N cows, as well as a higher incidence of apoptosis in H embryos.

Key words: heat stress, IGF, embryo

T244 Cytological endometritis incidence in crossbred dairy cows. R. M. Santos*, L. C. Carneiro, J. P. E. Saut, A. F. Ferreira, M. F. S. Padua, and N. Bortoletto, *FAMEV-UFU, Uberlândia, Minas Gerais, Brazil.*

The objective was to evaluate the incidence and risk factors for cytological endometritis in crossbred dairy cows (Holstein/Gyr) maintained in a hot climate in Southwestern Brazil. The cytological endometritis diagnostic was performed in primiparous (n = 26) and multiparous (n = 100) cows, from a herd with 480 lactating cows maintained in pasture during the rainy season and at loose housing in the dry season. Average milk production was 18.75 kg/day. At 48.18 ± 9.10 DIM the cows had their body condition scored using a 5-point system and were examined by ultrasound to determine CL and uterine fluids. The vaginal discharge was evaluated by the gloved hand method. The cytological samples were collected only in cows with clear or translucent vaginal mucus and no uterine fluids. Cytological sample of the endometrium were collected using a cytobrush adapted for use in cattle. Slides for cytological examination were prepared on farm by rolling the cytobrush on a glass microscope slide and air-dried. The cytology slides were stained with modified Wright Giemsa stain. Each slide was examined at 400× magnification to perform the differential cell count of 200 cells (polymorphonuclear neutrophils and endometrial cells) by 2 observers. Cytological endometritis was defined when the proportion of neutrophils were ≥5% (Gilbert et al., 2005). The incidence of cytological endometritis was analyzed by the binary logistic regression including in the model calving season, BCS, presence of CL, parity and DIM. The cytological endometritis incidence in crossbred dairy cows was 25.40%. Cows calving at spring/summer season had tendency (34.04 vs. 20.25%; $P = 0.057$) to have higher cytological endometritis incidence than cows calving at autumn/winter. Cows with BCS ≤2.5 had higher (31.25 vs. 15.22%; $P = 0.04$) cytological endometritis incidence than cows with BCS ≥2.75. The effects of the CL, parity, and DIM were not different. In conclusion, cytological endometritis was related to BCS but not other production factors. Supported by FAPEMIG.

Key words: uterine disease, endometritis, dairy cows

T245 Effect of simultaneous thawing of multiple semen straws and sequence of insemination on pregnancy rate for timed-AI in suckled multiparous Nelore cows. L. Z. Oliveira*[1], V. F. M. Hossepian de Lima[1], R. M. Santos[2], T. Martins[3], R. F. G. Peres[4], H. B. Graff[4], E. R. Carvalho[4], A. F. C. de Andrade[5], and R. P. Arruda[5], *[1]FCAV-UNESP, Jaboticabal, SP, Brazil, [2]FAMEV-UFU, Uberlândia, MG, Brazil, [3]FMVZ-UNESP, Botucatu, SP, Brazil, [4]Agropecuária Fazenda Brasil, Nova Xavantina, MT, Brazil, [5]FMVZ-USP, Pirassununga, SP, Brazil.*

Because of large breeding herds and the frequent use of fixed-time artificial insemination (TAI) in Brazil, multiple cows are often bred simultaneously. This results in the routinely practice of thawing simultaneously more than one straw of semen. The objective of this study was to determine the effect of simultaneous thawing of multiple 0.5-mL semen straws and sequence of insemination on pregnancy rate (PR) at TAI in suckled multiparous Nelore cows. All cows (n = 479) received 2 mg of estradiol benzoate and an intravaginal progesterone releasing device on d 0. On d 8 the device was removed and the animals were treated with 500 µg of PGF2α, 300 UI of eCG and 0.5 mg of estradiol cipionate. At 48 h after device removal the cows were TAI. Ten 0.5-mL frozen straws were thawed simultaneously in an electric water-bath (36°C) for a minimum of 30s. Semen doses from 3 Angus bulls were utilized. The sires and the straw sequence were equally distributed across 2 AI technicians. The records also included sequence of insemination (first, second, third, until tenth) and time of seminal deposition. The cows were divided into different groups: cows inseminated with 1st, 2nd and 3rd semen straws (G1); cows inseminated with 4th, 5th and 6th semen straws (G2); cows inseminated with 7th, 8th, 9th and 10th semen straws (G3). Ultrasound pregnancy diagnosis was performed 40 d after TAI. The PR at TAI was analyzed using PROC LOGISTIC of SAS, including model effects of bull, inseminator and group. The mean time (±SD) of straws remaining in the thawing bath were 01:30 ± 00:51 (G1), 03:36 ± 01:10 (G2) and 06:13 ± 01:44 min (G3). The PR was affected ($P = 0.009$) by sequence of insemination (G1: 52.78%; G2: 53.85%; G3: 39.06%). An important point when considering simultaneous thawing of straw groups is the thawing bath would serve as an incubating environment for the semen, and could have influenced the sperm viability and the fertility of the spermatozoa.

Key words: Nelore, pregnancy rate, simultaneous thawing

T246 An individual cow-based model to aid in decision making about reproductive management of dairy cows. P. Federico*[1], A. De Vries[2], G. M. Schuenemann[3], and K. N. Galvão[2], *[1]Capital University, Columbus, [2]University of Florida, Gainesville, [3]The Ohio State University, Columbus.*

Many factors influence the reproductive and productive performance of dairy herds, consequently, profitability. Choosing the most effective reproductive protocol for a given herd is a critical managerial decision. To assess the effectiveness and profitability of different AI protocols, we developed an individual-based model to simulate a dairy herd. The reproductive status and milk production of each individual cow is tracked over time accounting for the stochastic nature of events such as estrus, conception, abortion, and mortality. Novel components of this model include: 1) implementation of various reproductive strategies [estrus detection (ED) only, Ovsynch, Presynch-Ovsynch, and Presynch-Ovsynch with ED]; 2) effectiveness of protocol implementation (e.g., accuracy of ED, compliance with administration of injections); 3) daily dynamic tracking of all events (e.g., milk, pregnancy, replacements, birth) that occur based on probability distributions; and 4) user-friendly interface to set up strategies, parameter values, and to visualize daily outcomes of the model. Components 1 and 2 provide quantitative information on best AI programs according to the effectiveness of protocol implementation (e.g., ED only is better than Ovsynch with poor compliance). Component 3 allows decision makers to estimate the timing to reach the new level of pregnancy and milk yield after a reproductive change is implemented at the farm level. Moreover, component 4 facilitates the understanding of the magnitude and the time to attain the expected true benefits. This is a key tool for outreach programs to motivate the adoption of best strategies for a particular farm. Additionally, the stochastic nature of the model helps the decision makers to be aware of the variability of the outcomes (e.g., percent pregnant) due to herd size and pure chance. Sensitivity analysis quantifies the influence of some of the factors affecting the reproductive performance. Through a mechanistic and bottom-up approach we obtained herd level parameters comparable to real on-farm values (e.g., percent pregnant, milking, or culled).

Key words: dynamic model, dairy cow, reproduction

T247 Efficacy of embryo transfer in lactating dairy cows during summer using fresh or vitrified embryos produced in vitro with sex-sorted semen. II. Calving data. T. R. Bilby*[1], J. Block[2], B. M. Stewart[1], P. Morelli[1], L. Bonilla[3], and P. J. Hansen[3], *[1]Texas AgriLife Research and Extension, Texas A&M System, Stephenville, [2]OvaTech LLC, Gainesville, FL, [3]Department of Animal Sciences, 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 calving rates and percentage of heifers born 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 examined by ultrasound for presence of a corpus luteum (CL). An 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 were no treatment by farm interactions. The percentage of cows with live births was significantly increased for ET-F than for ET-V and AI among all cows (27.5 vs. 17.1 and 14.6%) and synchronized cows (29.9 vs. 18.5 and 20.0%). The percentage of cows giving birth to a live heifer was significantly increased for ET-F and ET-V compared with AI among all cows (79.1 and 72.5 vs. 50.0%) and synchronized cows (79.1 and 72.5 vs. 50.0%). There was no difference between ET-F and ET-V for percent live heifer births but both were greater than for AI. There was no effect of treatment on embryo loss. The transfer of fresh embryos produced in vitro using sex-sorted semen to lactating dairy cows during summer can effectively increase the percentage of cows that calve and also the percentage of cows that give birth to a live heifer compared with AI with conventional semen.

Key words: embryo, heat stress, dairy

T248 Economic evaluation of embryo transfer in dairy cows during the summer using linear programming. A. De Vries*[1], T. R. Bilby[2], J. Block[3], and P. J. Hansen[1], *[1]University of Florida, Gainesville, [2]Texas AgriLife Research and Extension, Texas A&M System, Stephenville, [3]OvaTech LLC, Gainesville, FL.*

The objective of this study was to estimate the economic value of the transfer of sexed female embryos (ET) to dairy cows in the summer compared with the use of conventional AI year round. Summer heat stress reduces fertility of dairy cows, but transfer of fresh sexed embryos in the summer may double the chance of pregnancy per transfer and result in more heifer calves. However, ET is more expensive than conventional AI, and the greater generation of pregnancies in the summer changes the calving pattern and seasonal cash flows. An economic analysis was carried out using a Markov chain dairy herd simulation model combined with linear programming. The model simulated cows from first calving up to the end of the ninth parity, used weekly steps, and assumed a 50% service rate. Seasonality was modeled as 52 periods per year. Heat stress was assumed to affect milk yield production, fat yield production, fertility, involuntary culling, and death risk. Decision variables were the number of purchased heifers per period. Embryo transfer was assumed to cost $60 per transfer compared with $20 per AI. Herd constraints were a maximum of 1300 cows (dry and lactating) or 1000 lactating cows during each week of the year. Results showed that the use of ET in the summer increased profit/cow per yr by $22 for the total cow constraint. Revenues were not changed, but the use of ET resulted in $39 less replacement cost per yr, as well as $20 greater total breeding costs and $3 greater feed cost. The use of ET reduced the maximum percentage of milking cows in the spring from 94% to 91% and reduced the number of dry cows. When the number of milking cows was the herd constraint, profit/milking cow per yr was increased by $42 when ET was used in the summer. Total costs were reduced by $4 per milking cow per yr and total revenues increased by $39, mostly due to increased milk sales and heifer calf sales. In conclusion, embryo transfer during the summer in heat stressed dairy cows is profitable, especially when the number of milking cows is the main constraint.

Key words: embryo transfer, heat stress, economics

T249 Economic comparison of two resynchronization protocols initiated at different intervals after insemination on fertility in lactating dairy cows. J. G. N. Moraes*[1], R. G. S. Bruno[2,3], P. R. B. Silva[1], A. L. A. Scanavez[1], L. G. D. Mendonça[1], J. A. Hernandez-Rivera[2], K. J. Lager[2,3], T. R. Bilby[2], J. Fetrow[1], and R. C. Chebel[1], *[1]Department of Veterinary Population Medicine, University of Minnesota, St. Paul, [2]Texas AgriLife Research and Extension Service, Texas A&M System, Stephenville, [3]Department of Agricultural Science, West Texas A&M University, Canyon.*

Objectives were to evaluate the effect resynchronization protocol on rate of re-insemination and economic outcomes. Cows from 2 dairies (MN = 3,069 and TX = 2,149) at 17 ± 3 d after pre-enrollment AI (PreEAI) were enrolled in the study. Cows were examined for pregnancy 31 ± 3 d after PreEAI. Cows in the early presynchronized resynchronization (EG) and early resynchronization (EOV) treatments started the resynchronization protocol (Ovsynch56) at 24 ± 3 d after PreEAI and EG cows received a GnRH at 17 ± 3 d after PreEAI. Cows in the late presynchronized resynchronization (LG) and late resynchronization (LOV) treatments started the resynchronization protocol at 31 ± 3 d after PreEAI and LG cows received a GnRH at 24 ± 3 d after PreEAI. Cows were re-inseminated when observed in estrus throughout the study. Cost of GnRH and PGF were $1.92/dose, value of pregnancies $275, value of pregnant cow $1,000, value of non-pregnant cow $600, and cost of a day open $3. Pregnancy to PreEAI was not (P = 0.54) different among treatments (44.2%). Smallest (P < 0.01) percentage of EG cows were re-inseminated before pregnancy diagnosis (EG = 28.8, EOV = 44.1, LG = 42.6, LOV = 47.6%), re-insemination rate was smallest (P < 0.01) for EG cows, and more EG cows were re-inseminated at timed AI (EG = 65.9, EOV = 49.6, LG = 42.4, LOV = 38.7%). Interval between AI was smallest (P < 0.01) for EOV cows (EG = 31.2 ± 0.3, EOV = 29.0 ± 0.3, LG = 32.7 ± 0.3, LOV = 32.0 ± 0.3d). Treatment did not affect pregnancy per AI of cows diagnosed non-pregnant to PreEAI (29.2%;P = 0.24) and the percentage of cows pregnant to PreEAI and resynchronized AI (55.4%; P = 0.78). Cost of resynchronization was greatest for EG treatment (EG = 9.1 ± 0.1, EOV = 5.0 ± 0.1, LG = 5.6 ± 0.1, LOV = 2.8 ± 0.1), but return per resynchronized cow was not affected by treatment (EG = 778.8 ± 11.6, EOV = 766.6 ± 11.6, LG = 786.3 ± 10.9, LOV = 790.3 ± 10.2). Because the EG treatment suppressed estrus signs, the difference in interval between AI among treatments was very small and because treatment did not affect percentage of cows pregnant to re-insemination there were no differences in economic return per cow non-pregnant to PreEAI.

Key words: economics, dairy cow, resynchronization

T250 The effects of probiotic, prebiotic, and plant extract on egg quality in layer hens. V. Kalderon[1] and V. Akay*[2], [1]*Cakabey High School, Izmir, Turkey,* [2]*Global Nutritech Biyoteknoloji Ltd., Kocaeli, Turkey.*

Researchers have been looking for alternative solutions to antibiotics for several reasons including the ability of microorganisms to develop resistance against antibiotics, the detrimental effects of antibiotics on the environment, and the high cost. This study was conducted to determine the effects of probiotic, prebiotic and plant extract on hen weight, various egg parameters, and egg bacterial growth in layer hens. Fifty 16-wk-old Bovans Brown layer hens were purchased from a local company and at 24 wks of age were randomly assigned to 5 treatments and kept in cages (70 × 93 × 114 cm). Treatments were: 1) Control; 2) Probiotic [1 kg BENESACC (*Saccharomyces cerevisiae* NCYC R618, 4 billion cfu/gr)/ton feed, Global Nutritech Ltd., Turkey]; 3) Prebiotic [1 kg EXCELMOS (mannanoligisaccharides)/ton feed, Global Nutritech Ltd., Turkey]; 4) Probiotic+Prebiotic (1 kg BENESACC and 1 kg EXCELMOS/ton feed); and 5) Oregano extract (2 lt ROPADIAR/ton water, Ropa Pharm Inc., The Netherlands). Feed and water were provided ad libitum; feeding was done manually several times a day. Hens were weighed weekly. Egg yields and egg weights were recorded daily and eggs were kept at 4°C for later analysis of protein content and bacterial growth. The trial continued 6 wks, and data were reported on a weekly basis. There were no differences for hen weights among treatment groups. Egg weights increased during trial for only the Probiotic, Prebiotic and Oregano groups compared with the Control and Probiotic+Prebiotic groups. Egg size increased for only the Probiotic and Prebiotic groups compared with the Control, Probiotic+Prebiotic and Oregano groups. There were no differences among groups for egg protein content. No bacterial growth was observed for the Probiotic+Prebiotic group, while bacterial growth was recorded for other groups. In conclusion, probiotic, prebiotic and oregano extract, or a combination of probiotic and prebiotic, can be used in layer hens to improve egg quality. However, a combination of probiotic and prebiotic provided the best results against bacterial growth in eggs.

Key words: probiotics, prebiotics, layer hen

T251 The in vitro antibacterial activity of extracts by different extraction of Chinese pulsatilla root, purslane herb, dyers woad leaf, and ash barks—traditional Chinese medicine. F. Rejun*[1], W. Xiangrong[1], H. Jianghua[1], Y. Yulong[2], and C. Caihui[1], [1]*Department of Animal Science and Technology, Hunan Agricultural University, Changsha, Hunan, P. R. China,* [2]*Institute of Subtropical Agriculture, Chinese Academy of Sciences, Changsha, Hunan, P. R. China.*

Conventional drugs usually provide effective antibiotic therapy for bacterial infections but there is an increasing problem of antibiotic resistance and a continuing need for new solutions. The aim of present study is to develop novel antibacterials replacer to overcome effectively bacterial resistance. Aqueous extracts and ethanolic extracts from Chinese pulsatilla root, purslane herb, dyers woad leaf and ash barks, were screened against *E. coli* C 84008 and *Salmonella pullorum* C (79–13) by using the disk diffusion test technique. The minimum inhibitory concentrations (MIC) were determined by micro-dilution method. As a result of this finding, The ethanolic extract of dyers woad leaf was not inhibitory to *E. coli*. Chinese pulsatilla root, purslane herb, dyers woad leaf (water) extracts were active against all the bacteria tested. The aqueous extracts of Chinese pulsatilla root and dyers woad leaf and the ethanolic extracts of ash barks had the lowest MIC against Salmonella pullorum (0.025 g/mL); the ethanolic extracts of ash barks had the lowest MIC against *E. coli* (0.025 g/mL).

Key words: traditional Chinese medicine, aqueous extracts, ethanolic extract

T252 Effect of season on four categories of fresh and current new mastitis infections in Minnesota. R. F. Leuer* and J. K. Reneau, *University of Minnesota, Saint Paul.*

New infection rates are a leading indicator of a dairy's udder health. Seasonal climate changes make it challenging to produce milk at a consistent quality level. Identifying problem months is important to focus effort on preventing spikes of high new infections. The objective of this study was to identify and quantify the months where herds have the highest percent of fresh cows with new infections (FNI) and percent of current lactating cows with new infections (CNI). Minnesota DHIA monthly average herd somatic cell count (SCC) records were collected from January 2007 to November 2010. Monthly herd tests without SCC information were removed and only herds with an average of 10 tests per year over the collection period were included. Herds were divided into 4 categories based on average herd SCC over the collection period. Low herds (L) with less than 200,000 SCC (n = 325), medium low (ML) herds between 200,000 and 300,000 SCC (n = 547), medium high herds (MH) herds between 300,000 and 400,000 SCC (n = 470), and high herds (H) above 400,000 SCC (n = 438). Monthly records (n = 66,296) were analyzed using PROC GLM with

significant differences determined at $P < 0.05$ using Tukey's multiple comparisons test. FNI was different in all categories except for MH and H (L = 11.8, ML = 14.1, MH = 15.6, H = 15.7). The statistically highest month for FNI was June (L = 12.7, ML = 15.1, MH = 17.2, H = 17.6) for all categories, with FNI similar for MH and H. The 4 categories were all significantly different in overall average CNI (L = 8.1, ML = 10.5, MH = 12.5, H = 14.2). High months of CNI for L herds were July and August (9.1, 9.3), ML high months were July, August, and September (11.6, 11.9, 11.2), MH high months were July, August, and September (13.6, 13.6, 13.1), and H high months were January, February, July, and August (15.1, 14.4, 15.3, 14.9). The greatest challenge for FNI appeared to be spring when cows may be exposed to the dampest environments. The summer months were the worst for CNI, with the addition of the deep winter months for the poorest milk quality herds.

Key words: SCC, DHIA, new infections

T253 Effect of somatic cells counting on milk composition of Holstein cows. J. A. De Freitas*[1], A. F. Garcez Neto[1], J. C. De Souza[2], J. Da Silva[1], V. L. De Souza[1], and T. M. Dos Santos[1], *[1]Federal University of Parana, Palotina, Parana, Brazil, [2]Federal University of South Mato Grosso, Aquidauana, Mato Grosso do Sul, Brazil.*

The subclinical mastitis is among the main diseases causing changes in milk composition and reducing their quality. Therefore, the somatic cell counting has been widely used as a tool for monitoring milk quality, which is an important factor to the milk industry and the health of the mammary gland. The objective of this study was to evaluate the correlation between somatic cells counting (SCC) and the contents of fat, protein, lactose, total solids, urea and milk production in Holstein cows of a Brazilian herd. It were used 3544 data of milk yield and composition from 467 cows of a commercial heard with an average milk production of 27.46 L / day during the year of 2006. Animals were kept in free stall system receiving a ration presented 17% of crude protein and 75% of total digestible nutrients (TDN) in dry matter (DM). The roughage:concentrate ratio used was 50% in DM . The roughage was based in corn silage and the concentrate feed was composed by soybean meal, cottonseed meal, vitamin and mineral premix. Individual milk samples were made monthly and from each sample were analyzed the percentage of protein, fat, lactose, total solids, urea and SCC. Data of production and milk composition were compared using ANOVA and correlation. There was no significant effect ($P > 0.05$) between SCC and fat content although there was found inverse correlation between SCC and % of milk fat (Table 1). There were significant negative correlations ($P < 0.05$) between SCC and lactose, total solids, urea and milk production, and positive and significant correlation ($P < 0.05$) between SCC and protein content. It can be concluded that the increase in SCC affect negatively the milk quality.

Table 1. Coefficients of correlation between somatic cell counting (SCC) and the levels of fat, protein, lactose, total solids, urea and milk production in dairy cows

Component	Coefficients of correlation	Level of significance
% Fat	−0.02098	0.2117
% Protein	0.13497	0.0001
% Lactose	−0.36840	0.0001
% Total solids	−0.10684	0.0001
% Urea	−0.11734	0.0001
Daily milk production (kg/d)	−0.20438	0.0001

Key words: lactation, mastitis, milk quality

T254 Immunoglobulin G1 concentration and bacterial contamination of colostrum fed to newborn Holstein heifers in Central California dairies. I. Z. Zhelev*[1], N. D. Spiro[1], J. D. Robison[1], J. Quigley[2], and A. Lago[2], *[1]California State University, Fresno, [2]APC Inc., Ankeny, IA.*

Objectives of this study were to evaluate the current status of immunoglobulin G1 (IgG1) concentration and bacterial contamination of first feeding colostrum under existing management practices of 7 Central California dairies ranging in herd size from 800 to 4000 adult cows. Colostrum samples (n = 546) were collected before first colostrum administration to newborn Holstein heifers. Three of the 7 dairies added supplement to colostrum (n = 312). On these dairies, 2 colostrum samples were obtained, one before adding supplement and one after supplementation. Colostrum collection began July 2009 and continued monthly through June 2010. Samples were analyzed for IgG1 using ELISA and bacteriology assessed through Standard Plate Count (SPC). Mean (SD) IgG1 concentration of colostrum fed was 35.96 (±16.13) mg/ml with a range of 0.45 to 114.94 mg/ml. Within dairy mean IgG1 concentrations varied from 21.20 to 47.21 mg/ml. Within the 3 dairies supplementing colostrum, mean IgG1 concentrations before and after supplementation was 45.39 and 47.21 mg/ml, 32.13 and 35.39 mg/ml, 27.20 and 37.07 mg/ml, respectively. Colostrum fed contained SPC ranging from 13,420 to 2,171,835 cfu/ml. A total of 41 (17.52%) of the pure colostrum fed (n = 234) were contaminated (>100,000 cfu/ml). Supplemented colostrum fed (n = 312) was contaminated in 179 (57.37%) of the cases. Thus, 220 (40.29%) of the total 546 calves were fed contaminated colostrum. A dramatic increase in SPC (52,817 to 2,171,835 cfu/ml) in supplemented compared with unsupplemented colostrum was observed in one dairy. The range of colostral IgG1 and SPC concentrations between herds suggests the potential exists to produce quality colostrum. However, this same data also suggests major flaws in the consistency of colostrogenesis and management of colostrum being fed to calves. Colostrum supplementation may lead to increases in colostrum IgG1 concentrations. Colostrum management practices markedly influence SPC concentrations.

Key words: colostrum, immunoglobulin, standard plate count

T255 Use of a blood glucose meter compared with laboratory analysis in dairy calves . M. R. Stafne* and S. I. Kehoe, *University of Wisconsin-River Falls, River Falls.*

Measuring glucose levels in calves is a key component in many research studies. However, testing the glucose levels at a laboratory can prove to be expensive and can delay progression of a project if the data are needed immediately. As an alternative to laboratory testing, it was hypothesized that a hand-held glucose meter would provide the same accurate results but faster. Therefore, the objective of the study was to determine the accuracy of a glucose meter when used on dairy calves compared with results from a laboratory test. Sixty-eight samples were collected from 34 calves with a 2-wk interval between the 2 sampling periods. Testing and housing of the calves was performed at Merrick's Research Facility (Union Center, WI). The calves used were fed a standard 20/20 milk replacer at 10 oz. DM per day which included various supplements due to an ongoing nutrition trial. Calves were housed in plastic hutches and were fed water and grain (18% CP; Prince, Marshfield, WI) ad libitum. Blood was collected using a blood collection vacutainer containing sodium fluoride (BD Diagnostic Systems, Franklin Lakes, NJ). Samples were first tested on whole blood

using a glucose meter and then centrifuged. Plasma was extracted using a pipette and frozen for later analysis at Marshfield Laboratories (Marshfield, WI). Measurements were statistically analyzed using the Proc Ttest in SAS 9.2 and were determined significant at $P < 0.05$. Least squares means for the laboratory glucose test and glucose meter were 93.97 ± 17.79 mg/dL and 121.66 ± 25.84 mg/dL, respectively ($P < 0.001$). It was concluded that the 2 testing methods did not produce comparable results. The variation in glucose concentration may have been due to the type of blood sample needed to run each test. Additional research containing more samples and other various tests would be recommended.

Key words: glucose, calves, glucose meter

T256 Study on the metabolic mechanism of melamine in dairy cattle. X. Jin, Y. Zhang, S. Li*, H. Zhang, Q. Zhang, and Z. Cao, *State Key Laboratory of Animal Nutrition, College of Animal Science and Technology, China Agricultural University, Beijing, China.*

This trial was to study the effects of dietary supplementation of melamine byproducts on residual concentration of melamine in rumen fluid, blood, urine, feces and milk of dairy cows. The further object was to reveal the metabolic mechanism of action of melamine in dairy cows by single factor experiment. The experiment was divided into 3 phases with 10 d in each phase (7 d for pre-feeding and 3 d for sampling). Five cannulated multiparous cows with similar milk yield and body weight were assigned to the experiments. There were 3 levels set in the melamine byproducts experiment, using 0.516%, 0.860%, 1.204% melamine byproducts to replace 3%, 5%, 7% soybean meal relatively. Feeding the dairy cows with the same concentration of pure melamine or melamine byproducts in each part of the experiments, the supplementing level was from low to high, and fed melamine byproducts to the cows with concentration in the morning. Data were analyzed as a completely randomized single factor design by ANOVA using the general linear model procedure in SPSS. The results showed that residual concentration of melamine in each kind of samples was durative increasing. When the melamine byproducts level rose to 0.860% in the concentration, the residual concentration of melamine in samples of milk was significantly different from that of 0.516% ($P = 0.02$), while the residual concentration in other samples were not significantly different; when the melamine byproducts level rose to 1.204%, the residual concentration in ruminal fluid and urine were very significantly different from that of 0.516 ($P \leq 0.01$), the residual concentration in blood, raw milk were significantly different from that of 0.516 ($P = 0.02$). The residual concentration in feces was not significantly different from that of 0.516% and 0.860% ($P = 0.27$), though the concentration of melamine was durative increasing; The concentration of melamine in the raw milk, feces and urine from the phase with the highest supplemental level were 1.31, 3.30 and 107.75mg/kg, respectively. It is concluded that renal excretion is the primary metabolic pathway of melamine while defecation and lactation are only auxiliary pathways. It was consistent with the report that melamine had negative effect on kidney.

Key words: dairy cattle, melamine, metabolic mechanism

T257 Association between milk urea nitrogen and fertility of Brazilian dairy cows. M. C. Doska[1], J. A. Horst[2], A. A. Valloto[2], and R. Almeida*[1], *[1]Universidade Federal do Paraná, Curitiba, PR, Brazil, [2]Associação Paranaense de Criadores de Bovinos da Raça Holandesa, Curitiba, PR, Brazil.*

The objective of this study was to associate milk urea nitrogen (MUN) values with reproductive performance of dairy cows from Paraná State, south of Brazil. With this purpose, 16,569 test-days from 2,145 dairy cows belonging to 3 large Holstein herds were analyzed. Monthly MUN concentrations measured using infrared test method before conception in these 3,926 lactations obtained from official milk recording program were used in this analysis. Generalized linear model methodology was adopted to determine the relationship between days open and the included fixed effects and the covariable peak milk yield, assuming gamma distribution. Animals were categorized into quartiles based on MUN values. General means in this data set were 154.4 ± 77.6 for days open, 48.6 ± 9.7 kg for peak milk yield, and 44.9 ± 21.2 mo of age. First, average, and maximum MUN values before conception were 13.85 ± 3.83, 15.36 ± 2.78, and 18.10 ± 3.57 mg/dL, respectively. Correlations between days open and the first MUN test after parturition (r = 0.03) and between days open and average MUN before conception (r = 0.07) were weak, but the association between days open and maximum MUN test before conception was higher (r = 0.30). Correlation between days open and peak milk yield also was positive (r = 0.16), which means that higher producing cows showed a trend for lower fertility. Days open from dairy cows calving in the fall were lower ($P < 0.01$) than in the remaining seasons; 135.5 ± 1.0 versus 152.6 ± 1.0, 155.4 ± 1.0, and 171.2 ± 1.0, respectively for summer, winter, and spring calving seasons. Primiparous cows showed lower ($P < 0.01$) days open than older cows; 144.9 ± 1.0 for first-lactation cows, 152.5 ± 1.0 for second-lactation cows, and 162.6 ± 1.0 for 3 or more lactation cows. Maximum MUN test before conception is more closely associated with increased days open than average MUN before conception or the first MUN test after calving. Maximum MUN values before conception greater than 15.5 mg/dL were associated with decreased fertility in Brazilian lactating dairy cows.

Key words: reproduction, protein, days open

T258 Metabolic profiles and immune status of periparturient dairy cows transitioning from conventional to organic management system. J. F. Odhiambo*, Q. Zebeli, S. Iqbal, D. A. Mansmann, U. Farooq, S. Sharma, S. M. Dunn, and B. N. Ametaj, *University of Alberta, Edmonton, AB, Canada.*

Metabolic profiles and plasma haptoglobin (Hp) in dairy cows transitioning from conventional to organic management system were compared with those of dairy cows managed conventionally. Blood samples were collected from Holstein and Jersey dairy cows during the dry period (DP), 0–30, 30–60, and 60–90 d in milk (DIM, n = 7 cows for each lactation stage). Concentrations of NEFA, BHBA, cholesterol, lactate and Hp in the serum were measured by ELISA. Data were analyzed by the mixed procedures of SAS. Results showed that concentrations of NEFA and BHBA were highest ($P < 0.001$) at 0–30, intermediate at 30–60 and 60–90 DIM, and lower during the DP. Interestingly, BHBA was greater ($P < 0.001$), at all stages of lactation, in conventional cows (e.g., 1289.4 ± 88.6 vs. 883.6 ± 47.5μmol/L at 0–30 DIM). Serum concentrations of cholesterol increased with increasing DIM and returned to nadir levels during DP and was higher ($P < 0.001$) in conventional than organic cows. Low glucose concentrations were observed 0–30 DIM, levels were intermediate at 30–60 and 60–90 DIM, and peaked during the DP ($P < 0.001$). Glucose concentrations did not differ ($P = 0.54$) between conventional and organic cows. Lactate did not ($P = 0.24$) vary with DIM or day × farm type but was higher ($P < 0.001$) in organic cows than in conventional ones. Serum concentrations of Hp were elevated during the DP; reached peak levels 0–30 DIM, and decreased gradually with increasing days postpartum

and were much higher ($P < 0.001$) at all periods in conventional than organic cows. Overall, concentrations of Hp were 528.1 ± 45.2 μg/mL in conventional cows vs. 261.1 ± 16.9 μg/mL in organic cows ($P < 0.001$). Taken together, data indicated that metabolic changes associated with initiation of lactation are preceded by an acute phase response in dairy cows, and that cows in organic systems seem to be healthier than cows under conventional systems. These differences might be due to differences in nutritional management and milk production expectations in the 2 systems.

Key words: organic dairy cows, metabolic profile, immunity

T259 Season and stage of lactation affected metabolic profiles and innate immunity of periparturient dairy cows. J. F. Odhiambo*, Q. Zebeli, S. Iqbal, D. A. Mansmann, U. Farooq, S. Sharma, S. M. Dunn, and B. N. Ametaj, *University of Alberta, Edmonton, AB, Canada.*

Blood metabolic profiles and innate immunity were evaluated in 4 dairy herds during their periparturient period. Blood samples were obtained during dry period (DP), 0–30, 30–60, and 60–90 DIM from dairy cows (n = 7 for each lactation group) by tail venipuncture during summer and winter of 2009 and 2010, respectively. Concentrations of NEFA, BHBA, glucose, cholesterol lactate and haptoglobin (Hp) in serum were analyzed by ELISA. Data were evaluated by the mixed procedures of SAS. Interactions between season and stage of lactation affected blood NEFA ($P < 0.001$) and Hp ($P < 0.02$) but tended ($P < 0.10$) to affect cholesterol and glucose. No effects were observed for BHBA and lactate. Concentrations of NEFA in cows during summer were greater 0–30 DIM, intermediate 30–60 DIM and DP, and lower between 60 and 90 DIM. The pattern was similar in winter except for greater values at 60–90 DIM compared with summer values (301.9 ± 29.3 vs. 174.2 ± 28.6 μEq/L, respectively). Concentrations of Hp in serum were elevated during the DP, peaked between 0 and 30 DIM and gradually declined to nadir levels between 60 and 90 DIM. At 0–30 DIM concentrations of Hp were higher in summer than in winter (495.9 ± 47.9 vs. 334.3 42.9 μg/mL, respectively). Cholesterol was lower ($P < 0.01$) during the DP and 0–30 DIM but higher ($P < 0.01$) 30–60 and 60–90 DIM in both seasons. In the latter periods, winter concentrations of cholesterol were numerically greater than those of summer (202.2 ± 8.7 vs. 187.7 ± 9.3, and 227 ± 9.2 vs. 207.6 ± 10.9 mmol/L, for 30–60 and 60–90 d, respectively). Glucose was higher during the dry period, lower immediately post calving, and gradually increased thereafter in both seasons. However, the concentrations during 0–30 and 30–60 DIM tended to be higher in the winter than during summer (46.6 ± 1.9 vs. 56.5 ± 1.7, and 52.9 ± 2.1 vs. 58.1 ± 1.8 mg/dL, respectively). In conclusion, differences in nutrition regimens and likely in milk yields for summer and winter seasons exacerbated cow responses to negative energy balance variably and the effects were more pronounced in summer than in winter.

Key words: dairy cows, season, metabolic profile

T260 Management factors affecting microbial contamination of bovine colostrum. E. Conrad*[1], K. Morrill[1], J. Quigley[2], and H. Tyler[1], *[1]Iowa State University, Ames, [2]APC Inc., Ankeny, IA.*

Our objective was to determine management practices that affect the level of bacterial contamination of maternal colostrum (MC) on US dairy farms. Samples of MC (n = 892) were collected from 65 farms in 12 states. Samples of MC were obtained from Holstein (n = 629), Jersey (n = 191), and unidentified (n = 102) breeds of cattle. Total plate count (TPC) and coliform count (CC) were determined for each sample (DHI, Dubuque, IA). An investigator completed a management survey assessing 53 factors associated with management practices on each farm. The average TPC for the MC was 5.50×10^5 cfu•ml^{-1}, well above the recommended industry standard of $<1.0 \times 10^5$ cfu•ml^{-1}. MC with TPC counts greater than $1.0x10^5$, $5.0x10^5$, and 10.0×10^5 accounted for 45.9, 27.2, and 16.6% of samples, respectively, indicating that bacterial contamination of colostrum is a significant problem. Industry standards recommend that MC CC be $<1.0 \times 10^4$ cfu•ml^{-1}. The average CC of MC was 115.16 cfu•ml^{-1}, 77.0% of the samples were <50.0 cfu•ml^{-1}, indicating that the industry standard of $<1.0 \times 10^4$ cfu•ml^{-1} may not be a good indicator of MC coliform contamination. Based on survey responses (n = 804) MC was transferred to an average of 2.48 containers before feeding. 42.29% and 8.96% of MC was transferred to >3 and >4 containers respectively. The average time from MC collection to the feeding or storage was 48 min, with 54.3% of the samples being fed or stored >60 min after collection. Colostrum was allowed to sit at room temperature for an average of 33 min after being removed from storage before feeding, with 20.1% of samples sitting out for >60 min before being fed. These survey results indicate that MC management practices may be responsible for the high levels of bacterial contamination observed in this data set.

T261 Effect of short-term treatment with bovine somatotropin on milk yield of Brazilian dairy cows. R. Almeida*[1] and S. L. Viechnieski[2], *[1]Universidade Federal do Paraná, Curitiba, PR, Brazil, [2]StarMilk Farm, Céu Azul, PR, Brazil.*

The objective of this trial was to evaluate short-term milk yield response of 2 commercial sources of bovine somatotropin (bST) administered every 14 d in a high-producing dairy herd. One hundred sixty Holstein cows from the StarMilk Farm, Paraná State, south of Brazil, averaging 53.9 ± 13.5 mo of age, 217 ± 148 DIM, 43.5 ± 11.7 kg/d of milk, 680 ± 65 kg of BW, and 2.90 ± 0.21 BCS were assigned to one of 2 treatments in a randomized block design using milk production during the 7-d pretreatment period as the blocking criterion. Treatments were 4 consecutive subcutaneous injections of 500 mg of bST (Boostin, Intervet Schering-Plough Saúde Animal, Brazil) or 500 mg of bST (Lactotropin, Elanco Saúde Animal, Brazil), both given at 14-d intervals. All cows were milked 3x a day and received the same TMR fed 5x daily, consisting of corn silage, ryegrass silage, corn grain ground, soybean meal, whole cottonseed, soybean hulls, urea, minerals, and vitamins. The DM, CP, and NDF contents of the offered diets were similar between treatments, as well as cow's BCS and reproductive status. The estimated nutritional levels of this diet were 53.7% DM, 1.64 Mcal/kg NE_{lac}, 17.0% CP, 33.3% NDF, 19.5% ADF, 19.0% $_{pe}$NDF, 38.0% NFC, and 4.2% EE. Each group of cows was housed in a side of a free stall and no cow entrance was allowed during the trial. Data was analyzed with the mixed procedure of SAS with a model containing the continuous effect of the covariate and the fixed effects of block, treatment, day, and the interaction between treatment and day. The mean square of cow nested within treatment was used as the error term to test the treatment effect. Boostin-treated cows yielded 1.6 kg/d more milk ($P = 0.02$) than Lactotropin treated cows; 38.8 ± 0.5 versus 37.2 ± 0.5 kg/d, respectively. Treatment and day interaction also was an important source of variation ($P < 0.01$), and milk yield differences between the 2 bST sources were observed mainly in the first half of each 14-d cycle of bST administration. In this short-term trial it was observed differences in the milk yield response between the 2 commercial sources of bST.

Key words: dairy cow, growth hormone

T262 Chop length, dry matter and density of corn and wheat silage structures in California dairies. N. Silva-del-Río*[1] and C. Heiman[2], *[1]University of California Cooperative Extension, Tulare, [2]Alltech, Lexington, KY.*

The aim of this study was to describe chop length, dry matter and density of corn (n = 25) and wheat (n = 16) silage structures in California dairies. Corn silage was stored in conventional piles (n = 22), drive over piles (n = 2), and bunkers (n = 1), that averaged 24 ft in height (range: 14–30 ft). Wheat silage structures were either conventional piles (n = 15) or bunkers (n = 1) and averaged 20 ft in height (range = 10–30 ft). Corn silage chop length was 1.3 cm (n = 6), 1.6 cm (n = 1), 1.9 cm (n = 14) and 2.2 cm (n = 4). Wheat silage chop length was 1.3 cm (n = 6), 1.9 cm (n = 9) and 2.2 cm (n = 1). Three density samples were taken at 6 ft from the bottom (B), and 2 samples at 6 ft from the top (T). The average of all the density samples collected was expressed as dry matter (DM) and as fed (AF). As fed density indicates porosity (resistance to air penetration) and may be a better indicator of silage preservation than DM density. Densities were compared with paired *t*-test (T and B) and chi-squared test (DM and AF). Average silage DM was 35.7% (range: 27.0–42.0%) for corn and 32.9% (range: 26.3–38.2%) for wheat. Silage DM was 35.4% (B) and 37.0% (T) for corn, and 35.5% (B) and 35.3% (T) for wheat. A greater ($P < 0.001$) proportion of corn silage structures met the desired density benchmark when expressed as DM (88.0%; 15 lb DM/ft3than AF (44.0%; 44 lb AF/ft3). Corn silage structures (88.0%) had at least one density sample below 44 lb AF/ft3, and 60.0% below 35 lb AF/ft3. Density of corn silage structures was higher at B than at T (47.6 vs. 36.6 lb AF/ft3; $P < 0.001$). There were no differences in the proportion of wheat silage structures meeting the desired density benchmark as AF (18.7%; 40 lb AF/ft3) or as DM (31.2%; 14 lb DM/ft3). Wheat silage structures (87.5%) had at least one density sample below 40 lb AF/ft3, and 68.7% below 30 lb AF/ft3. Density of wheat silage structures was higher at B than at T (40.0 vs. 29.1 lb AF/ft3; $P < 0.001$). The units (DM or AF) and sample location (B and T) need to be accounted for when interpreting silage density results. There are opportunities to improve silage packing density in California dairies.

Key words: corn silage, wheat silage, density

T263 Molecular aspect of laying hens feed cottonseed meal supplemented with lysine and enzyme. K. Pournia*, H. Kermanshahi, and A. Golian, *Ferdowsi University of Mashhad, Mashhad, Iran.*

The objective of this study was to evaluate the effect of cottonseed meal supplemented with lysine and NSP-depredating enzyme on jejunum cell efficiency and magnum protein synthesis as measured RNA:DNA and Protein:RNA ratio, respectively. Eighty White Leghorn hens (80 weeks old) were used in this experiment for 12 weeks. Hens were randomly divided into 4 treatments of 5 replicates with 4 birds in each. The experiment was conducted in 2 × 2 factorial experiment in completely random design (CRD). The hens were fed by mash basal diet supplemented with 1% lysine + 0% enzyme (Treatment 1), 1% lysine+0.025% enzyme (Treatment 2), 2% lysine+0% enzyme (Treatment 3), 2% lysine+0.025% enzyme (Treatment 4). Feed and water were provided ad libitum. The result indicated that protein content in magnum was not significantly affected by different levels of lysine and enzyme. Although magnum Protein: RNA ratio increased as lysine level increased ($P < 0.05$). However, results have shown that jejunum DNA concentration was not significantly affected by lysine ($P > 0.05$). Moreover, jejunum RNA: DNA ratio increased with 2% of lysine ($P < 0.50$). It was concluded cottonseed meal supplemented with lysine and enzyme had improved jejunum cell efficiency (RNA: DNA), and magnum protein synthesis (Protein: RNA) ratio in laying hens.

Key words: cottonseed meal, cell efficiency, protein synthesis

T264 Performance evaluation of Santa Ines ewes and lambs weaned at 60 days of lactation. M. M. Stradiotto*[1], A. D. Rodrigues[2], and J. A. Negrão[1], *[1]University of Sao Paulo – USP; Faculty of Animal Science and Feed Engineering – FZEA, Pirassununga, SP, Brazil, [2]University of Sao Paulo State – UNESP; Faculty of Agronomy and Veterinary Sciences – FCAV, Jaboticabal, SP, Brazil.*

The objective of this work was to verify how the maternal stress influenced lambs performance during suckling and after weaning. For that, milk production of 50 ewes was measured during 90 d of lactation. Before weaning, milk production was measured twice a month by the system weigh-suckle-weigh of lambs. Weaning occurred abruptly, at 60 d of lambs life, and after that, milk production was daily measured for 30 d. During lactation, animals were submitted to stressful stimulus called ACTH, where ewes received 1 mL/10kg BW of ACTH (adrenocorticotropic hormone) with saline solution 0.9%, which corresponded to the administration of 0.6 UI of the hormone by intravenous injection (jugular). Blood samples were collected by jugular vein puncture in 5 times: −20 min (20 min before the stressful stimulus ACTH), 0 min (soon after the stimulus) and 60, 120, and 300 min after the stimulus. The variables were analyzed in subdivided parcels, which means as repeated measures in time through MIXED procedure. Means were compared by Tukey test with a significance level of 0.05 and, when necessary it was performed the Pearson correlation analysis through statistical program SAS (2000). Mean milk production before weaning was influenced by cortisol levels at 60 min after ACTH administration, with linear correlation of 0.36 ($P < 0.01$). However, mean milk production after weaning and weight of lambs were not influence by imposed stress to the animals. Milk production was greater at 90 d, as in the fourth week after weaning, mean production was 195.2 mL (±17.74), showing that the breed has satisfactory mean milk production.

Key words: milk, sheep, weigh-suckle-weigh

T265 Comparison of pork characteristics of antibiotic free Yorkshire crossbreds raised in the hoop barn. S.-H. Oh*[1], D. Bautista[2], D. Hanson[2], M. Morrow[2], and T. See[2], *[1]North Carolina A&T State University, Greensboro, [2]North Carolina State University, Raleigh.*

The objective of this study is to compare pork characteristics for antibiotic free Yorkshire crossbreds to be raised in the hoop barn. The experiments have been accomplished in North Carolina Agricultural and Technical State University Farm and The Center for Environmental Farming Systems (CEFS) in Goldsboro, NC, where have been raising antibiotic free Yorkshire sows. Twenty 4 sows were impregnated in each research farm with the semen of Berkshire, Large Black, Tamworth and Yorkshire as a control group. Litters were weaned, and reared within deep-bedded hoop houses. The deep bedding, generally straw, corn stalks, or hay, was spread approximately 14–18 inches thick and provided a comfortable environment for the animals, which allows rooting and other natural behaviors. One hundred four pigs were used to compare pork characteristics which include pH, color score, L*, a*, b*, marbling score, drip loss, hot carcass weight, backfat thickness (BF), loin muscle area (LMA), and shear force. The data was analyzed with GLM in SAS 9.01 including research farm, season, breeding

group and sex as fixed effects. Backfat thickness, LMA, and drip loss were significantly different among breeding groups ($P < 0.05$). Large Black breeding group showed significantly higher backfat thickness followed by Berkshire, Yorkshire and Tamworth groups. However, Tamworth breeding group had significantly higher drip loss (4.50 g) than other groups; 3.77 g, 3.26 g, and 2.62 g in Yorkshire, Berkshire, and Large Black groups, respectively. This information helps the small farmers who raise rare breeds to choose better breed combinations for outdoor environments.

Key words: antibiotic-free Yorkshire, crossbred, pork characteristics

T266 Comparison of body weights in Berkshire and Large Black crossbreds produced by the use of antibiotic-free Yorkshire sows. S.-H. Oh*[1], M. Morrow[2], and T. See[2], *[1]North Carolina A&T State University, Greensboro, [2]North Carolina State University, Raleigh.*

The objective of this study was to compare body weights of Berkshire and Large Black crossbreds produced by the use of antibiotic free Yorkshire sows raised in a hoop facility. Pigs were reared within deep-bedded hoop houses at finishing phase. The swine unit at North Carolina A&T State University has a 48 × 96 ft hoop facility that is different from standard confinement facilities. The deep bedding, generally straw, corn stalks, or hay, is spread approximately 35–45 cm thick and provides a comfortable environment for the animals which allows rooting and other natural behaviors. It is relatively difficult to measure feed intake and growth rates for pigs raised in outdoor systems compared with confinement systems. Eight Feed Intake Recording Equipment (FIRE, Osborne Industries Inc. Osborne, Kansas) stations were used to collect body weight, feed intake, feeding time, feeding rate, number of feedings per day, and feed conversion. This abstract was limited to comparison of body weights among 3 breeding groups that were 23 finishing pigs (5 Berkshire × Yorkshire; 10 Large Black × Yorkshire; 8 Yorkshire × Yorkshire) in total. Before analysis, each individual′s feed intake records were evaluated for outliers by plotting feed intake by day and testing each feed intake observation with the Cook′s D test statistic and studentized residuals. After removal of outliers, 5 time points at 64, 125, 162, 176, 197, and 229 d of age, were selected to analyze the data with the repeated measurement method, which included 138 observations (30 records in Berkshire × Yorkshire; 60 records in Large Black × Yorkshire; 48 records in Yorkshire × Yorkshire). As a result, Berkshire breeding group (Berkshire × Yorkshire) showed significantly higher weights than Yorkshire purebred ($P < 0.05$), however, there was not significantly different between Berkshire and Large Black breeding groups as well as between Large Black and Yorkshire groups. This information helps the small farmers who raise rare breeds to choose better breed combinations for outdoor environments.

Key words: antibiotic free, Yorkshire, crossbred

T267 Evidence that maternal conjugated linoleic acid alters secondary metabolites in plasma of late-stage chick embryos that may lead to increased embryonic mortality. V. A. Leone*[1], D. Haughey[2], E. A. Bobeck[2], M. E. Cook[2], and F. M. Assadi-Porter[2], *[1]University of Chicago, Chicago, IL, [2]University of Wisconsin-Madison, Madison.*

Previous work in our lab shows that hens fed 0.5% conjugated linoleic acid (CLA) in a low-fat diet results in nearly 90% embryonic mortality in non-cooled, fertile eggs. Mortality appeared to be a result of decreased yolk lipid utilization by the developing embryo during the last week of development. Since the chick embryo relies on lipid for nearly 90% of its energy needs via β-oxidation during incubation, we hypothesized that if embryos from CLA-fed hens were lipid "starved," changes in blood secondary metabolites (metabolome) may be altered when compared with embryos from hens fed 0.5% canola oil. Single Comb White Leghorns (8 per treatment) were individually housed and fed standard layer mash with 0.5% canola oil or 0.5% CLA. After one month on diet, hens were artificially inseminated and eggs were incubated. On d 20 of incubation, 3 to 6 viable eggs from each treatment that had not pipped were removed from incubation and plasma was collected aseptically and immediately placed on ice. Plasma metabolites were analyzed via nuclear magnetic resonance (NMR) using a Varian 600 MHz instrument and integrated using MetaboAnalyst software. A 2-tailed *t*-test with unequal variance was conducted to determine significant differences ($P < 0.1$) using SAS. Embryos from hens fed CLA showed decreased plasma leucine ($P = 0.01$), alanine ($P = 0.03$), methionine ($P = 0.03$), glutamine ($P = 0.06$), tyrosine ($P = 0.03$), phenylalanine ($P = 0.07$), formate ($P = 0.06$), and glucose ($P = 0.01$). The significant decreases in plasma amino acids in embryos from CLA-fed hens suggest they are undergoing starvation, hence embryos from hens fed dietary CLA could be in a state of metabolic acidosis and undergoing protein catabolism to counterbalance these effects. This is further supported by the significant decrease in plasma glucose. These results provide preliminary data to show that embryos from CLA-fed hens exhibit a different pattern of metabolism than their control counterparts that may be associated with CLA's negative effects on embryonic mortality.

Key words: CLA, embryonic mortality, metabolomics

T268 Suitability of visual ear tags, electronic boluses and retinal images for tracing and auditing lamb traceability. M. A. Rojas-Olivares, G. Caja, S. Carné, A. Costa-Castro, A. K. K. Salama, A. Ait-Saidi, and M. Rovai*, *G2R, Universitat Autònoma de Barcelona, Bellaterra, Barcelona, Spain.*

Lamb traceability using different identification (ID) devices was studied under farm and slaughterhouse conditions. Lambs were intensive fattened and slaughtered as Spanish Recental lamb (23 to 25 kg BW). Lamb primary ID was done at birth with temporary official visual ear tags (V1; polyurethane rectangular flags, 2.8 g, 40 × 15 mm; n = 241) in the left ear. Lamb secondary ID was done at weaning with permanent official visual ear tags (V2; polyurethane triangular flags, 5.2 g, 38 × 39 mm; n = 104) inserted in the right ear and with electronic mini-boluses (MB; ceramic capsules, 19 g, 56 × 12 mm) applied orally. Moreover, 81 lambs were ID with glass encapsulated transponders s.c. injected (IT) in the left armpit for tracing carcasses through the slaughtering line. Electronic ID by MB and IT used 32-mm half-duplex transponders. Retinal images of live lambs (n = 98) were taken at 80 d of age (both eyes) for auditing lamb ID. Head position was compared (normal, n = 67; reversed, n = 31) after harvesting. On-farm traceability did not vary according to ID device ranging from 98.6 to 100%; $P > 0.05$). The V1 and V2 were removed at beheading, and MB at evisceration, enabling carcass ID that was assumed to be the same as the slaughtering order. Although only 78.8% IT were retained after slaughter, they proved that carcass order was altered at weighing, reducing the carcass traceability in the slaughterhouse to 68.3%. All retinal images matched in live lambs, but live vs. slaughtered image matching markedly decreased in the normal vs. reversed head position (56.4 vs. 75.0%; $P < 0.05$). In conclusion, V1, V2, MB and IT were efficient devices for individually tracing live lambs but all of them failed for tracing carcasses efficiently. Individual tracing from farm to

carcass using radiofrequency ID devices would be possible if carcass order is maintained in the slaughterhouse. Retinal images efficiently audited live lambs and most of carcasses. We do not recommend the use of injects for lamb ID, agreeing with previous research, but they may be a useful tool for tracing carcasses when their order is compromised.

Key words: traceability, electronic identification, retinal image

T269 Retrospective analysis of the effects of feeding pelleted versus meal diets on growth performance of 12- to 30-kg nursery pigs over a 5-year period. E. D. Frugé*[1], E. L. Hansen[1], S. A. Hansen[1], K. A. Frerichs[1], and C. W. Hastad[2], *[1]Hubbard Feeds, Mankato, MN, [2]New Fashion Pork, Jackson, MN.*

A retrospective analysis was conducted on 5 trials (TRL) over 5 years (2006–2010) to determine the effects of feeding pigs pelleted (P) vs. meal (M) diets on growth performance. The TRL were combined and analyzed as a randomized complete block design with TRL and BW as blocking factors. Treatment (TRT) replication for each TRL were 12, 6, 12, 5 and 5, for TRL 1 to 5, respectively for a total of 40 replicates, with 25 to 28 pigs per pen (n = 2,129; 12.3 ± 1.05 kg initial BW). Trials were conducted using the same research barn and similar genetics (FAST/PIC dam × TR4 sire). The TRT were; 1) meal diet; and 2) as 1 pelleted. All diets were corn-soybean meal-DDGS based and contained 15, 15, 30, 23.5, and 30% DDGS, in TRL 1 to 5, respectively. Diets were formulated to be adequate in all nutrients and contained 1.20% TID Lys in all TRL except TRL 2 at 1.10% TID Lys. The average TRL length was 26.6 d, ranging from 24 to 29 d between TRL. Consistent improvements in performance for pigs fed pelleted diets were noted in each TRL (Table 1). Overall ADG, GF, and final BW were improved ($P < 0.01$) in pigs fed pelleted diets. Pigs fed pelleted diets had increased ADG by 5.4% and improved GF by 5.9%. These data provide the ability to determine economic benefits of feeding pelleted vs. meal diets in nursery pigs.

Table 1.

TRL[1]	ADG, g	SEM	GF	SEM	ADFI, g	SEM	ENDWT, kg	SEM
1M	618	4.45	0.60	0.002	1024	6.22	30.3	0.170
1P	645*		0.64*		1009		31.0*	
2M	631	9.28	0.66	0.002	950	14.00	28.8	0.379
2P	688*		0.71*		972		30.3**	
3M	615	7.08	0.67	0.005	918	9.21	27.0	0.211
3P	645*		0.72*		900		27.8**	
4M	641	14.0	0.64	0.004	995	25.00	29.9	0.509
4P	666		0.67*		987		30.6	
5M	623	8.64	0.63	0.007	986	13.49	29.0	0.324
5P	665**		0.67**		987		30.2***	
Cum. M	627	4.02	0.64	0.002	978	6.02	29.1	0.139
Cum. P	663*		0.68*		974		30.1*	

[1]TRT × TRL; $P > 0.35$; *$P < 0.01$; **$P < 0.05$; ***$P < 0.10$.

Key words: growth, nursery pigs, pellet

T270 Comparative assessment of boar spermatozoa having different cryopreservation potential. J. M. Feugang*[1], M. M. Ferraz[2,1], J. C. Rodriguez-Munõz[1], B. S. Grillis[1], S. T. Willard[3], and P. L. Ryan[1,4], *[1]Department of Animal and Dairy Sciences, Mississippi State University, Mississippi State, [2]Faculdade de Medicina Veterinariae Zootecnia, Universidade de Sao Paulo, Brasil, [3]Department of Biochemistry and Molecular Biology, Mississippi State University, Mississippi State, [4]Department of Pathobiology and Population Medicine, Mississippi State University, Mississippi State.*

Introduction of semen cryopreservation is still limited in swine industries due to their poor freezability. Indeed, a subset of boars, known as "bad freezers" induces low pregnancy and farrowing rates compared with "good freezers" when using same amounts of spermatozoa per insemination. Numerous studies have been conducted to improve the cryosurvival of boar semen, but there are still no clear indicators of freezability potential of boar semen. To this end, the present study was conducted to evaluate the motility and viability of boar spermatozoa with known cryotolerance status. Commercial proven fertile boars were selected upon conception rates after artificial inseminations (AI) using fresh semen. Semen of 3 independent ejaculations were collected from 4 "good" and 4 "bad" freezers as indicated by their differential conception rates after AI using frozen-thawed semen. Collected-semen were diluted and either stored in cooling solution or frozen in 5-mL plastic straws. Both semen types were centrifuged through a discontinuous percoll gradient to remove all contaminants. Motile spermatozoa were washed in PBS-PVP or extender for motility (CASA) and viability analyses. The proportions of motile, progressive, rapid, and viable spermatozoa were evaluated. Data were analyzed using a Student′s *t*-test, and $P \leq 0.05$ was fixed as threshold of significance. Sperm motility of cool-diluted semen was similar between "good" and "bad" freezers (82 ± 20% and 78 ± 16%). After freezing-thawing, the proportions of motile (24 ± 8% vs. 22 ± 10%), progressive and rapid spermatozoa were comparable between both boar groups. The proportions of (viable) spermatozoa with intact plasma membrane (94 ± 7% vs. 95 ± 4%), acrosome (29 ± 11% vs. 23 ± 6%) and mitochondria (87 ± 11% vs. 87 ± 10%) membranes were not significantly different between "good" and "bad" freezers. Our data confirm the inability of routine criteria of sperm evaluation to identify the freezability status of boars, suggesting the existence of induced-molecular cryodamages that may characterize "bad" freezer boars′ semen. Work supported by USDA-ARS Biophotonics Initiative #58-6402-3-0120.

Key words: spermatozoa, cryopreservation, motility

T271 Performance and carcass traits of bulls fed different levels of crude glycerin. J. R. R. Carvalho, M. M. Ladeira*, M. L. Chizzotti, T. M. Gonçalves, P. D. Teixeira, J. S. F. Hostalácio, P. T. Silva, and O. R. Machado Neto, *Federal University of Lavras, Lavras, MG, Brazil.*

The use of crude glycerin to partially replace corn in feedlot diets might be interesting if performance and carcass quality are unchanged. The aim of this study was to evaluate the performance and carcass traits of bulls finished in feedlot fed different levels of crude glycerin. Forty-four Red Norte bulls received the following levels of crude glycerin (83% glycerol): 0, 6, 12 and 18% of DM. The basal diet consisted of 30% of corn silage, 12% of soybean meal, 56% of ground corn grain and 2% of mineral mixture. Glycerin was added to partially replace corn and to achieve an isonitrogenous diet, corn gluten meal (21% CP) was used. The experiment lasted 112 d, with 28 d for adaptation. Animals were weighed at the beginning and at the end of the experiment to obtain the average daily gain (ADG). All animals were slaughtered after fasting for 16 h and hot carcass weight (HCW) was recorded. After 24 h of cooling at 4°C, there were measured cold carcass weight, subcutaneous fat thickness (SFT) and longissimus muscle area (LMA) between the 12nd and 13rd ribs. The experiment was conducted in a completely randomized design and data were analyzed using PROC GLM and PROC REG of SAS 9.1. The inclusion of glycerin in the diet did not affect ADG, HCW, LMA and SFT (Table 1). The dressing percentage (DP) increased linearly with glycerin inclusion, likely due to a higher energy intake. The level of 18% of crude glycerin in diet DM to finishing beef cattle does not compromise performance or carcass traits. Funded by Fapemig, CNPq, CAPES, and INCT-CA

Table 1. Performance and carcass traits of bulls fed different levels of crude glycerin

	Crude Glycerin level, DM basis					
Item	0%	6%	12%	18%	SEM	*P*-value
Slaughter weight, kg	513	522	527	516	14.9	0.90
ADG, kg	1.75	1.92	1.88	1.80	0.10	0.62
HCW, kg	284	289	299	291	9.21	0.71
CCW, kg	278	283	287	279	8.59	0.87
DP, %[a]	55.4	55.5	56.8	56.5	0.43	0.05
SFT, mm	3.18	3.27	3.18	3.19	0.43	0.99
LMA, cm^2	83.13	78.15	85.45	87.84	2.69	0.11

[a]Y = 55.34* + 0.078*X (*$P < 0.05$).

Key words: dressing percentage, glycerol, longissimus

T272 Effects of distillers grain supplementation on beef cow performance. M. J. Faulkner*[1], P. M. Walker[1], R. L. Atkinson[2], J. L. Veracini[1], L. A. Forster[3], J. M. Carmack[1], and K. L. Jones[2], *[1]Illinois State University, Normal, [2]Southern Illinois University, Carbondale, [3]Archer Daniels Midland Co, Decatur, IL.*

The objective of this 3-yr study is to determine the optimum inclusion rate for wet corn distillers grains with solubles (DGS) in late gestation and early lactation beef cow diets and the effect of including higher dietary levels of DGS on dystocia, postpartum conception rate, and other measures of cow and calf performance. During yr. 2, 128 cows were blocked by parity (first parity vs. 2 or more parities) and stratified by BW, subject to variation in BCS, to 16 pens, equivalent to 8 cows/pen. Four diets were fed until completion of timed (AI). Control cows (T1) were fed corn silage, shelled corn, and soybean meal based diets to meet NRC estimates. In treatment diets DGS replaced shelled corn, soybean meal, and a portion of the corn silage, resulting in DGS inclusion rates (DM basis) of 11.4% (T2), 39.2% (T3), and 54.4% (T4). Analyzed dietary values for CP intake were 10.0%, 10.6%, 14.8%, and 18.3%, for T1, T2, T3, and T4, respectively. Mean DMI were 6.2 ± 0.6, 5.5 ± 0.04, 7.3 ± 1.0, 7.7 ± 1.1kg for T1, T2, T3 and T4, respectively. No differences ($P > 0.05$) between treatments were observed for AI conception, calf birth weight, and milk production. Calving ease scores were not significantly different ($P = 0.27$) but a numerical increase toward increased difficulty was shown for T4 compared with other treatments. Differences in calf BW at AI ($P = 0.01$), cow BW change ($P = 0.001$), and cow BCS change ($P = 0.001$) were observed where T1 = T2 < T3 = T4. Higher ($P = 0.003$) DMI were observed for T3 and T4 than for T1 and T2. These data suggest that cows fed 39% to 54% of their diet as DGS consumed more DM and had increased BW, BCS and calf BW than cows fed to meet NRC recommendations with either DGS or shelled corn and soybean meal.

Key words: distillers grains, beef cow performance

T273 Effect of a mixture of cinnamaldehyde, carvacrol and capsicum oleoresin on performance and rumen development of weaning calves. C. Oguey*[1], J. Trautwein[2], H. Hendrik Kuhrmann[2], G. Dusel[2], and D. Bravo[1], *[1]Pancosma, Geneva, Switzerland, [2]Universtiy of Applied Sciences, Bingen, Germany.*

Weaning is a critical period for the calf as its diet changes from liquid to solid feeding. Plant extracts are known to optimize rumen function in ruminants and growth performance in ruminants and monogastrics. The objective was to test the effect of a blend of cinnamaldehyde, carvacrol and capsicum oleoresin (XT, XTRACT 6930 and XTRACT Instant Pancosma) on performance and rumen parameters of weaning calves. Forty suckling calves aged of 14 d (initial BW 45 kg) were randomly allocated to 2 treatments for 68 d: CT: standard milk replacer (MR) and concentrate feed (CF), and XT: MR + 250 ppm XT and CF + 100 ppm XT. Animals were restricted fed MR from d1 to 60, and ad libitum fed CF, hay and corn silage from d 1 to 68. Individual daily intakes of MR and CF, daily hay and silage intake per group, individual weekly BW and BWG and blood and rumen parameters at d 56 were recorded. Data were analyzed using the GLM procedure of SAS. For the whole weaning duration calves fed XT exhibited a concentrate intake greater by 26.4% ($P < 0.01$) compared to CT. XT increased BWG and final BW respectively by 8.11% ($P = 0.14$) and 3.8% ($P = 0.097$). From d 1 to 42, compared to CT, calves fed XT exhibited greater concentrate intake (90.89 vs. 174.03 g/animal daily, P = 0.015) and BWG (470.75 vs. 536.718 g/animal daily, $P = 0.012$). From d 43 to 68, XT tended to increase concentrate intake (+14.5%, $P = 0.125$), but did not affect BWG ($P = 0.300$). However, at d 56, animals fed XT tended to have greater blood leucocytes (+13.8%, $P = 0.11$), monocytes (+39.0%, $P = 0.19$) and basophiles (+60.0%, $P = 0.13$), suggesting that these calves were subject to an infection. XT did not affect ruminal concentrations of total VFA and acetate ($P > 0.76$), but numerically increased ruminal concentrations of propionate and butyrate (respectively +10.3%, $P = 0.64$ and +39.0%, $P = 0.15$), suggesting that calves supplemented with XT can be more prone to a quick development of their rumen.

Key words: calf, essential oil, plant extracts

T274 Effect of fescue toxicosis on the expression of selected hepatic genes in Angus cattle. J. Bryant*, J. Johnson, B. Scharf, D. Kishore, E. Coate, P. A. Eichen, K. Wells, J. Green, and D. E. Spiers, *University of Missouri-Columbia, Columbia.*

Fescue toxicosis may result from intake of ergot alkaloids found in endophyte-infected (E+) tall fescue. The liver is the major organ involved in the pathology of fescue toxicosis, as it is the site where the toxic ergot alkaloids are metabolized. A study performed with rats consuming an E+ diet reported increased expression of phase I detoxification enzymes and a decreased expression of antioxidants, to suggest an increase of cellular oxidative stress. This study was performed to determine if intake of E+ fescue had the same effect on the expression of detoxification enzymes and antioxidants in cattle. Missouri- (MO; n = 10; 513.6 ± 13.6 kg BW) and Oklahoma- (OK; n = 10; 552.8 ± 12.0 kg BW) derived Angus steers, maintained at 19–22°C air temperature, were fed diets containing either endophyte-free (E-) or E+ seed (30 µg ergovaline/kg BW/day) for 8 d. Feed intake (FI) was recorded daily. Blood and liver tissue samples were collected during pretreatment followed by blood samples at d4 and liver tissue samples on d8 of treatment. A significant reduction (2.84 kg, $P < 0.05$) in FI of E+ steers occurred from treatment start to Day 7. Blood alkaline phosphatase was significantly lower in E+ steers compared with E- steers with a difference of 14.5 U/L ($P < 0.05$) to confirm the presence of fescue toxicosis. Real-time PCR was performed to determine expression of selected hepatic phase I detoxification enzymes and specific antioxidant proteins. Illumina deep sequencing was performed on samples from the fescue-naïve OK steers. Tiling of the sequences to a ~23,500 member reference allowed for the quantification of mRNA transcript abundance in each sample. Real-time PCR demonstrated that cattle consuming E+ fescue did not have a significant change in the expression of phase I detoxification enzymes or antioxidants. Illumina transcriptome analysis confirmed that E+ fescue did not have any significant effect on the expression of phase I genes; however, there were over 250 genes whose expression was significantly affected by E+ fescue, including several genes involved in lipid and carbohydrate metabolism and several involved in phase II conjugation reactions.

Key words: cattle, fescue

T275 Evaluation of Nellore steers′ performance supplemented with two levels of concentrate and sugar cane in feedlot. R. M. Silva*[1,2], J. T. Pádua[2], J. Restle[2], R. Z. Taveira[1], B. A. S. R. Leite[1], and D. A. Lima[2], *[1]Universidade Estadual de Goiás, São Luís de Montes Belos, Goiás, Brazil, [2]Universidade Federal de Goiás, Goiânia, Goiás, Brazil, [3]FAPEG, Goiânia, Goiás, Brazil.*

The aim of this research was to evaluate the BW gain associated to the DMI of Nellore steers fed in feedlot. Two levels of concentrate, 40% and 60%, were used in the diets, which t were composed by 36.71% and 59.45% of sugar cane, 27.08% and 53.74% of ground corn, 9.55% and 5.45% of cottonseed meal, 0.91% and 0.98% of urea, and 3.01% and 3.12% of a mineral mix, respectively. Twenty animal′s with 24 mo of age and average weight of 347.60 kg were used. The animals were weighted every 21 d and on the last day of the trial, resulting in 90 d of trial. The mean intake of sugar cane was evaluated by weighing and colleting the orts twice a week. The mean results were compared by Tukey test ($P < 0.05$). The initial BW was not different among between ($P > 0.05$). There wasn′t a difference in the ADG between the first and fourth weightings ($P > 0.05$). However, differences in ADG between the fourth and fifth weightings were detected ($P < 0.05$). The DMI wasn′t different between the first and second weightings ($P > 0.05$). Considering the final mean weight, the increase in the concentrate level from 40% to 60% did not result in significant weight gain.

Key words: average daily gain, beef cattle, nutrition

T276 The influence of glycerol supplementation during late gestation on beef cow performance and dietary digestibility. S. J. Winterholler*, N. L. Hojer, R. H. Pritchard, and K. VanderWal, *South Dakota State University, Brookings.*

Glycerol (GLY) was evaluated as an energy supplement for spring-calving beef cows during late gestation (n = 30; 637 kg of initial BW; 5.8 initial BCS) consuming medium-quality forage. Treatments were formulated to provide equal CP and included (DM basis): 1) 1.06 kg/d soybean meal (SBM); 2) 1.06 kg/d soybean meal and 0.86 kg/d glycerol (GLY); 3) 0.65 kg/d soybean meal and 1.74 kg/d soybean hulls (SBH). Glycerol and SBH were fed for isocaloric intake; SBM was the positive control. Glycerol was mixed with SBM daily and diets were fed individually. Cows had ad libitum access to medium-quality bromegrass hay (7.6% CP%; 79% NDF, DM basis). Change in cow BW over the feeding period was similar among treatments (29 kg; $P = 0.20$). Change in BCS over the feeding period tended ($P = 0.12$) to be greater for GLY and SBH as compared with SBM (0.42, 0.15, −0.08, respectively). Cow BW (645 kg) and BCS (5.4) before breeding were similar among treatments ($P > 0.20$). Fecal grab samples were collected twice throughout the 60-d supplementation period and were composited to estimate dietary digestibility, using ADIA as an internal marker. Diet digestibility of DM (52.6%; $P = 0.64$), NDF (66.8%, $P = 0.82$), and ADF (68.3%, $P = 0.77$) were similar among treatments. Supplementation of GLY in a forage-based diet had no negative impacts on fiber digestibility. Additional energy from GLY was an effective replacement for SBH to maintain BCS during late gestation.

Key words: beef cow, glycerol, supplement

T277 The effect of feed additive and sulfur intake on rumen fluid pH and rumen gas cap hydrogen sulfide concentration in feedlot steers. K. L. Neuhold*[1], J. J. Wagner[1], T. E. Engle[1], E. M. Domby[1], and M. Branine[2], *[1]Colorado State University, Fort Collins, [2]Alpharma Animal Health, Canon City, CO.*

Crossbred yearling steers (n = 432) were used to study the effects of Cattlyst and Aureomycin (CA) vs. Rumensin and Tylan (RT) and variation in Sulfur (S) intake on rumen fluid pH and rumen gas hydrogen sulfide (H_2S) concentration. An unbalanced randomized block design using a 2 × 2 factorial was utilized. Factors included feed additive (CA vs. RT) and S concentration (constant vs. variable). The variable concentration (VAR) was intended to simulate the use of random loads of wet distillers grains (WDG). Random numbers were generated for each d of the study. High S diets (S = 0.60% of DM) were fed to VAR on d associated with an even number. Low S diets (S = 0.48% of DM) were fed to CON all d of the study and to the VAR only on d associated with an odd number. From d 0 through 35, a high S meal supplement was fed to VAR on the appropriate d. Since variation in S concentration in WDG is driven by rate of inclusion and S concentration in distillers solubles (DS), 2 DS based liquid supplements (low S, 0.99% vs. high S, 2.35%) were used to create the constant (CON) vs. VAR S intake from d 36 through slaughter. Sulfuric acid was added to the high S DS used to obtain the intended dietary S concentration. On d 35, 70, and 105 rumen fluid and gas cap samples were obtained via rumenocentesis from a subsample (3 hd/pen and 3 pens/treatment) of steers to determine rumen fluid pH and H_2S concentration. The effects

of feed additive, dietary S, or the interaction on rumen fluid pH were not significant ($P > 0.38$). An interaction between feed additive and dietary S treatment ($P < 0.02$) existed suggesting that the effect of feed additive on H_2S concentration was influenced by dietary S. Steers fed the CON diet receiving RT exhibited lower H2S concentration than steers fed CA (1053 vs. 2519 mL/L). Steers fed the VAR diet receiving RT exhibited a higher H_2S concentration than steers fed CA (2567 vs. 2187 mL/L). Rumen H_2S concentration was related to rumen fluid pH suggesting that management of rumen pH is likely a key in dietary S management.

Key words: sulfur, ionophore, antibiotic

T278 The effect of feed additive program and dietary sulfur concentration in steam-flaked corn diets containing wet distillers grains on feedlot performance and carcass merit in yearling feedlot steers. E. M. Domby*[1], K. L. Neuhold[1], J. J. Wagner[1], T. E. Engle[1], and M. Branine[2], *[1]Colorado State University, Fort Collins, [2]Alpharma Animal Health, Canon City, CO.*

Crossbred yearling steers (n = 432, BW = 329 ± 10.5 kg) were used in an unbalanced randomized block design to examine the effect of feed additives and dietary sulfur (S) on performance and carcass merit. Treatment factors were arranged as a 2 × 2 factorial and included ionophore and antibiotic [Rumensin/Tylan (R/T) or Cattlyst/Aureomycin (C/A)] and dietary S (constant or variable). High S diets (0.60% S, DM basis) were fed on random days to the variable (VAR) treatment. Low S diets (0.48% S, DM basis) were fed to the VAR treatment on remaining days and to the constant (CON) treatment all days. From d0 to 35 the high S diet was achieved by using a high S meal supplement; however, since S concentration in wet distillers grains (WDG) is associated with distillers solubles (DS) added to WDG and H_2SO_4 added to the DS, the VAR S diets were achieved from d36 to d159 by using 2 DS sources at 0.99 versus 2.35% S. Cause of cattle death was verified by necropsy. No interaction between S and additive treatments existed for feedlot performance; therefore, only main effects are presented. Steers receiving VAR had higher ($P < 0.05$) BW compared with CON supplemented steers. Overall DMI was greater ($P < 0.05$) for VAR compared with CON steers. Average daily gain and feed efficiency were similar for CON and VAR. Steers receiving VAR diets had a higher mortality rate ($P < 0.02$) than steers fed CON diets (5.21 versus 0.67%). Feedlot performance and carcass merit were similar for feed additive treatments. The S by feed additive interaction was significant ($P < 0.05$) for dressing percentage indicating that S treatment had no effect on dressing percentage if R/T was fed but when steers were fed C/A, dressing percentage was reduced by 0.72% ($P < 0.02$) if VAR diets were fed. All other carcass characteristics were similar across S treatments. Results indicate that performance and carcass characteristics were not affected by feed additive program. Varying S in diets increased mortality rate; however, feedlot performance and carcass merit were not affected.

Key words: sulfur, ionophore, antibiotic

T279 Effects of dietary chromium propionate on performance traits of stocker/growing cattle. J. L. Veracini*[1], P. M. Walker[1], M. J. Faulkner[1], and R. E. Hall[2], *[1]Illinois State University, Normal, [2]Cooperative Research Farms, Richmond, VA.*

Chromium propionate is a trace mineral when in the +3 state will increase the uptake of glucose by insulin sensitive organs. How this change in glucose metabolism affects growth performance has varied depending on the dietary concentrations of Chromium and the different substrates to which chromium is bound. The objective of this study was to determine if providing supplemental chromium to receiving calves in the feedlot improves growth performance and health status. Two hundred forty crossbred steer calves (260 ± 49 kg) were blocked by source and stratified within each block (3 blocks) by BW to 32 treatment pens (either 10 or 12 pens/block). All steers were fed a concentrate with or without chromium for 70 d, at 1.25% of BW along with forage ad libitum (ground grass hay for 55 d, followed by corn silage for 15 d). Two treatment concentrates containing either 0 (T1) or 717 ppb chromium (DM basis) from chromium propionate (T2) were randomly assigned to 16 pens each. Average chromium concentration in the total DM intake of steers on the chromium treatment was 328 ppb. There were no significant differences between treatments throughout the trial. Normal steer health status was maintained throughout the trial with the exception of d 14 to 28 when respiratory disease challenges were observed. Chromium supplementation (T1) tended to improve rate of gain 35% ($P = 0.074$) from d 14 to d 28 and 12% ($P = 0.058$) from d 0 to d 28. Feed efficiency tended to be improved 10% by chromium supplementation from d 0 to d 28 ($P = 0.106$). From d 28 to d 55, steers on the control diet (T2) exhibited some compensatory gain; which was nonsignificant. Steer performance subsequent to d 28 and for the overall 70 d trial was not ($P > 0.05$) influenced by chromium supplementation. The greatest advantage to chromium supplementation may occur during the receiving period when steers are subjected to respiratory disease challenges. During such periods ADG, and G/F may be improved up to 30% to 35%, respectively, for steers receiving supplemental chromium propionate compared with control steers.

Key words: chromium propionate, respiratory challenge, steers

T280 Nutrient digestibility and residual feed intake in Nellore heifers. R. H. Branco[1], E. Magnani[1], T. L. Sobrinho[2], S. F. M. Bonilha[1], L. T. Egawa[1], M. E. Z. Mercadante*[1], and F. M. Monteiro[1], *[1]Instituto de Zootecnia, Sertãozinho, São Paulo, Brasil, [2]Faculdade de Ciências Agrárias e Veterinárias, Jaboticabal, São Paulo, Brasil.*

Residual feed intake (RFI) as a tool for evaluating feed efficiency has been widely studied, however, associations among RFI, animal growth and nutrient digestibility are inadequate and existing data are contradictory. The objective of this study was to evaluate nutrient digestibility of Nellore heifers classified according to RFI. The experiment was conducted at Instituto de Zootecnia, Sertãozinho/São Paulo/Brazil with 32 Nellore heifers with 377 kg of average BW, previously classified according to RFI which was calculated by the difference between DMI observed and estimated by regression equation based on ADG and mid metabolic BW. Heifers were classified into high RFI (≥mean + 0.5 SD; less efficient) and low RFI (≤mean - 0.5 SD; more efficient). The diet was formulated with tifton hay, corn ground, cottonseed meal and urea, with 15.43% CP and 56.77% NDF. Animal feces were collected 2, 4 and 6 h after feeding, on consecutive 3 d, and analyzed for concentrations of DM, NDF, ADF, cellulose, ether extract (EE) and CP. Lignin was used as an internal marker. There were no differences between low and high RFI animals for CP digestibility (CPD; $P = 0.9506$) and EE digestibility (EED; $P = 0.6878$). Low RFI animals had higher DM digestibility (DMD), NDF digestibility (NDFD), ADF digestibility (ADFD) and cellulose digestibility (CELD) than the high RFI ones (Table 1). Differences in diet digestibility between RFI levels would be due to retention time and ruminal individual feeding behavior. Associations between RFI and nutrients digestibility, would indicate that the principle of equal digestibility for animals receiving similar diets would not be entirely accurate. Thus, it can be argued that small variations in nutrients digestibility provide great impact on

feed efficiency and may be a factor discriminating among levels of efficiency.

Table 1. Feed intake and nutrient digestibility of Nellore heifers classified for RFI

Traits	Low RFI	High RFI	CV	*P*-value
n	17	15		
RFI, kg/d	−0.419*	0.445	1.39E-4	<0.0001
DMI, kg/d	7.73*	8.43	10.4	0.0002
DMD, %	49.1*	45.4	10.5	0.0423
EED, %	54.5	57.1	32.6	0.6878
CPD, %	39.4	39.2	28.3	0.9506
ADFD, %	49.9*	45.1	11.5	0.0177
NDFD, %	56.6*	49.8	8.45	0.0002
CELD, %	61.6*	56.4	10.1	0.0203

Means followed by the symbol *, in the lines, differ significantly by t test at 5% of probability.

Key words: beef cattle, dry matter intake, efficiency

T281 Potential of calcium oxide-treated corn stover and modified distillers grains as a partial replacement for corn grain in feedlot diets. J. R. Russell*[1], D. D. Loy[1], and M. Cecava[2], *[1]Iowa State University, Ames, [2]Archer Daniels Midland Company, Decatur, IL.*

Effects of partial replacement of corn grain in the feedlot diets with calcium oxide (CaO)-treated corn crop residues and modified distillers grains with solubles (MDGS) were evaluated in sheep digestion and steer growth experiments. In 2009, corn stover (59.7% DM) was harvested and stored in silo bags untreated or treated with CaO at 5% of the DM. Large round bales of stover were also harvested, stored outdoors, and tub-ground before feeding. Baled stover was used as 5% of a Control diet containing corn grain, MDGS, and a mineral-vitamin supplement at 70, 20, and 5% of the DM. Three experimental diets containing 20, 35, 40, and 5% DM from baled (Baled diet), untreated (Untreated diet), or CaO-treated stover (CaO diet) with corn grain, MDGS, and mineral-vitamin supplements were also prepared. Baled, Untreated, and CaO-treated stover diets were fed at 1.5 × maintenance to 3 lambs (39 kg) in a 3 × 3 Latin-square digestion trial with 10-d adjustment and 5-d collection phases. Two hundred ten Angus-cross steers (294 kg) were allotted to 35 pens and fed the Control, Baled, Untreated, and CaO-treated stover diets to finish or fed the Baled, Untreated, and CaO-treated stover diets during growing to 454 kg and the Control diet to finish. The DM digestion coefficients ($P < 0.05$) were 75.9, 75.5, and 83.2% for the Baled, Untreated, and CaO-treated stover diets. Average daily gains (kg/d; $P < 0.05$) and feed-to-gain ratios (kg/kg; $P < 0.05$) of steers fed the Control, Baled, Untreated, or CaO-treated stover diets to finish and the Baled, Untreated, CaO-treated stover diets during growing and the Control diet to finish were 1.8, 5.5; 1.5, 6.2; 1.6, 5.8; 1.7, 5.2; 1.5, 5.8; 1.5, 5.5; and 1.6, 5.2 to finish. Steers fed the Control diet to finish had a higher ($P < 0.05$) marbling score than steers fed the stover diets. Economic returns per steers fed the CaO-treated stover diet to finish were greater than those fed the Control diet at a corn price of $4.00/bushel and became more favorable with increasing corn prices.

Key words: beef steers, corn stover, modified distillers grains

T282 Performance of Nellore steers from a genetic improvement program in feedlot. M. D. Freitas Neto[1,2], J. J. R. Fernandes*[1,2], D. A. Lima[1,2], P. L. P. Rezende[1,2], G. A. B. Queiroz[1], L. F. N. Souza[3], J. M. C. Silva[1], E. G. Moraes[3], and M. L. R. Pereira[1], *[1]Universidade Federal De Goias, Goiania, Goias, Brasil, [2]Conselho Nacional De Desenvolvimento Cientifico e Tecnologico, Brasilia, Distrito Federal, Brasil, [3]Nelore Qualitas, Goiania, Goias, Brasil.*

The objective of this trial was to evaluate the BW gain level of 113 Nellore non-castrated steers with an average age of 24 mo in feedlot. The animals were distributed into 16 pens, 15 pens with 7 steers and 1 pen with 8 steers, and divided into 4 treatments by grade of the genetic program: T1 = −0.067; T2 = 3.840; T3 = 7.049 and T4 = 10.763. The results were analyzed in a totally randomized design using the statistical software SAS (2002). The grade considers the BW at different ages and the scrotal circumference. The animals were fed once daily by a total mixed machine provided with a digital balance and the orts were weighed weekly. The diet was composed of 14.88% of sugar cane bagasse, 43.89% of corn germ, 4.36% of soybean meal, 19.15% of soybean hulls, 14.79% of cotton seed, 0.95% of urea and 1.99% of mineral. The animals were weighed before the beginning of the trial and then each 21 d. The animals with highest grade showed a higher DMI (kg/day) ($P < 0.05$), maybe because they had higher BW ($P < 0.05$). The treatments did not affect DMI (% of BW and $BW^{-0.75}$; $P > 0.05$). The steers with higher grades (T4) showed higher ADG than the steers with lowest grade (T1). For T4, LM area was higher than the others ($P < 0.05$). There were no differences in rib fat thickness and rump fat thickness ($P > 0.05$). Correlations between the grade and DMI (kg/day), grade and ADG, grade and LM area and grade and rib fat thickness were (r = 0.57; $P < 0.05$), (r = 0.66; $P < 0.05$), (r = 0.84; $P < 0.05$) and (r = 0.53; $P < 0.05$), respectively.

Key words: carcass, fat thickness, longissimus muscle area

T283 Effect of partial or complete replacement of barley grain with wheat bran on voluntary intake, apparent nutrient digestibility and rumen pH of beef heifers fed backgrounding rations. A. D. Friedt*[1], T. A. McAllister[2], and B. Wildeman[3], *[1]University of Saskatchewan, Saskatoon, SK, Canada, [2]Agriculture and Agri-Food Canada, Lethbridge Research Centre, AB, Canada, [3]Pound-Maker Agventures Ltd., Lanigan, SK, Canada.*

Wheat bran (WB) is a high fiber, low starch by-product of the wheat processing industry. Few published studies are available on the nutritional value of WB for growing cattle. The objective of this trial was to evaluate the effect of replacing rolled barley (RB) with WB on apparent nutrient digestibility, voluntary intake and rumen pH of beef cattle fed a moderate energy growing diet. Five spayed and rumen cannulated Angus heifers (584 ± 40 kg) were used in a 5x5 Latin square design. The control diet consisted of 36% barley silage, 24% grass hay, 8% supplement and 32% RB (DM basis). Dietary treatments replaced RB with WB at 8, 16, 24 and 32% of the diet (DM basis). Voluntary DM intake was highest in the control ration and decreased ($P < 0.01$) as level of WB increased. Mean rumen pH, as well as duration (min) and area under pH cut off values of 6.0, 5.8 and 5.5 were not affected ($P > 0.05$) by WB inclusion. Maximum and minimum daily pH values were not affected ($P > 0.05$) by treatment. Feeding WB at levels greater than 8% of ration DM decreased ($P < 0.01$) DM and gross energy ($P < 0.05$) digestibility, while feeding WB at levels greater than 24% decreased ($P < 0.05$) organic matter digestibility. However, digestible energy content was not affected ($P > 0.05$) by WB treatment. Acid (ADF) and neutral (NDF) detergent fiber digestibility decreased ($P < 0.05$) in all

diets containing WB when compared with the control diet ($P < 0.05$) with the exception that NDF digestibility of the 24% wheat bran diet was similar to that of the control diet. Crude protein digestibility was not affected ($P > 0.05$) by treatment. These results indicate that due to reduced dry matter intake and apparent nutrient digestibility, WB is unlikely to support similar performance to barley grain in backgrounding diets for cattle.

Key words: wheat bran, digestibility, beef heifers

T284 Effect of different doses of chitosans to modulate ruminal fermentation in Nelore steers. F. P. Renno*[1,2], A. P. C. Araujo[1], J. E. Freitas Junior[2], J. R. Gandra[1], R. Gardinal[1], G. D. Calomeni[1], L. N. Renno[3], M. C. B. Santos[1], and R. T. Trimboli[1], *[1]University of Sao Paulo, Sao Paulo, Sao Paulo, Brazil, [2]State University Julio de Mesquita, Jaboticabal, Sao Paulo, Brazil, [3]Vicosa Faculty of Life Sciences and Health, Vicosa, Minas Gerais, Brazil.*

The objective of this study was to evaluate the inclusion of different doses of chitosan in the diet of beef cattle on intake and in the pattern of ruminal fermentation. Eight Nellore steers (540 ± 28.5 BW/kg of SD) cannulated in the rumen were used and divided into 2 4 × 4 balanced Latin squares with a experimental period of 21 d, being 14 d for adaptation and 7 d of sample collection. The daily doses of chitosan (0, 50, 100 and 150 mg/kg BW) were inserted directly through the rumen cannula, twice daily. Daily intake was measured individually so to be kept a percentage of orts between 5 and 10% of the total supplied in the previous day. Samples of ruminal fluid were collected at 0 (before feeding) and 2, 4, 6, 8, 10 and 12 h after feeding. For variables measured at long time, the statistic model included treatment (doses), the time and the interaction between time and treatment as fixed effects. There was no effect of doses on the DMI, pH and NH3-N concentrations. There was linear effect for concentrations of propionate (mmol/L) with increasing doses of chitosan (21.40; 20.88; 21.66 and 22.08 for 0, 50, 100 and 150 mg/kg BW, respectively). There was linear effect for concentrations of acetate (mol/100mol) and decrease of relation C2/C3 with increasing doses of chitosan (69.17; 69.00; 68.67 and 67.97 for 0, 50, 100 and 150 mg/kg BW, respectively). Similarly there was a linear effect for concentrations of propionate (mol/100 mol of VFA) with increasing doses of chitosan (19.56; 19.57; 20.20 and 21.13 for 0, 50, 100 and 150 mg/kg BW, respectively). At the significance level of 5% the analysis in SAS 9.1 by Proc Mixed pointed as best dose for that occurs increase of the energy efficiency 150 mg/kg BW. The increase addition of chitosan in diets change the pattern of ruminal fermentation in Nellore steers.

Key words: energetic efficiency, intake, short chain fatty acids

T285 Evaluation of residual feed intake of Nelore bulls from a genetic improvement program. M. D. Freitas Neto[1,2], J. J. R. Fernandes*[1,2], D. A. Lima[1,2], P. L. P. Rezende[1], L. F. N. Souza[3], E. G. Moraes[3], R. A. Nogueira[1], and M. L. R. Pereira[1], *[1]Univerdidade Federal de Goias, Goiania, Goias, Brasil, [2]Conselho Nacional de Desenvolvimento Cientifico e Tecnologico, Brasilia, Distrito Federal, Brasil, [3]Nelore Qualitas, Goiania, Goias, Brasil.*

The goal of this trial was to evaluate the residual feed intake (RFI) relating to performance and carcass characteristics of 117 Nellore bulls from a genetic improvement program. The animals were an average of 24 mo of age and were located in individual pens. The production measures evaluated were: dry matter intake (Kg/day, %BW and g.BW$^{-0.75}$), average daily gain (Kg/day), feed efficiency (gain:feed), feed conversion (feed:gain). For carcass characteristics, longissimus muscle area (LMA), rib fat thickness (RFT) and rump fat thickness (RUFT) were measured by ultrasound. Dry matter intake (Kg/day) was determined weighing the orts every day. The diet was composed by 5.92% of corn silage, 30.89% of sugar cane bagasse, 26.01% of corn germ 15.12% of soybean meal, 19.53% of soybean hulls, 0.94% of urea and 1.60% of mineral mix. The animals were weighed in the beginning of the trial and each 21 d, so the average daily gain (ADG) could be determined. The estimated dry matter intake (Kg/day) was calculated by the regression of dry matter intake (Kg/day), ADG and BW$^{-0.75}$. The residual feed intake (RFI) was obtained by the difference between the DMI and the EDMI. The bulls were divided in 3 treatments: low, middle and high RFI and the results were analyzed using the statistical software SAS (2002). The animals with low RFI showed less dry matter intake (%BW and g.BW$^{-0.75}$) ($P < 0.05$). A better rate of feed efficiency and feed conversion was showed by the animals with low RFI ($P < 0.05$), because of low dry matter intake. Any difference was found for LMA, RFT and RUFT measured by ultrasound ($P > 0.05$). There were no difference ($P > 0.05$) for first weight, final BW and final BW$^{-0.75}$, showing no relation between RFI with final weight and feed conversion. Correlations between RFI and feed conversion, dry matter intake (%BW) and RFI and dry matter intake (g/Kg g.BW$^{-0.75}$) and RFI were (r = 0.27; $P < 0.05$), (r = 0.81; $P < 0.05$) and (r = 0.88; $P < 0.05$), respectively. No significant correlation for carcass characteristics (LMA, RFT and RUFT) and RFI was found.

Key words: feed efficiency, fat thickness, average daily gain

T286 Effect of different doses of chitosans on ruminal microbial protein synthesis in Nelore steers. F. P. Rennó*[1], A. P. C. Araujo[1], J. E. Freitas Junior[2], J. R. Gandra[1], G. D. Calomeni[1], R. Gardinal[1], L. N. Rennó[3], B. C. Venturelli[1], T. H. A. Vendramini[1], and F. G. Vilela[1], *[1]São Paulo University, São Paulo, São Paulo, Brazil, [2]State University Julio de Mesquita, São Paulo, Jaboticabal, Brazil, [3]Faculty of Life Sciences and Health, Facis, Viçosa, Minas Gerais, Brazil.*

The addition of controllers of rumen fermentation in ruminant diets has been explored in last year aiming to increase energy efficiency and the animal performance. The objective of this study was to evaluate the inclusion of different doses of chitosan in the diet of beef cattle on ruminal microbial protein synthesis. Eight Nellore steers (540 ± 28.5 BW/kg of SD) cannulated in the rumen were used and divided into 2 4 × 4 balanced Latin squares with a experimental period of 21 d being 14 d for adaptation and 7 d of sample collection. The daily doses of chitosan (0, 50, 100 and 150 mg/kg BW) were inserted directly through the rumen cannula, twice a day. Urine samples were collected on d 16 of the experimental period. The estimation of microbial protein synthesis was performed by the method of total excretion of purine derivatives. There was no effect of doses evaluated on concentrations of microbial nitrogen and microbial protein to the 5% level of significance by SAS Proc Mixed 9.1. The values observed for microbial nitrogen were 53.31; 59.53; 48.75 and 79.55 g/day for the doses 0, 50, 100 and 150 mg/kg BW, respectively. The values of microbial crude protein observed were 352.02; 373.33; 302.85 and 448.48 g/day for the doses 0, 50, 100 and 150 mg/kg BW, respectively. The addition of different doses of chitosan did not influence ruminal microbial protein synthesis in Nellore steers.

Key words: microbial nitrogen, purine derivatives, chitosan, beef cattle

T287 Effect of crude glycerin on nutrient intakes and apparent digestibility in Nellore feedlot steers. E. H. C. B. van Cleef*, J. M. B. Ezequiel, A. C. Homem Júnior, A. P. D'Áurea, J. B. D. Sancanari, F. B. O. Scarpino, D. A. V. Silva, and V. R. Fávaro, *São Paulo State University, Jaboticabal, São Paulo, Brazil.*

Thirty Nellore steers (277.7 ± 23.8 kg BW) were used to compare effects of diets containing increasing levels of crude glycerin to a control on nutrient intake and apparent digestibility. Cattle were blocked by weight and assigned randomly to one of the 5 treatments during 103 d. Animal was the experimental unit, and model effects included block and treatment. Orthogonal contrasts were used to determine the linear, quadratic, and cubic effects of glycerin, and 0% glycerin vs glycerin treatment. Experimental diets consisted of 30% corn silage and 70% concentrate (corn grain, soybean hulls, sunflower meal, glycerin) and were labeled as: 1) diet with no added glycerin (CON), 2) 7.5% glycerin on diet dry matter basis (7.5GLY), 15% glycerin on diet dry matter basis (15GLY), 22.5% glycerin on diet dry matter basis (22.5GLY), 30% glycerin on diet dry matter basis (30GLY). Indigestible neutral detergent fiber was used as internal marker to determine nutrient apparent digestibility. Five ruminally cannulated Nellore steers were adapted to experimental diets and used to incubate diets, orts and fecal samples from the 30 finishing study animals for 264 h. DM intake tended ($P = 0.09$) to decrease linearly with glycerin level. NDF and EE intakes decreased ($P < 0.01$) when glycerin was added to the diets. CP intake was not influenced ($P > 0.05$) by the inclusion of glycerin, and the ADF intake showed a quadratic effect ($P = 0.04$). Feeding glycerin caused linear ($P = 0.03$) reductions in NDF apparent digestibility while simultaneously increasing CP apparent digestibility. The DM, EE and ADF apparent digestibilities were not altered ($P > 0.05$) by glycerin. The inclusion of crude glycerin in feedlot cattle diets becomes a viable alternative since it provides no significant decrease in dry matter intake and digestibility of most nutrients in Nellore cattle. Caution should be taken to the level of roughage used, once the glycerin has a negative effect on fiber digestibility. Further studies are needed to elucidate the relative feed value of glycerin and its effects on performance, carcass characteristics and meat quality.

Key words: biodiesel, co-products, feedlot cattle

T288 Performance and carcass traits of bulls fed lipids sources and ionophore. L. C. Santarosa, M. M. Ladeira*, O. R. Machado Neto, M. L. Chizzotti, T. M. Gonçalves, D. M. Oliveira, L. S. Lopes, J. S. F. Hostalácio, and M. C. L. Alves, *Federal University of Lavras, Lavras, MG, Brazil.*

The objective of this research was to evaluate the performance and carcass traits of Red Norte bulls fed soybean ground grain or protected fat (calcium salts) based on soybean oil, and with or without the inclusion of the sodic monensin. Forty animals were allotted in a completely randomized design using a 2 × 2 factorial arrangement. The diets had corn silage as forage (40% of DM basis), and were isonitrogenous (12.7% CP), with the same ether extract content (7.2%), and neutral detergent fiber (29%). When the ionophore was supplemented, the dosage used was 230 ppm/day. The animals were weighed every 28 d after fasting for 16 h. The duration of the experiment was 84 d, preceded by 28 d of adaptation. At slaughter, carcasses were identified, weighed, washed, divided into halves, and stored in a cold chamber for 24 h at 1°C temperature. After 24 h were measured cold carcass weight, the subcutaneous fat thickness and *Longissimus* muscle area between the 12th and 13th ribs. There were no interaction between lipid source and ionophore ($P > 0.15$) and for lipid source ($P > 0.13$). There were no effects of ionophore for most of the variables, except for dressing percentage (DP), which can be due to an improvement in the metabolizable energy content of the diet. It can be concluded that the ground soybean grain or protected fat did not affect the weight gain any of the carcass traits. Funded by Fapemig, CNPq, CAPES and INCT-CA

Key words: monensin, protected fat, soybean

T289 Effect of post-ruminal *Saccharomyces boulardii* on fecal parameters and nutrient digestibility in Holstein steers given abomasal oligofructose. K. Davison*, R. L. Hougentogler, C. Leonardi, M. M. McCarthy, L. M. Nemec, and T. F. Gressley, *University of Delaware, Newark.*

Dietary conditions that lead to increased carbohydrate fermentation in the large intestine of ruminants may damage gastrointestinal tissues. Probiotics such as *Saccharomyces boulardii* (SB) modify intestinal fermentation and may improve the response to a large intestinal carbohydrate load. This study evaluated the effects of SB on fecal parameters and nutrient digestibility in steers before and after an abomasal oligofructose challenge. Six ruminally cannulated Holstein steers were used in a crossover design experiment with 18 d periods. Treatments were abomasal delivery of 0 or 10 g/d SB. On d 16 of each period, steers were abomasally dosed with 0.25 g/kg BW oligofructose every 6 h for 24 h. Pre-challenge fecal samples were collected every 6 h for 24 h before the first dose, and post-challenge samples were collected every 6 h for 48 h following the first dose. Dry matter, pH, and organic acid concentrations were measured on each sample. Fecal samples were composited by day and used to quantify apparent total tract nutrient digestibility. For DM, pH, and organic acid data, pre- and post-challenge results were each statistically evaluated using a mixed model including fixed effects of treatment, hour, their interaction, sequence, and period, and the random effect of steer. Time was included as a repeated measure. For digestibility data, all results were analyzed in one model. Treatment did not affect pre-challenge fecal DM, pH, or organic acid concentrations ($P > 0.10$). Post-challenge, SB decreased total organic acid concentration (56 vs. 65 mM, $P = 0.05$) and tended to increase fecal pH (6.96 vs. 6.81, $P = 0.09$). Treatment did not affect digestibility of OM, starch, or CP, but there tended to be a treatment × time interaction for NDF ($P = 0.07$). Pre-challenge, SB increased NDF digestibility (45.8 vs. 43.2%), but there was no difference during or following the challenge. The SB treatment modified hindgut fermentation as evidenced by decreased fecal pH and VFA changes following a fermentable carbohydrate challenge and by increased NDF digestibility pre-challenge.

Key words: feces, hindgut, yeast

T290 Can forage-based nutritional strategies offset weaning stress in calves? S. R. Blevins*, A. E. Tanner, W. S. Swecker, B. F. Tracy, D. A. Fiske, J. P. Fontenot, and R. M. Lewis, *Virginia Tech, Blacksburg.*

Weaning is stressful for calves. Calves often vocalize and pace rather than eat, resulting in weight loss and poor gains. Spring-born calves are typically weaned in late summer or early fall, where forages adequate for a mature animal may be insufficient for the maintenance and growth requirements of newly weaned calves. The purpose of this study was to determine if alternate forages could increase gains of newly weaned calves. The study was conducted at a research farm in western Virginia (latitude: 37°56′ N; longitude: 79°13′ W; elevation: 537m). After weaning, 24 moderate and 24 large framed Angus-cross

steer calves were assigned to 1 of 4 forage types: (i) nil-ergot, endophyte-infected fescue, (ii) endophyte-free fescue, (iii) orchardgrass + alfalfa, and (iv) orchardgrass + red and white clover. Three replicates of each forage type (1 ha area each) were grazed for 42 d by 4 calves (2 per frame size). Blood and fecal samples, and BW, were collected on d 0 and 42. Serum was analyzed for blood urea nitrogen, NEFA, glucose, and cortisol. Fecal samples were analyzed for cortisol. The experiment was repeated over 2 years. Data were analyzed (GenStat) using a split-plot design, with year and replicate fitted as random. Fixed effects were forage type, frame size, and their interaction. Age at weaning was a covariate. Between April and September paddocks received on average 59 cm of rain. An additional 8 cm fell during the experiment. Forage on offer did not differ between paddocks (748 (SD 131) kg/ha; $P > 0.10$), with no difference in CP (13 (SD 4) % DM basis) or NDF (33 (SD 4) % DM basis) between forage types ($P > 0.10$). As expected, large frame steers were heavier than medium frame steers ($P < 0.01$) at both the beginning and end. However, no differences were detected ($P > 0.05$) in ADG (0.48 (SD 0.22) kg/d) among forage types or frame sizes. Blood and fecal chemistry results also did not differ among treatments ($P > 0.05$). The forage types considered did not result in different ADG. The question remains whether other forages may be better suited to increasing post-weaning gains in fall-weaned calves in forage-based systems.

Key words: alternative forages, stress, weaning

T291 Urea supplements for beef steers grazing on marandu-grass pastures during dry season in the Brazilian savannas. D. G. de Quadros*[1], H. N. de Souza[2], G. L. Franco[3], R. G. de Almeida[1], and D. N. de Oliveira[1], *[1]Universidade do Estado da Bahia (UNEB), Barreiras, Bahia, Brazil, [2]PETROBRAS, Rio de Janeiro, Rio de Janeiro, Brazil, [3]Universidade Federal do Mato Grosso do Sul (UFMS), Campo Grande, Mato Grosso do Sul, Brazil.*

During the dry season in the Brazilian savannas, pastures become mature, lowering the nutritive value. The objective of this work was to evaluate urea supplements on the grazing behavior and performances of beef steers grazing marandugrass (*Brachiaria brizantha* 'Marandu') pastures. Twenty Nellore steers, weighting 300 ± 24.9 kg of initial liveweight, were used, 5 for treatment, grazing on 5 paddocks of 4 ha, rotating every 7 d, from July to October of 2010, in Barreiras, Bahia, Brazil. The supplements tested were: commercial mineral (M), mineral + urea (MU), and 3 multiple mixes (45.5% TDN) with corn, soybean meal, and 10 (MM10), 15 (MM 15), and 20 (MM20) % of urea, containing 0, 70, 41, 51, and 63% CP, respectively. Grazing behavior was observed every 14 d, registering every type of behavior (grazing, feeding supplements, ruminating/resting, others) during a 24h period. Dry matter and height of pasture were sampled monthly. Weekly, the intake of supplements was measured and the cattle were weighted every 28 d. The experiment was conducted using a completely random design, with 5 treatments and 4 replications. Data were submitted to ANOVA, using Tukey test to compare average values ($P \leq 0.05$). Dry matter was reduced by almost 50% compared from the beginning (7 ton) to the finishing time, mainly leaves, although the height just decreased 10 cm (from 61 to 51 cm). Supplementation reduced grazing time and simultaneously increased rumination/resting time. However, the patterns of behavior were not affected by supplementation. The daily intake of supplements changed with treatment, being 106, 196, 852, 666, and 400 g for M, MU, MM10, MM15, and MM20, respectively. The utilization of mineral alone (M) resulted in expressively less liveweight (150 g/day). Urea in the supplement (MU) maintained cattle liveweight. However, if gains are expected, the mixes should be used. In these cases, liveweight gain reached 324 g/day. Comparing economic performance, the best treatment was MM20, followed by MM10. Urea supplements were shown to be an indispensable tool to beef cattle production.

Key words: multiple mix, performance, protein

T292 Influence of nonmedicated additives as alternatives to antibiotics on calf plasma and intestinal measurements. S. M. Katzman*[1], S. I. Kehoe[1], and D. B. Carlson[2], *[1]University of Wisconsin-River Falls, River Falls, [2]Milk Products LLC, 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 on intestinal function and electrolyte profiles. Twelve bull calves were purchased from a local farm 3 separate times and were fed 1 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 of jejunum. Plasma samples were obtained weekly and analyzed for sodium, chloride, potassium, calcium, bicarbonate, phosphorus, BUN: creatinine ratio, and anion gap. Proc Mixed in SAS 9.2 was used with a repeated week statement to analyze blood results and repeated calf statement to analyze intestinal results. Plasma results indicate no significant differences between treatments except for sodium concentrations which were significantly lower for C calves (139.5, 140.1, and 141.5 for C, NM, and MED, respectively) and chloride concentrations which were significantly higher for MED (95.3, 95.4, and 97.3 for C, NM, and MED, respectively). Villus lengths were significantly longer for MED (40.4, 40.9, and 53.7 for C, NM, and MED, respectively). Crypt depths were significantly shorter for NM (28.8, 23.5, and 31.4 for C, NM, and MED, respectively). Villus diameter was not significantly different between treatments. These results indicate that medicated milk replacers may enhance intestinal morphology and both nonmedicated and medicated additives may improve electrolyte concentrations in the blood.

Key words: calves, milk replacer, intestinal morphology

T293 Effects of using near infrared spectroscopy to segregate and feed high and low energy barley on feedlot cattle performance, animal health, and carcass characteristics. E. M. Hussey[1], R. E. Peterson[1], D. Plett[2], C. W. Booker[1], G. K. Jim[1], L. O. Burciaga-Robles[1], and M. L. May*[1], *[1]Feedlot Health Management Services, Okotoks, AB, Canada, [2]Western Feedlots, High River, AB, Canada.*

The feed cost of gain accounts for 65–80% of the total cost of production, thus understanding the nutrient profile of the feed consumed by animals is important to investigate. A feeding trial was conducted to evaluate segregating barley by its estimated digestible energy value using near infrared reflectance spectroscopy (NIRS) measuring cattle health, performance, and carcass characteristics. In the study 9,007 heifers (initial BW 255.9 kg ± 4.59) were randomly allocated to one of 3 dietary treatments with 10 pens per treatment. The treatments were low energy barley (LOW), high energy barley (HIGH) and a 50:50

blend of the low and high energy barley (50:50). The data were analyzed as a randomized complete block design using the PROC MIXED (SAS Institute, NC) with the fixed effect of treatment and the random effect replicate with linear and quadratic contrasts. Compared with LOW, HIGH had greater ($P < 0.001$) DE, DM, fat, NE, CP, and bushel weight, with lower values ($P < 0.001$) of ash, ADF, crude fiber, and waste. There was an effect ($P < 0.05$) to increase overall mortality with increasing energy content of the diet (LOW 1.9%; 50:50 2.97%; HIGH 2.94%). In addition, increasing the barley energy increase ($P = 0.04$) metabolic mortality and ($P = 0.06$) miscellaneous mortality. Increasing the energy of the barley fed to cattle tended ($P = 0.06$) to decrease ADG, carcass adjusted ADG ($P = 0.08$), decrease DMI ($P < 0.001$) and decrease on G:F ($P < 0.05$). There was a linear effect to decrease ($P = 0.02$) Canada 2 yield grade carcasses with increasing energy of the diet, with no effect of dressing percentage, or quality grade ($P > 0.16$). Use of NIRS technology to procure feedstuffs has considerable merit, however the implications of segregating barley by its nutrient content needs to be better understood.

Key words: near infrared spectroscopy, feedlot cattle, barley

T294 Supplementation of methionine hydroxy analog, chelated trace mineral and dietary antioxidants in the diet of beef bulls for color stability. I. Castillo*, G. I. Zanton, and M. Vazquez-Anon, *Novus International Inc., St. Charles, MO.*

In the Mexican Southeast Beef Region during the winter of 2009 and spring of 2010, 2 experiments were conducted at commercial feedlots to evaluate methionine hydroxy analog, chelated trace minerals, and a dietary antioxidant on ribeye color stability. The 2 experiments were designed similarly with the same treatment and control diets. The treatment diets were supplemented with methionine hydroxy analog (5g/hd/d; MFP), chelated trace minerals (250 mg/d of Zn, 77 mg/d of Cu, 167 mg/d of Mn; Mintrex), 3 mg/d of Se yeast (Zorien SeY), and dietary antioxidants (125mg/kg DM of Agrado Plus); minerals for the control group were formulated according to NRC 2000. For each experiment, 100 bulls (Zebu x European; 18 ± 2 mo and 455 ± 5 kg) housed in a commercial feedlot were randomly assigned to the control or treatment group pens. Bulls were on trial for a minimum of 42 and maximum of 45 d. Bulls were fed an isoenergetic (1.10 Mcal NEg/kg) and isonitrogenous (14% CP) diet twice a day that was composed of 70% corn, 12% DDGS, 8% of tropical grass hay and 10% of base mix (sugar cane molasses, urea, soybean meal, and vitamins and trace minerals). Following harvest, color was assessed at time 0 (30 min after cut), 3, 6, 9, 12, 24, 48 and 72 h for color stability during cooler storage with a Minolta 508d spectrophotometer with d65 light at 10° observer and AUSMET color scale. For experiment 1, meat from treatment-fed bulls compared with control-fed bulls (n = 8/treatment/experiment) had significantly lower visual color assessment ($P < 0.05$) at time 6, 9, 12, 48, and 72 h while lightness (L*) was significantly higher at all times. For experiment 2, meat from treatment-fed bulls had significantly lower visual color assessment at all times and significantly higher lightness at all times except for 12 and 24 h. There were no differences in average daily gain (1.6 kg/d) during the trials. From these studies it can be concluded that supplementing methionine hydroxy analog, chelated trace minerals, and dietary antioxidant to diets fed to finishing bulls significantly improved beef color shelf life.

Key words: antioxidant, beef color, trace minerals

T295 Evaluation of bimodal distributions to determine meal criterion in heifers fed a high-grain diet. J. C. Bailey*, L. O. Tedeschi, E. D. Mendes, and G. E. Carstens, *Texas A&M University, College Station.*

Meals are clusters of bunk visit (BV) events separated by short intervals that are differentiated from the next meal by a non-feeding interval that is long compared with the intervals within a meal. The longest non-feeding interval considered to be part of a meal is defined as meal criterion. The objective of this study was to determine which combination of Gaussian normal (N) and Weibull (W) 2-population distribution models best fit non-feeding interval data to distinguish intervals within (1st population) and between (2nd population) meals in beef cattle. Feeding behavior traits were measured in 119 heifers fed a high-grain diet (3.08 Mcal ME/kg DM) using a GrowSafe system. BV frequency and duration averaged 75 ± 14 events/d and 73.0 ± 22.3 min/d. The following 2-population distribution models; NN, NW, WW and WN were fitted to the $\log_{10}$-transformed interval lengths between BV events for each animal using R mixdist package (2.9–2). The intersection of the 2 distributions was computed as the meal criterion and used to derive meal frequency and duration data. Akaike's Information Criterion (AIC) was used to assess goodness of fit of the 4 models. The range in AIC values for the 2-pool NN, NW, WW and WN distribution models were 580 to 2923, 575 to 2884, 509 to 3226, and 726 to 3227, respectively. The NN and NW models resulted in longer ($P < 0.0001$) meal criterion (15.3 and 14.2 ± 7.2 min) compared with WW and WN models (10.8 and 10.6 ± 7.2 min). Consequently, meal frequencies were shorter and meal durations were longer when the N distribution was used to describe the first population. Each of the 4 models was fitted to individual animal BV data, and the model with the lowest AIC identified. A Chi-squared analysis was conducted to assess the number of animals identified for each 2-popluation distribution model. The frequencies (2, 76, 2, and 39) were different ($X^2 = 126.55$, $P < 0.0001$) among treatments, suggesting that 63.9% of the heifers were best fit by the NW model. Therefore, these results indicate that the NW 2-population distribution model is most appropriate to define meal criterion in beef cattle fed high-grain diets.

Key words: meal criteria, normal, Weibull distribution

T296 Effects of temperament classification and breed type on feed efficiency and feeding behavior traits in heifers fed a high-grain diet. J. C. Bailey*, G. E. Carstens, J. T. Walter, A. N. Hafla, E. D. Mendes, L. O. Tedeschi, and R. K. Miller, *Texas A&M University, College Station.*

The objective of this study was to evaluate the effects of temperament classification and breed type on performance, feed efficiency and feeding behavior traits in heifers fed a high-grain diet. Six trials were conducted over 3 consecutive yr with Angus (AN; n = 185), Braford (BO; n = 241), Brangus (BN; n = 266) and Simbrah (SI; n = 196) heifers from the Deseret Ranch; with 2 trials conducted each yr during the fall (n = 415) and spring (n = 473). Initial ages were 337 vs. 501 ± 86 d for heifers used in the fall (younger) and spring (older) trials. DMI and feeding behavior traits were measured for 70 d using a GrowSafe system. Exit velocity (EV), which is defined as the rate at which heifers exit a squeeze chute, was used as an objective measure of temperament. Within trial, heifers were classified into calm, moderate and excitable temperament groups based on ± 0.5 SD from the mean EV. Initial BW (318 vs. 308 ± 9 kg), final BW (425 vs. 401 ± 11 kg), ADG (1.45 vs. 1.27 ± 0.06 kg/d) and DMI (10.29 vs. 9.62 ± 0.47 kg/d) were higher ($P < 0.0001$) for heifers with calm temperament compared with

excitable heifers. Feed conversion (F:G) (7.36 vs. 8.23 ± 0.21 kg/d) differed ($P < 0.005$) between calm and excitable temperament class, but residual feed intake did not. In BO and BN heifers, there were no differences in F:G between calm and excitable groups, but in AN and SI, F:G was lower in the calm temperament group (EV x breed interaction; $P = 0.02$). Calm heifers spent more time ($P < 0.0001$) at the feed bunk (58.3 vs. 50.6 ± 3.8 min/d) than excitable heifers, but bunk visit frequency was similar between temperament groups. Meal frequency was not affected by temperament classification, however, meal duration (138 vs. 132 ± 9 min/d), and the bunk visit per meal ratio (9.4, 9.3, 8.7 ± 1.1 events/meal) were higher ($P < 0.02$) for calm compared with excitable heifers. These results suggest that heifers with calm temperament have 13.5% greater ADG, consume 7.1% more DM, and have 10.6% lower F:G than heifers with excitable temperament.

Key words: feeding behavior, temperament

T297 Effect of concentration of flax hulls in the diet on intake, digestion, milk production, and milk composition of dairy cows. H. V. Petit*, *Dairy and Swine R&D Centre, Agriculture and Agri-Food Canada, Sherbrooke, QC, Canada.*

A total of 45 lactating Holstein cows averaging 617 kg of BW were allotted at wk 20 of lactation to 9 groups of 5 cows blocked for similar DIM to determine the effects of feeding different concentrations of flax hulls (FH) on DMI, milk production, milk composition, and digestion. Cows within each block were assigned to one of the 5 isoenergetic TMR containing 0, 5, 10, 15 or 20% FH. The experiment was carried out from wk 20 to 24 of lactation and diets were fed for ad libitum intake. Milk samples were obtained from 2 consecutive milkings on wk 5 of the experiment and were analyzed separately to determine milk composition. Total tract digestibility was determined on wk 5. Data recorded during the digestibility trial were analyzed as a randomized block design and block and treatment were the main sources of variation. Data on production were analyzed as repeated measurements using PROC MIXED of SAS. Treatment sum of squares were partitioned to provide linear, quadratic, and cubic contrasts after a significant F-test (i.e., $P < 0.05$). There was no significant cubic effect of treatment on any parameter measured. Intake of DM averaged 20.9 kg/d and was similar among treatments. Concentration of FH in the diet had no effect on milk yield, proportions of protein and fat and yields of protein, fat and lactose. There was a linear increase in proportion of lactose in milk and a quadratic effect of feeding level of FH on somatic cell count. Total tract apparent digestibility of DM, ADF, and NDF was similar among diets. Ether extract digestibility increased with higher proportions of FH in the diet but the increase was more important from 0 to 50 g/kg. These data suggest that corn and barley can be partially substituted by flax hulls (up to 20% of the DM) as the energy source in the diet of mid-lactating dairy cows.

Key words: dairy cattle, flax, milk production

T298 Body condition score at the initiation of bST supplementation does not affect milk response in dairy cows of Chile. F. Bargo[1], S. Follert*[1], A. Hinostroza[1], L. Lastra[2], and R. Navarrete[2], *[1]Elanco Animal Health, Southern Cone (Argentina & Chile), [2]Ancali Dairy, Los Angeles, Chile.*

Three hundred Holstein dairy cows (150 primiparous and 150 multiparous) from the commercial dairy farm Ancali (Los Angeles, Chile) were used to evaluate the interaction between body condition score (BCS) at the beginning of recombinant bovine somatotropin (bST) supplementation at 67 DIM and milk response to bST in a completely randomized design. Cows were sorted out by lactation (primiparous vs. multiparous) in 2 free-stall corrals and within each corral randomly assigned to 2 treatments: control or bST (Lactotropina, Elanco Animal Health). Cows on bST received a total of 15 subcutaneous injections of 500 mg bST every 14 d during 210 d starting June 13th at 67 DIM. Daily milk yield (Alpro, De Laval), monthly BCS (scale 1 to 5 by 2 independent experienced observers), and days open (DC305) were measured. Data were analyzed by ANOVA with a repeated measures mixed model using the PROC MIXED procedure of SAS (1999) where cows nested within treatment were considered as random effect. A significant interaction between health status and milk response to bST was found ($P < 0.05$). Healthy cows showed a milk response to bST of 5.2 kg/d ($P < 0.05$), while cows with mastitis or foot problems did not respond to bST ($P > 0.05$). The interaction between BCS at 67 DIM (≤ 2.75 vs. ≥ 3.00) and milk response to bST was not significant ($P = 0.67$). Cows on bST did not loss BCS and at the end of supplementation gained 0.19 points of BCS (3.03 at 67 DIM vs. 3.22 at 277 DIM; $P < 0.05$). Days open did not differ ($P > 0.05$) between treatments and averaged 105.5 and 97.5 d in primiparous and multiparous cows, respectively. When bST supplementation was initiated at 67 DIM in healthy Holstein cows, milk response to bST was not related to initial BCS averaging 5.2 kg/d without affecting days open.

Key words: body condition score, bST, milk response

T299 Associations among digestive tract lesions and abnormal serum chemistries in cull dairy cattle. M. B. Hall*[1], G. R. Oetzel[2], G. B. Huntington[3], F. M. Moore[4], and D. M. Hertzke[4], *[1]U.S. Dairy Forage Research Center, USDA-ARS, Madison, WI, [2]School of Veterinary Medicine, Univ. of Wisconsin, Madison, [3]Dept. of Animal Science, Univ. of North Carolina, Raleigh, [4]Marshfield Labs Veterinary Services, Marshfield, WI.*

All animals accrue tissue damage with age, but types and prevalence of damage are not known. Tissue lesions could signal impaired organ function, which could affect performance. The study objective was to assess prevalence of microscopic lesions in digestive tracts of cull dairy cows, and determine associations among lesions and with abnormal serum chemistry values. Cull dairy cows (79) were sampled at 3 commercial abattoirs on 5 occasions. Tissue samples from reticulorumen (RR), small intestine (SI), large intestine, pancreas (PAN), cecum, and liver (LIV), and a blood sample were obtained immediately postmortem. Additionally, jugular blood samples and RR biopsies of papillae were obtained from 19 clinically normal live, noncull, ruminally cannulated Holsteins (11 lactating cows and 8 nonlactating bred heifers). Associations among lesions and with serum chemistries were evaluated with logistic regression analysis. Odds ratios for pairs of lesions described the increased likelihood of presence of both if 1 was found. Infiltration by lymphocytes observed in all SI, large intestinal and cecal samples suggests that this is normal, possibly related to barrier immune function. Serum chemistries were generally not good predictors of specific tissue lesions. Noncull animals had lower prevalence of RR inflammation and pustules than cull cows ($P < 0.03$). For cull animals, no lesions were detected in 36% of RR, 49% of SI, and 64% of PAN samples. Only 8% of LIV samples showed no lesions. Associations among lesions were found between RR and PAN, and among PAN, SI, and LIV. Among the odds ratio results: 4.7 for RR pustules and PAN inflammation ($P = 0.12$), 8.7 for SI hemosiderin laden macrophages (HLM) and decreased PAN zymogen ($P < 0.01$), and 3.0 for HLM and LIV mineralization ($P = 0.06$). Interrelatedness of lesion prevalence suggests that impact of disorders that created the lesions was not confined to a single organ. With implications for improved animal health, well-being, longevity, and performance, further investigation is warranted into how treatment or prevention of primary disorders and traits of economic importance relate to development of tissue damage.

Key words: dairy cattle, digestion

T300 Influence of a reduced-starch diet with or without exogenous amylase on lactation performance by dairy cows. L. F. Ferraretto*[1], R. D. Shaver[1], M. Espineira[1], H. Gencoglu[2], and S. J. Bertics[1], *[1]Department of Dairy Science, University of Wisconsin-Mad-*

ison, Madison, [2]Department of Animal Nutrition and Nutritional Diseases, Faculty of Veterinary Medicine, University of Uludag, Bursa, Turkey.

The objective of this trial was to determine lactation performance responses in high-producing dairy cows to a reduced-starch (RS) with or without exogenous amylase addition versus a normal-starch (NS) diet. Forty-five multiparous Holstein cows, 68 ± 29 DIM and 696 ± 62 kg body weight (BW) were randomly assigned to 1 of 3 treatments in a completely randomized design; a 2-wk covariate adjustment period with cows fed the NS diet followed by a 10-wk treatment period with cows fed their assigned treatment diets. The NS TMR did not contain exogenous amylase (NS-). The RS diets, formulated by partially replacing corn grain and soybean meal with whole cottonseed and wheat middlings, were fed without (RS-) and with (RS+) exogenous amylase addition to the TMR. Starch and NDF concentrations averaged 27.0% and 30.9%, 22.1% and 35.0%, and 21.2% and 35.3% (DM basis) for the NS-, RS-, and RS+ diets, respectively. Cows fed RS- tended ($P < 0.06$) to consume 1.9 kg/d more DM than NS-. Expressed as a percentage of BW, DMI was greater for cows fed RS- than NS- ($P < 0.01$) or RS+ ($P < 0.05$). Intake of NDF ranged from 1.09% to 1.30% of BW among the treatments with RS- being 21% greater ($P < 0.001$) than NS-. Milk yield tended ($P < 0.07$) to be 2.2 kg/d greater for cows fed NS- than RS- and was 2.6 kg/d greater ($P < 0.04$) for cows fed NS- than RS+. Milk fat content and yield were unaffected ($P > 0.10$) by treatment. Milk protein content and yield were greater for cows fed NS- than RS- ($P < 0.04$) and RS+ ($P < 0.01$). The MUN concentrations were greater ($P < 0.001$) for cows fed RS diets than the NS- diet. BW, BW change, and BCS were unaffected by treatment ($P > 0.10$), except for a trend for BW change of cows fed RS- to be greater than RS+ ($P < 0.09$). Feed conversion (kg milk/kg DMI) was 10% greater on average for cows fed NS- than for cows fed the RS diets ($P < 0.001$ and $P < 0.03$), and tended to be 6% greater for cows fed RS+ than RS- ($P < 0.09$). Feeding a RS diet compared with a NS diet without addition of exogenous amylase to either diet reduced ($P < 0.001$) milk and component-corrected feed conversions.

Key words: amylase, lactating cow, starch

T301 Effects of different ratios of extruded soybeans and whole cottonseeds on production performance of cows and conjugated linoleic acids (CLA) in milk fat. R. Yan*[1,2], S. Y. Chen[2], C. Jiang[1], Y. J. Zhang[1], and J. G. Han[1], *[1]Department of Grassland Science, China Agricultural University, Beijing, China, [2]Department of Agronomy, University of Wisconsin-Madison, Madison.*

The objective of this study was to investigate effects of different ratios of extruded soybeans (ESB) and whole cottonseeds (WCS) on production performance of cows and conjugated linoleic acids (CLA) in milk fat. 40 multiparous Holstein cows (averaging 100 ± 22 DIM) divided into 6 groups, were used in a randomized block design for a 14-week period. In this study, there were 4 treatments (dry matter basis): adding no ESB or WCS (control), 10% ESB, 5% ES+5% WCS, 10% WCS. All diets included 30% alfalfa hay, 10% corn silage, 10% *Leymus chinensis* and 50% concentrates. After adding ESB or WCS, crude protein content and ether extract content increased. In vitro crude protein digestibility and in vitro ether extract digestibility increased with the supplementation of ESB or WCS. Neutral detergent fiber content and in vitro neutral detergent fiber digestibility increased when 10% WCS was added to the diet. No change of dry matter intake was found in all 4 treatments. Compared with control (30.1kg/d), milk yield increased by 4.6 kg/d, 4.3 kg/d, and 2.1 kg/d respectively for 10% ESB, 5% ES+5% WCS or 10% WCS treatments. Because of the increase of milk yield, milk protein yield, milk fat yield, milk lactose yield and milk total solid yield increased. Milk cis9, trans11-conjugated linoleic acids content increased when cows were fed ESB or WCS. Cis9, trans11-CLA content in milk was increased comparing with control (0.88 g/100 g fatty acids)) and highest when cows were fed 10% ESB (1.43 g/100 g fatty acids), followed by 5% ES+5% WCS (1.48 g/100 g fatty acids) diets and the 10% WCS diet (1.24 g/100 g fatty acids). These results suggested that adding ESB or WCS in the diets could increase milk yield and milk cis9 (trans11-CLA).

Key words: production performance, conjugated linoleic acid, extruded soybean and whole cottonseed

T302 Effects of supplemental whole cotton seeds on production performance and milk fatty acids of dairy cows fed diets with different ratios of corn silage and alfalfa hay. R. Yan*[1,2], S. Y. Chen[2], R. Z. Zhang[1], Y. J. Zhang[1], and J. G. Han[1], *[1]Department of Grassland Science, China Agricultural University, Beijing, China, [2]Department of Agronomy, University of Wisconsin-Madison, Madison.*

The objective of this study is to investigate the effects of different ratios of corn silage (CS): alfalfa hay (AH), and whole cotton seeds (WCS) on milk yield, milk compositions, blood metabolites, and fatty acids in milk fat and plasma. 90 multiparous Holstein cows (73 ± 27 DIM) were arranged in a randomized block design which lasted 14 weeks. There were 3x3 treatments with 3 levels of WCS (0%, 5% and 10%) and 3 levels of forage addition (one is 30% corn silage (CS) and 10% alfalfa hay (AH); another is 20% CS and 20% AH; and the third is 10% CS and 30% AH). When part of CS was replaced by AH, protein content and digestibility, organic digestibility and neutral detergent fiber digestibility increased. After supplementation of WCS in diets, protein and ether extract contents, digestibility of protein and neutral detergent fiber increased. There was no change of dry matter intake when cows were fed the experimental diets. As more AH was added to the diets, milk yield ($P = 0.004$), milk protein content and yield (($P < 0.01$), and trans-9, cis-11 conjugated linoleic acids (CLA) concentration in milk fat and plasma ($P < 0.01$) increased. When WCS were supplemented to the diets, milk yield ($P = 0.04$), and trans-9, cis-11 CLA concentration ($P < 0.01$) in milk fat and plasma increased. When 10% WCS was added to the diet containing 30% AH, trans-9, cis-11 CLA content (1.46 g/100 g of total fatty acids) in milk was the greatest among all treatments. It suggested that AH could replace part of CS and be a good forage source of diet for dairy cows to improve milk yield and milk composition. Meanwhile, WCS could be included in the diet with high AH to improve production performance of dairy cows.

Key words: alfalfa hay, whole cottonseed

T303 Energy expenditure, feeding behavior and locomotion of grazed versus zero-grazed dairy cows throughout the lactation period. F. Dohme-Meier*[1], L. D. Kaufmann[1], S. Görs[2], P. Junghans[2], C. C. Metges[2], and A. Münger[1], *[1]Agroscope Liebefeld-Posieux, Research Station ALP, Posieux, Switzerland, [2]Research Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany.*

An experiment was conducted to determine the effect of grazing versus zero-grazing on energy expenditure (EE), feeding behavior and locomotion in dairy cows at different time points in lactation. Fourteen Holstein cows were subjected to 2 treatments in a repeated cross over design with 3 experimental series. At the beginning of each series, cows were on average 38, 94 and 171 ± 11.1 DIM, respectively. Each

series consisted of a 7-d adaptation and a 7-d collection period. Cows either grazed on pasture or had ad libitum access to grass cut from the same paddock in a free-stall barn. Grass intake was estimated using the double alkane technique. On each day of the collection period, EE of one cow in the barn and of one cow on pasture was determined by using the ^{13}C bicarbonate dilution technique, with blood sample collection done either manually in the barn or using an automatic sampling system on pasture. During the same time period cows′ locomotion and feeding behavior were recorded over 3 d using pedometers and behavior recorders. The model included production system, experimental series and their interaction as fixed effects (MIXED procedure of SAS). Milk yield decreased with increasing DIM ($P < 0.05$). Grass intake was lower ($P < 0.01$) for grazing cows (16.8 kg DM/d) compared with zero-grazing cows (18.9 kg DM/d). The lowest intake was observed in the first series and the highest in the second series ($P < 0.001$). Within the 6-h measurement period, grazing cows expended more ($P < 0.001$) energy (273 vs. 231 kJ/kg $BW^{0.75}$) than zero-grazing cows and differences in EE did not change with increasing DIM. Cows on pasture spent proportionally more ($P < 0.001$) time walking and less ($P < 0.001$) time standing and lying than cows in the barn. The proportion of time spent eating was higher ($P < 0.001$) and that of time spent ruminating was lower ($P < 0.001$) for grazing cows compared with zero-grazing cows. In conclusion, the unchanged milk production along with a lower feed intake indicates that grazing cows mobilized body reserves to cover additional energy requirements, which were at least partly caused by more locomotion.

Key words: dairy cows, energy expenditure, grazing

T304 Effects of combinations of probiotics on growth and blood biochemical parameters in preruminant calves. Y.-Q. Fu, Q.-Y. Diao, Y. Tu*, N.-F. Zhang, and C.-G. Jiang, *Key Laboratory of Feed Biotechnology of Ministry of Agriculture/Feed Research Institute, Chinese Academy of Agricultural Sciences, Beijing, P.R. China.*

This study examined the effects of different combinations of probiotics on growth performance and blood biochemical parameters in preruminant Chinese Holstein calves. Twenty-four newborn Holstein calves were randomly divided into 4 groups with 3 males and 3 females each group, and each group was offered a basal diet(a milk replacer and a starter) (control, group I), or the basal diet supplemented with *Bacillus licheniformis* (group II), or *Bacillus licheniformis* + *Bacillus subtilis* (group III), or *Bacillus licheniformis* + *Bacillus subtilis* + *Lactobacillus plantarum* (group IV). The ratio of each strain of *Bacillus* for group III and group IV was 1:1, 1:1:1, respectively. The amount of total probiotics supplemented to corresponding calves was at 200 × 10^8 cfu/(head•d) for 56d. Live weight of each calf was recorded fortnightly and blood samples were collected concomitantly to examine its blood biochemical parameters. Data were analyzed by mixed or GLM procedure of SAS software. Compared with the control, average daily gain of the calves from group II only was significantly higher than group I throughout the trial (0.65 vs. 0.53 kg/d, $P < 0.05$), and the average daily gain of the calves from group II was 15.1% and 14.0% higher than that from groups III and IV, respectively ($P > 0.05$). From 2 to 4 weeks of age, average daily gain of the calves from group II was higher ($P < 0.05$) than that from group I (0.46 vs. 0.28kg/d) or group III(0.46 vs. 0.25kg/d). At the end of the experiment, the serum concentration of globulin or total protein in group II was significantly lower than that in group IV ($P < 0.05$), and the serum concentration of glucose in group II was significantly higher than that in group IV ($P < 0.05$). No significant difference in the serum albumin or urea nitrogen was detected among groups. It was concluded that dietary probiotics, especially *Bacillus licheniformis*, improved growth of preruminant calves.

Key words: calves, probiotics, growth and blood biochemical parameters

T305 The limiting sequence and proper ratio of lysine, methionine and threonine for calves fed milk replacers containing soy protein. J.-H. Wang, Y. Tu*, N.-F. Zhang, X.-C. Xu, and Q.-Y. Diao, *Key Laboratory of Feed Biotechnology of Ministry of Agriculture/ Feed Research Institute, Chinese Academy of Agricultural Sciences, Beijing, P.R. China.*

This study estimated the amino acid (AA) sequence and relative ratio of AA for calves on milk replacers (MR) with 50% milk protein replacement from soy protein concentrate (39.8% CP) by supplementing lysine (Lys), methionine (Met), and threonine (Thr) to the MR. Method of partial deduction of AA was adopted, on the principle that N retention was determined by the intake of the first limiting AA. Twenty-four newborn calves were randomly offered 1 of 4 MR diets (22% CP, 14% fat) for 56 d (n = 6/diet, half males and half females): PC (2.34% Lys, 0.72% Met and 1.80% Thr) or the PC with either Lys, Met or Thr reduced by 30%, respectively (i.e., PC-Lys (1.64% Lys, 0.72% Met and 1.80% Thr), PC-Met (2.34% Lys, 0.50% Met and 1.80% Thr), and PC-Thr (2.34% Lys, 0.72% Met and 1.26% Thr)). MR were fed at 11% of BW, adjusted twice weekly as calves grew. Starter (20% CP, 1.03% Lys, 0.30% Met and 0.69% Thr) and hay (3.23% CP, 0.29% Lys, 0.12% Met and 0.23% Thr) were offered ad libitum beginning on d 36 and d 43, respectively. A 3-d total collection of feed refusals, feces, and urine were recorded starting at d 33 and d 54 of age, respectively. Observations of N balance trials were analyzed using the GLM procedure of SAS. The results showed that the limiting sequence of the 3 AA was ranked as Lys, Met and Thr; the proper ratio of Lys, Met and Thr was 100:29:70 for the calves on MR alone and 100:30:60 for the calves on MR, starter and hay. Compared with PC, absorbed N/intake N was significantly lower for calves fed PC-Lys from d 33 to 35 and from d 54 to 56 (67.5% vs. 78.3% and 80.6% vs. 87.7%, $P < 0.05$), and for calves fed PC-Thr from d 33 to 35 (70.3% vs. 78.3%, $P < 0.05$); retained N/intake N was significantly lower for calves fed PC-Lys from d 33 to 35 and from d 54 to 56 (42.2% vs. 62.0% and 63.2% vs. 71.7%, $P < 0.05$), and for calves fed PC-Met from d 54 to 56 (67.5% vs. 71.7%, $P < 0.05$), also for calves fed PC-Thr from d 33 to 35 (45.7% vs. 62.0%, $P < 0.05$). In conclusion, digestion and utilization of N were negatively affected by AA deletion. The average relative ratio of the 3 AA was 100:29.5:65 for calves from 2 to 10 wk of age.

Key words: limiting amino acid, milk replacers, soy protein

T306 Feeding frequency for individually fed early lactation cows: enlightening the perplexing strategy. A. Nikkhah*, S. M. Karimzadeh, B. Sorkhroo, S. Asghari, M. Avaz Khanloo, and L. Bahramkhani Zarrin Goli, *University of Zanjan, Zanjan, Iran.*

Due to dependence on several cow, dietary and housing factors, feeding frequency (FF) is a perplexing strategy. The objective was to determine FF effects on feeding behavior, metabolism and production of early lactation cows. Eight multiparous Holstein cows (70 d in milk, 577.5 kg BW) housed in free individual boxes (4 × 3 m) received either once daily (1 ×) at 0700 h, or 4 times daily (4 ×) at 0100, 0700, 1300 and 1900 h an alfalfa hay, barley-corn grain based TMR with 63% concentrate (DM-based). The TMR delivered had 81% DM, 17.6%

CP, and 27.3% NDF. The study design was a 2 × 2 crossover with 2 periods of 20 d. Data were analyzed as a linear mixed model with fixed treatment effect, and cow plus period random effects. Once instead of 4 × feeding increased ($P = 0.05$) intakes of DM (21.1 vs. 20.0 kg/d) and NEL (36.4 vs. 34.3 Mcal/d). Orts as a % of the TMR fed were similar between 1 × and 4 × groups (7.6 vs. 10%, respectively). Milk yield (31.5 vs. 30.7 kg/d, $P = 0.16$), milk NEL output (21.7 vs. 21.4 Mcal/d, $P = 0.72$), fat content (3.5 vs. 3.6%, $P = 0.66$), protein content (3.2 vs. 3.2, $P = 0.81$), BW changes (−70 vs. 180 g/d, $P = 0.53$) and fecal pH (6.64 vs. 6.62, $P = 0.67$) were similar between 1 × vs. 4 × FF, respectively. Urine pH was higher for 4 × than 1 × FF (8.12 vs. 8.00, $P < 0.01$). Daily duration of eating (323 vs. 284 min/d, $P = 0.49$), ruminating (302 vs. 326 min/d, $P = 0.66$), total chewing (624 vs. 609 min/d, $P = 0.37$), laying (537 vs. 586 min/d, $P = 0.40$), and standing (691 vs. 640 min/d, $P = 0.50$), were comparable for 1 × vs. 4 × FF, respectively, as were serum glucose, urea, BHBA, albumin, total protein and triglycerides. The first meal length (defined as the time interval between feeding and the first non-eating bout of ≥ 20 min) was 106 min in the 1 × cows, while being on average 49 min per feeding and 196 min per day in the 4 × cows ($P < 0.01$). As such, the post-feeding serum insulin and NEFA concentrations were respectively higher and lower with 1 × than 4 ×. Reduced urine pH by 1 × feeding suggests less alkaline extracellular body fluids. Improved energy intake by less frequent feeding possesses metabolic and health implications.

Key words: feeding frequency, early lactation, individual

T307 Prolonged provision of protected methionine improves milk contents and yields of fat and protein in lactating cows. A. Nikkhah*[1], D. Kianzad[2], A. Haj Hosseini[2], A. Zalbeik[2], and G. Ghorbani[3], *[1]University of Zanjan, Zanjan, Iran, [2]Animal Breeding Center, Karaj, Iran, [3]Isfahan University of Technology, Isfahan, Iran.*

Metabolic challenges of early lactation superimposed on environmental stresses such as high ambient temperatures alter lactation curve and compromise cow health. The objective was to establish productive effects of prolonged feeding of protected methionine (PMT) in dairy cows. Twenty 4 fresh Holsteins (27 ± 9 d in milk, 617 kg BW, 2.8 BCS) including 12 s lactation and 12 higher lactation cows were randomly assigned to an either control (CN) or PMT (Smartamine) supplemented TMR (51:49% forage:concentrate), fed continuously for 5 mo. Cows were housed in free stalls, milked 3 times daily at 0000, 0800 and 1600 h in a milking parlor, and offered TMR post-milking plus top-dress alfalfa hay. The study was conducted from May through November of 2009 in central Iranian province of Isfahan. The monthly collected production data were analyzed as a linear mixed model with fixed effects of treatment, parity, time and 2- and 3-way interactions, plus random effects of cow (parity × treatment × time) and residuals. To adjust for correlated repeated measures on the same subject, covariance structures with minimum fit criteria were modeled for all parameters. The PMT group had greater 5 mo-long average milk yield (42.4 vs. 37.4 kg/d, $P = 0.06$), milk fat content (3.30 vs. 2.75%, $P = 0.007$), fat yield (1.40 vs. 1.04 kg/d, $P = 0.002$), milk protein content (2.96 vs. 2.75%, $P = 0.01$) and protein yield (1.25 vs. 1.02 kg/d). Mature cows tended to produce more milk (42.2 vs. 37.6 kg/d, $P = 0.08$) and milk fat (1.30 vs. 1.13 kg/d, $P = 0.10$) than second lactation cows. Findings provide compelling evidence for beneficial effects of prolonged PMT provision (e.g., 5 mo) on milk fat and protein contents and yields in high-producing early-mid lactation cows exposed to summer high ambient temperatures.

Key words: Smartamine, methionine, prolonged feeding

T308 Rumen degradation patterns of ground and steam-processed broomcorn and ground barley. A. Nikkhah*, *University of Zanjan, Zanjan, Iran.*

The objective was to determine rumen disappearance behavior of ground broomcorn (GBC), whole and ground steam-flaked broomcorn (SBC) and ground barley (GB). Three ruminally fistulated Naeini ewes, fed at maintenance an alfalfa hay based partially mixed ration, were used in a randomized complete block design to monitor grain in situ digestion properties. The methodology involved rumen incubation of 8 × 12 cm nylon bags (50 μm pore size) containing approximately 3 g of processed grains. Grains were finely ground by a hammer mill (screen size of 2 mm). Broomcorn was steamed for about 60 min to increase grain moisture up to 18% vs. 13% pre-processing, and flaked between preheated large rollers (46 × 90 cm) for a desired flake density (380 to 400 g/L). Samples were incubated ruminally for 2, 4, 8, 16, 24 and 48 h subsequently and were taken out all at once. For 0 h, bags were put in 39°C water for 15 min. To further differentiate between steam-flaking and particle size effects on rumen degradation, the SBC was incubated as both whole and ground flakes. All bags were rinsed under running tap water until the effluent was clear. The bags were dried at 55°C for 48 h, weighed, and residues were ground to pass a 1-mm screen. Data were analyzed with Mixed Models procedures of SAS program with repeated measures. At 0 h, DM of ground SBC (21.0%) was degraded to a greater extent ($P < 0.05$) than that of whole SBC (13.0%), GBC (14.0%) and GB (13.6%). However, at 2, 4, 8, 16 and 24 h post-incubation, respectively, GB (53, 69, 75, 80, 86%) had greater degradation extent than ground SBC (33, 43, 51, 61, 71%), whole SBC (29, 39, 48, 58, 63%) and GBC (17, 21, 37, 44, 50%). Thus, steam processing compared with grinding considerably increased rumen DM degradation of broomcorn, getting closer to that of GB. Results demonstrate the effectiveness of steam-flaking in improving rumen digestibility of broomcorn, which possesses a harder endosperm than corn and grain sorghum. Given its lower price compared with barley and corn grains, broomcorn may be included in dairy diets at higher levels should it be effectively steam-processed.

Key words: rumen degradation, broomcorn, barley

T309 Steam-flaking of broom sorghum improves effective rumen degradation of DM while controlling that of CP. A. Nikkhah*, *University of Zanjan, Zanjan, Iran.*

The objective was to determine effective rumen DM and CP degradation of ground (GBS) and steam-flaked broom sorghum (SFB) grains comparing ground barley grain (GB). Three ruminally cannulated Naeini sheep were fed at maintenance and utilized in an in situ randomized complete block design study with a 2-week pre-study adaptation period. Grains were finely ground by a hammer mill (2 mm mesh size). Broom sorghum was steamed for 60 min and up to a moisture content of 18% before flaking through preheated corrugated rollers (46 × 90 cm) for a flake density of 380–400 g/L. Nylon bags (8 × 12 cm, 50 μm pore size) containing 3 g of differently processed grains were incubated ruminally for 2, 4, 8, 16, 24 and 48 h to be taken all out at once. For 0 h, bags were put in 39°C water for 15 min. Sample and blank bags were all rinsed under running tap water until clearing the effluent, were dried at 55°C for 48 h, weighed, and residues were ground (1-mm) for wet chemistry analysis. Disappearance patterns data were fitted into a nonlinear equation to estimate rates and extent of rumen CP and DM digestion: $Y = a + b (1- e^{-ct})$; a = soluble %, b = slowly digestible %, c = disappearance rate/h, and t = incubation hour. Effective rumen DM and CP degradations were calculated by the equation:

a + (b × c)/(c + k); k = fractional outflow rate. Data were analyzed with Mixed Models Procedures of SAS program. Steam-flaking compared with grinding considerably increased rumen effective degradation of broom sorghum DM while to some extent reducing that of CP. With rumen outflow rates of 5 and 8%, respectively, effective rumen DM degradation was greater ($P < 0.01$) for GB (74 and 70%), ground SFB (58 and 52%) and whole SFB (53 and 47%) than for GBS (43 and 35%). assuming 5%/h rumen passage rate. The respective modeled values for CP effective degradation were 70 and 63% for GB, 39 and 30% for GBS, 33 and 25% for ground SFB, and, 31 and 24% for whole SFB. Findings provide evidence that steam-flaking under special circumstances can successfully improve rumen degradation of broom sorghum grains without elevating CP degradability.

Key words: broom sorghum, degradation, steam-flaking

T310 Steam-flaked broom sorghum a viable substitute for ground barley in midlactation dairy rations. A. Nikkhah*, *University of Zanjan, Zanjan, Iran.*

An objective was to determine effects of feeding cows ground (GBS) vs. steam-flaked broom sorghum (SFB) vs. ground barley (GB). Ten mid lactation Holstein cows (140 ± 10 d in milk, 570 ± 40 kg BW) in tie stalls were used in a 5 × 5 replicated Latin square design with 5 21-d periods. Each period had 14-d of adaptation. Treatments were diets with 1) GB, 2) GB + GBS, 3) GBS, 4) GB + steam-flaked broom sorghum (SFB), and 5) SFB. Diets were fed as total mixed rations with 30% alfalfa hay, 15% corn silage, and 20% cereal grain (DM based). Data were analyzed as a linear mixed model with fixed effects of diet and period, and random effects of cow (diet) and residuals. Dry matter intake was similar among treatments (19.1–19.7 kg/d). Feeding GB+SFB (66.7%), SFB (64.1%) and GB (63.7%) vs. GBS (55%) improved total tract apparent CP digestibility ($P < 0.05$). Fat corrected milk yield (FCM) increased by 2.3 kg by feeding SFB instead of GBS based diets (24.4 vs. 22.1 kg, $P < 0.01$). The FCM was 2.8 kg greater for GB + SFB than for GBS (24.9 vs. 22.1 kg, $P < 0.01$). Milk contents of fat (3.63% and 3.55% vs. 3.44%), protein (3.02% and 3.04% vs. 2.94%), and total solids (11.86%, 11.88% vs. 11.61%) were greater for SFB and GB than for GBS, respectively, as were milk yields of fat (0.82 and 0.81 vs. 0.73 kg/d), protein (0.68 and 0.68 vs. 0.62 kg/d) and total solids (2.7 and 2.7 vs. 2.47 kg/d). Feeding SFB instead of GBS increased ($P < 0.05$) fecal pH (7.10 vs. 6.87) and feed efficiency (1.26 vs. 1.15). Feeding SFB and GB+SFB compared with GBS and GB+GBS decreased plasma urea (14.8 and 13.4 vs. 18.0 and 16.0 mg/dL) and increased plasma glucose (61 and 58 vs. 55 and 55 mg/dL) concentrations, respectively. Results demonstrate the effectiveness of steam-flaking over grinding in considerably improving feeding value of broom sorghum when included at 20% of diet DM. Hence, SFB may be feasibly fed to midlactation cows both alone and combined with GB.

Key words: broom sorghum, steam-flaking, milk

T311 Effect of dietary nitrogen levels and yeast supplementation on apparent diet digestibility and microbial population in the rumen content of dairy lactating cows. D. R. Ouellet* and J. Chiquette, *Dairy and Swine R&D Centre, Agriculture and Agri-Food Canada, Sherbrooke (QC) Canada.*

Eight rumen-fistulated Holstein dairy cows (679 kg BW; SEM = 5) were used in a duplicated 4 × 4 Latin square design, with a 2 × 2 factorial arrangement of treatments to evaluate the effect of dietary nitrogen levels and yeast supplementation on apparent diet digestibility and rumen microbial population of dairy lactating cows. Isoenergetic diets, highly or moderately deficient in metabolizable protein [-22% (HD) or −14% (MD) less than requirements], were fed with or without yeast supplement (10 g/head/d of a mixture of *Aspergillus oryzae* and *Saccharomyces cerevisiae*). Total mixed ration (60:40 grass silage:concentrate barley based) was fed 12 times daily. Apparent digestibility of DM, OM, NDF, ADF and N were measured. Ruminal fluid content was sampled to estimate protozoa using microscopic-counting method, and cellulolytic and total viable bacterial count (TVC) by the most-probable-number method. Plasma urea concentration was determined. There were no interactions between treatments for items evaluated ($P > 0.10$). Apparent digestibility of N (69.5% vs. 65.9%; SEM = 1.6) and urinary N excretion (261g/d vs. 162 g/d; SEM = 6) were higher ($P < 0.01$) in MD than in HD. Apparent digestibility (average %) of DM (72.4; SEM = 1.1), OM (74.4; SEM = 1.1), ADF (52.5; SEM = 2.3), and NDF (57.8; SEM = 2.5) were similar among treatments. Yeast supplementation did not affect apparent digestibility parameters. Compared with MD, HD reduced by 48% plasma urea concentration (10.6 vs. 15.7 mg/dL; $P < 0.02$). Average microbial counts were unaffected ($P > 0.05$) by treatments. Protozoa counts [geometric means (cfu/mL) and 95% confidence interval (CI)] were: 2.3×10^5 (CI = 1.6×10^5 to 3.4×10^5), TVC: 3.1×10^9 (CI = 2.6×10^9 to 3.7×10^9) and cellulolytic bacteria: 3.9×10^7 (CI = 2.8×10^7 to 5.5×10^7). In conclusion, addition of yeast to diets containing up to −22% the requirements in metabolizable protein had no effect on the apparent digestibility of the diet, ruminal content parameters and plasma urea.

Key words: direct-fed microbials, metabolizable protein restriction, digestion

T312 Ground broomcorn in dairy rations. A. Nikkhah*, *University of Zanjan, Zanjan, Iran.*

A main purpose was to determine nutritional effects of feeding ground broomcorn (BC, 1% tannin) vs. ground barley grain (GB) based mixed rations on dairy cow performance. Ten tie-stall-housed Holstein cows (averaged 140 d in milk, 570 kg BW) were fed twice daily alfalfa hay-corn silage based mixed rations with 1) 20% GB, 2) 10% GB + 10% BC, or 3) 20% BC, in a duplicated Latin square design. Each 21-d period had 14-d for adaptation. Diets were balanced for CP (15%), NEL (1.6 Mcal/kg) and NDF (38%). Cows were milked 3 times daily. Data were analyzed as linear Mixed Models with diet and period fixed effects, and cow within diet plus residuals random effects. Total tract apparent CP digestibility was decreased by feeding 20% BC vs. 20% GB (55 vs. 63%, $P < 0.05$). DM intake (kg/d) was maintained by GB+BC (19.7) and BC (19.1) vs. GB (19.1). Fecal pH (7.01, 6.93, 6.87, $P < 0.05$), milk yield (24, 22.2, 22.1 kg/d), feed efficiency (1.26, 1.12, 1.15), and milk total solids percent (11.88, 11.64, 11.61%) and yield (2.70, 2.50, 2.47 kg/d) decreased ($P < 0.05$), and plasma urea increased (14.3, 16.0, 18.0 mg/dL) as BC replaced GB, with similar rumen pH (6.6, 6.7, 6.6), urine pH (8.12, 8.15, 8.16) and plasma glucose (56, 55, 55 mg/dL). The quite similar values for BC vs. GB+BC suggest that cows are able to adapt to high dietary BC levels. These data, while biologically light, may not support feeding BC to high-producing cows at 20% of diet DM, especially if the optimum goal is maximizing milk production. On the other hand, given the lower price of BC (0.20$/kg) than of BG (0.35$/kg), where commercially available, BC partially replacing the strategic costly GB in mid and late lactation rations is commercially pursued.

Key words: broomcorn, dairy, production

T313 Effect of naturally extracted vitamin E (RRR-α-tocopheryl acetate) vs. synthetic vitamin E on blood and milk levels of vitamin E in lactating dairy cows. M. B. de Ondarza*[1], K. Daniels[2], and D. Bunting[2], [1]*Paradox Nutrition LLC, West Chazy, NY,* [2]*ADM Alliance Nutrition Inc., Quincy, IL.*

The trial objective was to determine the effect of supplementing synthetic vitamin E (545 IU/d) (SYN) vs. naturally extracted vitamin E at one-half the level of milligrams (NAT) on blood and milk levels of vitamin E in high-producing multiparous dairy cows. Half of the cows (n = 57) received SYN and half (n = 57) received NAT for 6 weeks. Treatment groups were housed in separate pens with ad libitum access to TMR. Cow groups were balanced pre-trial for parity, previous ME305 production, and previous 14-d milk yield. After 14 d, daily milk yield of individual cows was recorded. Individual milk samples were analyzed for component content pre-trial, wk 5 and wk 6. Data was analyzed using JMP statistical software (SAS, Cary, NC) with pre-trial data as covariates. Milk yield (40.95 and 39.80 kg/d for SYN vs. NAT, respectively), % milk fat (3.63 and 3.64% for SYN and NAT, respectively), kg milk fat, % true protein, kg true protein, 3.5% FCM (kg), milk urea nitrogen (mg/dl), and SCC (x 1000) (395 vs. 431 for SYN vs. NAT, respectively) were unaffected ($P > 0.10$) by treatment. Pre-trial and wk 6, blood and milk samples were taken from each cow. Individual blood samples and super-composite milk samples for each treatment group were analyzed for vitamin E and cholesterol. Blood serum vitamin E status was not affected ($P > 0.20$) by treatment with means of 8.98 and 9.04 μg/mL for SYN and NAT, respectively. Blood serum cholesterol was not affected ($P > 0.20$) by treatment with means of 252 and 253 mg/dL for SYN and NAT, respectively. Blood serum vitamin E: cholesterol ratio was not affected ($P > 0.20$) by treatment with means of 3.62 and 3.61($\times 10^{-3}$) for SYN and NAT, respectively. Pooled milk vitamin E concentrations were 1.20 and 1.19 μg/mL for SYN vs. NAT, respectively. Considering that naturally extracted vitamin E was fed at one-half the weight amount, this form of vitamin E appears to be at least twice as potent as synthetic vitamin E at NRC recommended levels.

Key words: RRR-alpha-tocopheryl acetate, synthetic vitamin E, lactating dairy cattle

T314 Large-scale production effects of an intestinally releasable methionine product in dairy cows. A. Nikkhah*[1], R. Kowsar[2], and G. Ghorbani[2], [1]*University of Zanjan, Zanjan, Iran,* [2]*Isfahan University of Technology, Isfahan, Iran.*

The objective was to determine productive effects of feeding an intestinally releasable methionine product (Met, Mepron-85) in lactating cows. A total of 195 free-stall-housed Holstein cows were fed either a control (C, n = 110, 71 ± 51 d in milk, 47.0 ± 0.12 kg milk/d) or a Met-supplemented (M, n = 85, 85 ± 59 d in milk, 47.5 ± 0.12 kg milk/d) alfalfa hay-corn silage based mixed ration 4 times daily in a completely randomized design study. The DM in control vs. Met diet had, respectively, 1.78 vs. 1.70 Mcal/kg NEL, 19.6 vs. 19.0% CP, and 34.5 vs. 35.5% NDF. Cows were milked 3 times daily and monitored for 8 weeks. The weekly collected data were analyzed as linear Mixed Models with fixed effects of diet, week and the interaction, and random effects of cow (diet × week) plus residuals. To account for correlated repeated measures on the same cow, covariance structures with least fit criteria were adopted. DM intake was greater for M than for C (26.6 vs. 25.8 kg/d, $P < 0.05$), whereas NEL intake tended to be greater for C than for M (45.9 vs. 45.2 Mcal/kg, $P < 0.10$). Actual milk volume (40.1 vs. 40.7 kg/d) and milk lactose content (4.90 vs. 4.95%) were similar for M vs. C, while protein content was higher for M (3.1 vs. 3.0%, $P = 0.01$) and fat content tended to be higher for C (3.0 vs. 2.9%, $P = 0.06$). As a result, milk energy density (0.63 vs. 0.64 Mcal/kg) and output (25.5 vs. 26.3 Mcal/d) remained similar for M vs. C. Milk urea N (17.6 vs. 18.1 mg/dL) and urine N (4.24 vs. 4.37 g/kg) concentrations were lower for M vs. C ($P < 0.05$), supporting the increased milk protein by M. These data may imply reduced hepatic N detoxification into urea, and reduced environmental N excretion by feeding the rumen protected Met to high-producing cows.

Key words: methionine, protection, lactation

T315 Study on the metabolic mechanism of melamine in dairy cattle. X. Jin*, Y. Zhang, S. Li, H. Zhang, and Q. Zhang, *College of Animal Science and Technology, China Agricultural University, Beijing, China.* This trial was conducted to study the effects of dietary supplementation of melamine byproducts on residual concentration of melamine in rumen fluid, blood, urine, feces and milk of dairy cows. The further object was to reveal the metabolic mechanism of action of melamine in dairy cows by single factor experiment. The supplemental levels in the concentrate were 0.516%, 0.860% and 1.204%, respectively. The experiment was divided into 3 phases with 10 d in each phase (7 d for pre-feeding and 3 d for sampling). The same 5 Holstein dairy cows were fed the same experimental diet in each phase. The results showed that the residual concentration of melamine in milk, feces and urine were all increased with the growing supplementation level. The results showed that residual concentration of melamine in each kind of samples was durative increasing. When the melamine byproducts level rose to 0.860% in the concentration, the residual concentration of melamine in samples of milk was significantly different from that of 0.516% ($P = 0.02$), while the residual concentration in other samples were not significantly different; when the melamine byproducts level rose to 1.204%, the residual concentration in ruminal fluid and urine were very significantly different from that of 0.516 ($P < 0.01$), the residual concentration in blood, raw milk were significantly different from that of 0.516 ($P = 0.02$). The residual concentration in feces was not significantly different from that of 0.516% and 0.860% ($P = 0.27$), though the concentration of melamine was durative increasing. The concentration of melamine in the raw milk, feces and urine from the phase with the highest supplemental level were 1.31, 3.30 and 107.75mg/kg, respectively. It is concluded that renal excretion is the primary metabolic pathway of melamine while defecation and lactation are only auxiliary pathways. It was consistent with the report that melamine had negative effect on kidney.

Key words: dairy cattle, melamine, metabolic mechanism

T316 Conjugated linoleic acid (CLA) supplementation around calving affects glucose metabolism in dairy cows. H. M. Hammon*[1], K. Hötger[1], S. Görs[1], M. Becker[1], C. Weber[1], A. Tröscher[2], and C. C. Metges[1], [1]*Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany,* [2]*BASF, Limburgerhof, Germany.*

CLA (in particular the t10,c12 CLA isomer) is well established for its reducing effects on milk fat content. Although CLA supplementation causes changes in fat metabolism of dairy cows, less is known about CLA effects on glucose metabolism. The objective of the study was to investigate endogenous glucose production (eGP), especially gluconeogenesis (GNG), in German Holstein cows supplemented either with 50 g rumen-protected CLA fat (10% t10,c12 CLA, Lutrell® pure, BASF, Ludwigshafen, Germany; n = 10) or 50 g linoleic acid (Ctrl; n

= 10) from 14 d before expected calving to 63 DIM. Diets based on grass and corn silage were fed *ad libitum*. DMI and milk yield were recorded daily, BW and milk composition were measured weekly, and BCS and back fat thickness every second week. Plasma concentrations of glucose, nonesterified fatty acids, and β-hydroxybutyrate were determined at 14 and 7 d before calving and once weekly up to 84 DIM. On 21 and 63 DIM, eGP was measured after overnight food withdrawal by primed [U-^{13}C]glucose infusion. Additionally, on 21 DIM, cows received 2 oral boli of deuterium-labeled water (70 atom% D) within 4 h (n = 7 per diet) and blood samples were taken to measure fractional GNG (GNG_{frac}) using deuterated glucose enrichment in plasma. Data were analyzed by SAS PROC MIXED with diet and time as fixed effects. Milk fat content was reduced ($P < 0.01$) and milk and lactose yield increased in both groups after calving and were higher ($P < 0.05$) from 35 DIM on in CLA cows than in Ctrl, respectively. Energy balance tended to be less negative ($P < 0.1$) in Ctrl than in CLA cows. Plasma concentrations of glucose were higher immediately after calving in CLA cows than Ctrl (diet × time interaction $P < 0.01$). The eGP increased ($P < 0.05$) from 21 to 63 DIM and CLA supplement reduced ($P < 0.05$) eGP on 21 DIM, but not on 63 DIM. GNG_{frac} on 21 DIM tended to be higher ($P < 0.1$) in CLA cows than in Ctrl. These findings suggest a glucose-sparing effect due to CLA supplementation, using less glucose for milk fat synthesis and more glucose for lactose production and other tissues, resulting in an increased milk yield and blood glucose level.

Key words: dairy cow, CLA, glucose

T317 Lactation performance and milk fatty acid profile in dairy cows fed linseed oil in diets with different forage to concentrate ratios. L. Saliba*[1,2], R. Gervais[1], Y. Lebeuf[1,2], J.-C. Vuillemard[1], and P. Y. Chouinard[1,2], *[1]Département des sciences animales, Université Laval, Québec, Québec, Canada, [2]Institute of Nutraceuticals and Functional Foods (INAF), Québec, Québec, Canada.*

The composition of basal diet is known to influence the response to dietary unsaturated fatty acids (FA) in lactating dairy cows. To evaluate the interaction between the levels of concentrates and linseed oil on milk yield and composition, 24 Holstein cows were used in a randomized complete block design based on DIM with a 2 × 2 factorial arrangement of treatments. Within each block, cows were fed one of 4 experimental diets containing 30% (LC) or 70% (HC) concentrates, with (LO) or without linseed oil (NLO) supplemented at 3% DM. After 4 weeks of treatments body weight was not different among treatments (654 ± 6 kg). Compared with LC, feeding HC increased ($P < 0.01$) DMI (20.5 vs. 24.7 kg/d), milk yield (26.1 vs. 33.1 kg/d), FCM (26.4 vs. 30.6 kg/d), milk lactose (4.59 vs. 4.76%; 1205 vs. 1582 g/d), and milk protein (3.22 vs. 3.50%; 832 vs. 1148 g/d). Milk fat content was lower (4.15 vs. 3.56%; $P < 0.01$), and milk fat yield tended to be higher (1076 vs. 1162 g/d; $P = 0.07$) for cows fed HC compared with LC. Feeding LO decreased DMI (23.5 vs. 21.7 kg/d; $P < 0.05$), milk fat content (3.99 vs. 3.72%; $P < 0.01$), and milk protein content (3.45 vs. 3.27%; $P < 0.01$) compared with NLO. Interaction between linseed oil and concentrates was observed for milk fat content of c9,c12,c15–18:3 (4.1, 3.2, 5.1, and 5.9 mg/g FA for LC-NLO, HC-NLO, LC-LO, and HC-LO, respectively; $P < 0.05$). Concentrations of c9,t11,c15–18:3 increased with LO compared with LNO (0.5 vs. 0.2 mg/g FA; $P < 0.001$), and decreased with HC compared with LC (0.3 vs. 0.4 mg/g FA; $P < 0.001$), while c9,t13,c15-C18:3 was not detected in any milk samples. Feeding linseed oil increased t11,c15–18:2 in milk fat, especially when cows were fed LC diets (1.6, 0.4, 9.8, and 3.6 mg/g FA for LC-NLO, HC-NLO, LC-LO, and HC-LO, respectively; $P < 0.01$). The same interaction was observed for t11–18:1 (11.5, 6.6, 24.1, and 11.0 mg/g FA for LC-NLO, HC-NLO, LC-LO, and HC-LO, respectively; $P < 0.01$). In conclusion, the level of concentrates in the basal diet influenced milk fat content of FA originating from rumen biohydrogenation in response to linseed oil supplementation.

Key words: concentrate levels, milk fatty acids, linseed oil

T318 Rumen volume and passage kinetics depend on feeding time (0900 vs. 2100 h). A. Nikkhah*[1], J. C. Plaizier[2], and A. D. Kennedy[2], *[1]University of Zanjan, Zanjan, Iran, [2]University of Manitoba, Winnipeg, MB, Canada.*

The objective was to determine effects of providing a total mixed ration (TMR) at either 0900 h or 2100 h on rumen volume as well as on fluid and solids retention time and outflow rates in lactating cows. Three primiparous and one multiparous Holstein cows (80 d in milk; 26 kg/d milk yield) with rumen cannula (10 cm d) were used in a crossover design study with 2 6-wk periods. Each period had 3-wk of adaptation. The diet had forage to concentrate ratio of 50.2:49.8 (DM based). Co-EDTA and Cr-mordanted alfalfa were used as markers to measure rumen outflow rates of fluid and solids, respectively. A total of 50 g Co-EDTA was dissolved in 300 mL of distilled water and ruminally infused via cannula at feed deliveries (0090 h vs. 2100 h). Simultaneously, 300 g of Cr-mordanted alfalfa fiber was dosed into 10 different rumen sites. Next, rumen fluid and solids were sampled subsequently at 2, 3, 4, 6, 8, 12, 16, 24, 36, 48, and 72 h post-marker-infusion. The rumen marker concentrations were regressed against time using a first-order exponential equation to acquire passage rates (slopes). Rumen fluid volume was calculated by dividing the amount of Co infused by the intercept for individual cows. Data were analyzed as Mixed Models with fixed feeding time (FT) effect and random period, cow within treatment, and residuals effects. Rumen fluid total volume tended to increase by feeding at 2100 h instead of at 0900 h (107 vs. 89 L; $P = 0.07$). Rumen fluid outflow rate (11.9 vs. 11.7%/h) and retention time (8.2 vs. 8.9 h), and rumen solids retention time (32.8 vs. 31.4 h) were similar between 0900 h and 2100 h FT, respectively. Feeding at 2100 h vs. 0900 h increased ($P < 0.05$) rumen solids outflow rate in primiparous cows (3.7 vs. 3.1%/h). Data suggest that rumen volume and passage kinetics depend on when TMR is delivered to once-daily-fed cows.

Key words: feeding time, rumen, kinetics

T319 Influence of method of surfactant supplementation on characteristics of digestion and feeding value of fat in Holstein steers fed a high-energy finishing diet. H. Dávila-Ramos*[1], A. Gonzalez-Castellon[1], A. Barreras-Serrano[1], A. Estrada-Angulo[2], M. A. López-Soto[1], J. V. Macias-Zamora[1], A. Plascencia[1], S. H. Vega[1], and R. A. Zinn[3], *[1]IICV - Universidad Autónoma de Baja California, México, [2]FMVZ - Universidad Autónoma de Sinaloa, México, [3]Department of Animal Science, University of California, Davis, El Centro.*

Four Holstein steers (271 ± 11 kg) with cannulas in the rumen and proximal duodenum were used to study the influence of method of surfactant (Tween 80) supplementation on characteristics of digestion and feeding value of fat. Treatments consisted of a steam-flaked corn-based finishing diet supplemented with: 1) no supplemental fat, no surfactant; 2) 6% supplemental fat (yellow grease, no surfactant; 3) 5.75% supplemental fat plus 0.25% Tween 80 (TW) added to the diet as part of the premix (TW was mixed with premix before incorporation with grain in the mixer, as second step in diet preparation), and 4) 5.75%

supplemental fat plus 0.25% TW combined directly with the supplemental fat (TW was mixed with supplemental fat before incorporation into the feed mix as penultimate step in diet preparation). The data was analyzed using MIXED procedures (SAS Inst. Inc., Cary, NC) based in a model for 4x4 Latin square experimental design Treatment effects were tested by means of orthogonal polynomials and differences were considered to be significant when $P < 0.05$. There were no surfactant by supplemental fat interactions ($P > 0.05$). Surfactant did not affect ($P > 0.05$) site and extent of OM, starch, N, ADF, and fatty acid digestion, or DE value of diet. Supplemental fat decreased ($P < 0.05$) ruminal and total tract digestion of OM and ADF and increased ($P < 0.05$) the DE value of diet. The decrease in postruminal FA digestion was mainly due to decreased ($P < 0.05$) digestion of C18:0. Digestible energy of supplemental fat averaged 6.87Mcal/kg. It is concluded, that independent of method of addition, supplementing high-fat diets with 0.22% of Tween 80 does not influence site and extent of digestion or the feeding value of supplemental fat.

Key words: fat supplementation, Holstein steers, surfactant

T320 Evaluation of limit feeding and bunk management strategies for gravid dairy replacement heifers. N. M. Esser[1], J. Larson[1], P. C. Hoffman*[1], C. L. Liu[2], and W. K. Coblentz[3], *[1]University of Wisconsin, Madison, [2]Northeast Institute of Geography and Agricultural Ecology, CAS, Harbin, Heilongjiang, China, [3]USDA-ARS Dairy Forage Research Center, Marshfield, WI.*

To assess effects of bunk access and limit feeding on dairy heifer growth and nutrient intake, 96 Holstein heifers (394 ± 31 kg) were fed one of 2 diets, and allotted to full (F) or partial (P) bunk access. Pens (n = 12) of heifers were limit fed a TMR without (NS) straw or fed a TMR with straw (S). Feed access times for NS and S were 6 and 24 h respectively. Heifers, fed NS or S, were assigned to pens with F (8 stalls/8 heifers) or P (4 stalls/8 heifers) to complete the 2 × 2 factorial arrangement (FS, PS, FNS, PNS). Heifers were evaluated for growth, and nutrient intake. Bunk occupancy time and rate, 0–6 h post-feeding, were evaluated using timed digital photography. Data were analyzed using PROC MIXED with pen replication as the experimental unit. Bunk occupancy for F was longer ($P < 0.01$; 149.8 vs. 111.2 min) than heifers allotted to P. Feeding S (S vs. NS) increased ($P < 0.02$) heifer bunk occupancy by 16.2 min. Bunk occupancy rate was 27.6, 20.0, 24.4 and 18.1 min/h for FS, PS, FNS and PNS respectively. Feeding S increased dietary NDF by 7.0% units and decreased ($P < 0.04$) DMI of heifers 0.28 kg/d as compared with limit feeding NS. Heifers fed S consumed 0.55 kg more ($P < 0.01$) NDF/d but consumed less ($P < 0.01$) CP, and Mcals of ME than heifers fed NS. Bunk access (F vs. P) had no effect ($P > 0.55$) on DMI or the intake of any nutrient. Despite lower CP and ME intakes, the ADG of heifers fed S or NS were similar ($P > 0.21$; 0.90 vs. 0.95 kg/d). Allotting heifers to F or P bunk access likewise had no effect ($P > 0.39$) on ADG (0.95 vs. 0.91 kg/d) and no interactions between bunk access and treatment diet on ADG were observed. Finally, bunk occupancy rate (min/h) and ADG were regressed using PROC REG procedures. For heifers assigned to PS ($r^2 = 0.25$) and FNS ($r^2 = 0.15$) there were weak positive relationships between bunk occupancy rate and ADG. For heifers assigned to FS or PNS there was no relationship between bunk occupancy rate and ADG. Data suggest adding straw to a limit fed diet with partial bunk access did not improve heifer nutrient intake, and induced a more variant relationship between bunk occupancy rate and ADG.

Key words: limit feeding, heifers, bunk space

T321 Effects of cinnamon essential oil, cinnamaldehyde and monensin on milk fatty acid profile of dairy cows. C. Benchaar*[1] and P. Y. Chouinard[2], *[1]Agriculture and Agri-Food Canada, Dairy and Swine R&D Centre, Sherbrooke, QC, Canada, [2]Université Laval, Département des Sciences Animales, Québec, QC, Canada.*

Eight multiparous lactating cows (BW = 614 kg; DIM = 71) were used in a duplicate 4 × 4 Latin square design (28-d periods) to examine the effects of no addition (CTL), or the addition of cinnamon essential oil (1 g/d; CIN), cinnamaldehyde (1g/d; CDH) and monensin (24 mg/kg DM; MON) on milk fatty acid (FA) composition. Analyses of FA were performed on pooled samples collected from 4 consecutive milkings (d 22 to 23). Differences between treatments were declared significant at $P \leq 0.05$ using the Tukey correction for multiple comparisons and trends were discussed at $0.05 < P \leq 0.10$. Feeding CIN and CDH to cows had no effect on milk FA composition (g/100 g of total FA) as compared with feeding CTL. Proportions of C18:0 (7.99 vs. 8.69%) tended to be lower while that of trans-11 C18:1 (0.74 vs. 0.70%) remained unchanged, those of trans-10 C18:1 were higher (0.39 vs. 0.30%), and those of cis-9, trans-11 C18:2 tended to be higher (0.40 vs. 0.35%) in milk fat of cows fed MON than in that of cows fed CTL. Cows fed CIN and CDH had lower proportion of trans-10 C18:1 (0.32%) than cows fed MON (0.39%). The proportion of trans-11 C18:1 was similar for cows fed CDH and those fed MON (0.74 and 0.66%) while it tended to decrease when cows were fed CIN as compared with MON (0.63 vs. 0.74%). The proportion of cis-9, trans-11 C18:2 was higher for cows fed MON than for cows fed CDH and CIN (0.40 vs. 0.35 and 0.34%, for MON, CDH and CIN, respectively). Results show that under the experimental conditions of this study, supplementing dairy cow diets with MON exerted minor effects on milk FA composition while no changes were observed when CIN and CDH were fed.

Key words: essential oil, monensin, milk fatty acid

T322 Fatty acids in milk of dairy cows fed diets containing propolis-based products. S. C. de Aguiar[1], S. M. Cottica[1], R. B. Samensari[1], E. M. de Paula[1], S. L. Franco[1], L. P. P. de Moura[1], G. T. dos Santos[1], J. V. Visentainer[1], W. B. R. dos Santos[2], E. H. Yoshimura[1], M. V. Valero[1], and L. M. Zeoula*[1], *[1]Universidade Estadual de Maringá, Maringá, Paraná, Brazil, [2]Instituto Federal do Amazonas, Maués, Amazonas, Brazil.*

Propolis is a resinous substance collected by bees from plants with various biological properties. The objective was to evaluate the addition of propolis-based products (PBP) in the diet of dairy cows, to decrease the amount of saturated fatty acids (SFA) in milk and the ratio of fatty acids (FA) n-6/n-3, as well as increase the amount of conjugated FA (CFA) and monounsaturated FA (MUFA). Four Holstein cows, with 550 kg of body weight and 147 d of lactation were subjected to 2 daily milkings (0600 and 1500h) and randomly assigned to a 4 × 4 Latin Square. The diets which were formulated with 60.27%:39.73% forage:concentrate, differed due to the inclusion or not of PBP as follows: control (no additives), PBP1, PBP2 and PBP3 (with 30.63, 71.88 and 78.45 mg of quercetin equivalents, respectively). Quercetin, a flavonoid, was used as a marker for flavonoids quantification. The PBP1 and PBP2 differ only in the concentration of propolis and have the same ethanol content, while the PBP3 has the same propolis concentration of PBP2 and higher ethanol content. Milk fat was transesterified and the methyl esters of FA were analyzed by gas chromatography. Quantification of FA was made in relation to the internal standard, methyl tricosanoate and the results expressed in $mg.g^{-1}$ of total lipids (Table 1). There was an increase in the amount of CFA in the milk from

PBP2 treatment when compared with control. Though, milk resulting from the addition of PBP3 treatment showed a significant increase in the amount of MUFA and n-3 FA, and a decrease (P = 0.00631) in the amount of SFA. The n-6/n-3 ratio decreased in all PBP treatments when compared with control. Concluded that the addition of PBP in dairy cows diets improves milk quality, which is more beneficial for human consumption.

Table 1. Sum of fatty acids in dairy cows milk for the different treatments

Fatty Acids (mg.g^{-1})	Control	PBP1	PBP2	PBP3
CFA	7.57 ^{c}	8.46^{c}	11.42^{a}	9.62^{b}
Polyunsaturated fatty acids	50.51^{a}	40.12^{c}	44.76^{b}	53.52^{a}
SFA	435.69^{a}	423.99^{ab}	432.90^{a}	403.01^{b}
MUFA	409.41^{b}	409.77^{b}	403.35^{b}	460.21^{a}
n-6	46.21^{a}	35.86^{c}	40.19^{b}	47.67^{a}
n-3	4.30^{b}	4.25^{b}	4.57^{b}	5.85^{a}
n-6/n-3	10.76^{a}	8.45^{b}	8.83^{b}	8.17^{b}
TOTAL	903.18	882.34	892.43	926.36

Different letters in the same line are statistically different (P < 0.05).

Key words: fatty acids, n-6/n-3 ratio, propolis ethanolic extracts

T323 Varying dietary dry matter concentration through water addition: Effect on nutrient intake of dairy cows in late lactation. J. A. Fish and T. J. DeVries*, *University of Guelph, Kemptville Campus, Kemptville, ON, Canada.*

Recent research suggests that adding water to a TMR containing wet forage sources can limit DMI. The objective of this study was to determine if DMI can be limited in late lactation cows through water addition to a TMR formulated for high production. Twelve lactating Holstein cows (214.8 ± 28.5 DIM) were exposed to 2 diets in a cross-over design with 28-d periods. Diets had the same ingredient composition (30.9% corn silage, 30.3% alfalfa haylage, 21.2% high-moisture corn, and 17.6% protein supplement; DM basis) and differed only in DM %, which was reduced by the addition of water. Treatment diets were: 1) DRY (61.7% DM) and 2) WET (51.9% DM). DMI and milk production (4% fat corrected milk; FCM) were recorded for the last 14 d of each treatment period. For the final 4 d of each period fresh feed and orts were sampled for particle size analysis. The particle separator had 3 screens (19, 8, 1.18 mm) and a bottom pan, resulting in 4 fractions (long, medium, short, fine). Sorting was calculated as the actual intake of each particle fraction expressed as a % of its predicted intake. Sorting values > 100% indicate selection for, while values < 100% indicate sorting against. Data were analyzed using a general linear mixed model. All cows sorted against long ration particles (P < 0.05); there was no difference in the extent of this sorting between the DRY and WET treatments (72.9 vs. 77.6%; SE = 4.5; P = 0.5). Across the study, there was no sorting (P > 0.05) for or against medium (99.9%) or small (101.4%) ration particles. There tended to be more sorting for fine ration particles on the DRY treatment compared with the WET (106.3 vs. 104.0%; SE = 1.0; P = 0.1). The addition of water had no effect on production parameters, with similar DMI (27.9 vs. 26.5 kg/d; SE = 1.1; P = 0.4), 4% FCM (28.7 vs. 27.6 kg/d; SE = 0.9; P = 0.4) and efficiency of production (0.98 vs. 1.00 kg 4% FCM/kg DMI; SE = 0.04; P = 0.6) between the DRY and WET treatments. The results suggest that, despite a tendency to reduce the degree of feed sorting, addition of water to a TMR had no effect on nutrient consumption and production efficiency of late lactation dairy cows.

Key words: dry matter, late lactation, sorting

T324 Effect of parity and stage of lactation on feed sorting behavior of lactating dairy cows. T. J. DeVries*[1], L. Holtshausen[2], M. Oba[3], and K. A. Beauchemin[2], *[1]University of Guelph, Kemptville Campus, Kemptville, ON, Canada, [2]Agriculture and Agri-Food Canada, Lethbridge, AB, Canada, [3]University of Alberta, Edmonton, AB, Canada.*

The objectives of this study were to determine if feed sorting differs between primiparous (PP) and multiparous (MP) cows, if sorting changes from peak lactation to peak DMI, and whether this sorting affects efficiency of production. Data on DMI, milk production, feed sorting (particle size of offered and refused feed), and plasma NEFA concentration were collected on 30 PP and 30 MP lactating Holstein dairy cows during 3 weeks of lactation. Cows averaged 53, 81, and 109 ± 10 DIM at each recording week. The particle separator had 3 screens (19, 8, 1.18 mm) and a bottom pan, resulting in 4 fractions (long, medium, short, fine). Sorting was calculated as the actual intake of each particle fraction expressed as a % of its predicted intake. Sorting values >100% indicate selection for, while values <100% indicate sorting against. Data were averaged per cow per week and analyzed in a repeated measures mixed model. Over the study period MP cows consumed more DM (25.2 vs. 21.9 kg/d; SE = 0.7, P < 0.001) and produced more milk (42.2 vs. 35.0 kg/d; SE = 1.5, P < 0.001) than the PP cows, but had similar efficiency of production (1.65 kg milk/kg DMI). Across the study period DMI increased (P = 0.002), while milk yield decreased (P < 0.001), resulting in decreased efficiency of production (P < 0.001) as cows moved further into lactation. All cows had higher plasma NEFA concentrations at 53 DIM compared with at 81 and 109 DIM (128.6 vs. 77.8 μEq/L; SE = 12.0; P < 0.001), suggesting they were mobilizing more body fat at that earlier stage of lactation. Across weeks all cows sorted against the long ration particles and sorted for fine ration particles. The PP cows sorted more against the long ration particles (92.8 vs. 95.5%; SE = 1.5; P = 0.05) and for the fine ration particles (104.0 vs. 102.9%; SE = 0.5; P = 0.01) than MP cows across all 3 recording weeks. The PP cows also sorted for the short ration particles (101.0%), while the MP cows did not (100.2%). The results demonstrate that despite changes in DMI, production, and efficiency, feed sorting remained consistent in cows across DIM. Further, our results demonstrate that PP cows engage in more feed sorting than MP cows.

Key words: parity, stage of lactation, sorting

T325 Effects of different physical processing of corn starter on performance of newborn Holstein dairy calves. A. Soltani[1], G. R. Ghorbani*[1], B. Omidian[3], M. Khorvash[1], S. Zaree-Shamsabadi[1], H. Beiranvand[1], M. Kazemi-Bonchenari[2], and M. Mirzaee[1], *[1]Department of Animal Sciences, Isfahan University of Technology, Isfahan, Iran, [2]Department of Animal Sciences, Arak University, Arak, Iran, [3]Department of Animal Sciences, Shahrekord University, Shahrekord, Iran.*

The objective of present study was to compare the effects of different corn processing of starter in neonatal dairy calves on feed intake, average daily gain (ADG), feed efficiency, rumen pH, and weaning weight. For this purpose, 20 Holstein dairy calves (10 male and 10 female) were used in a completely randomized block design. Calves were randomly allocated to 2 different treatments consisting of either steam flaked or finely ground corn. Starters were formulated to contain similar ingredients and nutrient compositions. The calves were housed

individually from d 3 after birth until 60 d old and the weaning also was done on 60 d old. Starter consumption was measured daily for each calf. Calves were weighed immediately after birth and also the weights were recorded weekly until 8 weeks. No significant differences were observed between calves received starter containing steam flaked versus finely ground corn for daily starter intake ($P = 0.28$). Calves fed steam flaked corn had significantly higher ADG compared with the calves fed grinded corn (0.89 vs. 0.68, $P < 0.01$). Consequently, feed efficiency was greater in calves consumed steam flaked versus grinded corn (0.73 vs. 0.56, $P < 0.01$). The reason probably is related to, lower rumen passage rate and higher digestibility of starch with steam flaked corn than grinded corn. As a result of higher feed efficiency and ADG, weaning weight tended to be higher for steam flaked corn compared with grinded corn ($P = 0.06$). Comparing the rumen pH on d 56 of experiment showed that no difference was observed between treatments ($P = 0.43$). In general, results of this study indicate that feeding steam flaked corn improve performance of newborn dairy calves in comparison to finely ground corn.

Key words: dairy calves, corn processing, starter

T326 Comparison of dairy cattle performance in Nebraska when fed silage and grain produced from second-generation insect protected (*B.t.*) corn (MON 89034), parental line, or reference corn grown during 2009. H. A. Paz*[1], E. Castillo-Lopez[1], K. Clark[1], T. H. Klusmeyer[2], G. F. Hartnell[2], and P. J. Kononoff[1], *[1]University of Nebraska-Lincoln, Lincoln, [2]Monsanto Company, St. Louis, MO.*

Sixteen Holstein cows were used to evaluate the effects on intake and performance of feeding grain and silage from a genetically modified corn (MON 89034), a parental control or 2 reference hybrids of non-genetically modified corn. Cows were randomly assigned to one of 4 4 × 4 Latin squares and periods lasted 28 d. Dietary treatments were 1) control hybrid DKC63–78 (Control), 2) second-generation insect protected corn MON 89034 (*B.t.*), 3) reference corn hybrid DKC61–42 (Ref 1), and 4) reference corn hybrid DKC62–30 (Ref 2). Diets had similar ingredient composition except for the source of corn silage and corn grain. Intake of DM was highest ($P = 0.01$) for cows consuming the *B.t.* corn diet (26.6 ± 0.59 kg/d) compared with those consuming other corn hybrids diets (25.4, 25.0, 25.6 ± 0.59 kg/d for the Control, Ref 1, and Ref 2 diets, respectively). Additionally, cows consuming the *B.t.* diet tended ($P = 0.09$) to produce more milk (38.2, 36.4, 36.5, and 36.1 ± 0.98 kg/d for *B.t.*, Control, Ref 1, and Ref 2). Milk percentage and yield of protein (3.01 ± 0.05% and 1.11 ± 0.03 kg/d) and fat (3.3 ± 0.10% and 1.22 ± 0.05 kg/d), 3.5% fat corrected milk (FCM; 35.7 ± 1.07 kg/d), FCM/DMI (1.39 ± 0.03 kg/kg), and milk urea N (14.01 ± 0.49 mg/dl) were not different ($P > 0.10$) across diets. Results from this experiment demonstrated that MON 89034 was as nutritious as conventional, non-transgenic corn grain and corn silage when fed to dairy cows.

Key words: corn silage, genetically modified corn, dairy cow

T327 Morphology of the omasum of dairy cows fed of high or low grain content diet before parturition. D. de O. R. B. Santoro, J. C. de Resende Júnior*, T. da S. Teófilo, R. F. de Lima, J. L. P. Daniel, M. B. Moreira, P. P. Bueno, T. A. Dell Vale, G. P. Lenzi, T. M. França, and S. de F. Costa, *Universidade Federal de Lavras, Lavras, Minas Gerais, Brazil.*

The high-energy diet before parturition is able to induce the proliferation of ruminal epithelium. However, nothing is known about the morphological response of the omasum of dairy cows that consume high-energy diet pre-partum. The aim of this study was to investigate whether the transition diet, with high grain content, is able to induce changes in omasum morphology. Four Holstein cows with cannula in the dorsal sac of the rumen, were allocated to 2 treatments in 2 blocks of 2 cows, defined by the date of the expected parturition. Six weeks before the expected calving, cows were fed a standardization diet and 4 weeks before delivery were subjected to diets with high (HGC) or low (LGC) grain content. After delivery, all cows were fed a high energy lactation diet. Fragments of the omasum and the rumen were collected by biopsy on days –42, –28, –14, –7, 2, 14, 28, 42 and 56 in relation to parturition. Data were submitted to variance analyze considering in the model the effect of the block; treatment; day related to calving; and interactions. The animals that received HGC had higher DMI ($P < 0.01$), greater ($P < 0.01$) intake of CP, NDF, fat and minerals and higher milk production ($P = 0.04$), milk fat ($P = 0.07$) and protein ($P < 0.01$). The mitotic index (MI) of the omasum epithelium tended ($P = 0.11$) to be higher in HGC and was higher ($P < 0.001$) than the MI in the rumen, but it was highly ($R^2 = 0.80$; $P = 0.01$) correlated. The papillae of the omasum in cows that received HGC had greater height and larger area, between one week before and 2 weeks after delivery, a fact demonstrated by the tendency of interaction between treatment and collection day ($P < 0.09$). Cows that received HGC had lower thickness of the keratin layer ($P < 0.01$) and not keratinized layers ($P = 0.03$) of the omasum epithelium, showing that the LGC diet stimulates thick epithelium. We conclude that the mucosa of the omasum of dairy cows responds positively to the diet high in grains before parturition, a fact demonstrated by the higher height and larger area of the papillae and by the higher epithelium MI.

Key words: acidosis, histology, transition diet

T328 Enteric methane production from dairy cows fed different silages with and without rapeseed supplementation. M. Johannes*, A. L. F. Hellwing, P. Lund, M. R. Weisbjerg, and T. Hvelplund, *Faculty of Agricultural Sciences, Aarhus University, Denmark.*

Enteric methane (CH_4) production is closely related to feed composition, mainly NDF, fat and starch content. The aim of the experiment was to study the methanogenic potential of common Danish silages, the effect of fat supplementation as well as the interaction. The study was conducted with six ruminally and intestinally cannulated lactating Holstein-Frisian dairy cows receiving six diets over four periods of 28 days according to an incomplete 6x4 Latin square design. The cows were 271 days in milk (sd 67) and had an ECM yield of 24.0 kg/d (sd 6.2). During the third week, samples were taken in order to determine digestibility. Methane production was measured in four open-circuit respiration chambers during the fourth week. The diets were based on early first cut grass silage (EG, harvested May 26th, 329g NDF/kg DM), late first cut grass silage (LG, harvested June 15th, 484g NDF/kg DM) or maize silage (M, 390g NDF/kg DM) supplemented with low fat concentrate (LF) or concentrate with whole crushed rapeseed (high fat, HF). Other concentrate ingredients were wheat and rapeseed meal. Content of fat-free rapeseed was equal for all diets. Fatty acid content was 20 g/kg DM in the LF diets and 50 in the HF diets. All diets were fed as total mixed ration with 64% forage. Absence of interaction between silage and fat supplementation was consistent for all parameters ($P > 0.7$). Later maturity (LG) reduced dry matter intake (DMI) by 1.05 kg DM compared to EG ($P = 0.02$). There was no significant difference in DMI between EG and M ($P = 0.28$). Fat supplementation tended to reduce DMI by 0.58 kg ($P = 0.09$). Silage had a significant effect ($P < 0.001$) on CH_4 production per kg DMI with most CH_4 on

LG (31.4 L/kg), 28.4 L/kg for EG and 26.0 L/kg for M. Fat supplementation reduced CH_4 by 1.6 L per kg DMI ($P = 0.05$). Energy loss for the different silages were 6.1, 6.8 and 5.6% of gross energy for EG, LG and M, respectively ($P < 0.001$). Fat supplementation reduced energy loss by 9% ($P = 0.004$). The results confirm that highly digestible forage and fat supplementation can reduce enteric CH_4 production, and that effects were additive.

Key words: methane, forage, fat supplementation

T329 Particle size and endosperm type of dry ground corn alter apparent ruminal synthesis of B-vitamins in lactating dairy cows. M. Seck*[1,3], 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 dry ground corn varying in particle size and endosperm type on apparent ruminal synthesis (AS) of thiamin (B1), riboflavin (B2), niacin (B3) and vitamin B6 (B6) were evaluated using 8 ruminally and duodenally cannulated dairy cows. The experiment was a duplicated 4 × 4 Latin square design with a 2 × 2 factorial arrangement of treatments. Main effects were corn grain vitreousness (floury or vitreous) and particle size (medium or fine). Endosperm was 25% vitreous for floury treatment and 66% vitreous for vitreous treatment. The fraction of grain passing through a 1.18 mm sieve was 43% for medium, vitreous, 42% for medium, floury, 57% for fine, vitreous and 62% for fine, floury. Diets included alfalfa silage, corn treatments, protein supplement, minerals, vitamins, and contained 29.2% starch, 27.2% NDF and 18.3% crude protein. Corn grain treatments supplied 86.2% of the dietary starch. Grinding and endosperm type had no effects on daily intakes of B-vitamins except for B2 where fine grinding decreased daily intake (175 vs. 181 ± 8.6 mg/d, $P = 0.04$). Reducing particle size increased duodenal flow (DF) of B2 (391 vs. 327 ± 26.6 mg/d, $P < 0.01$), B3 (3513 vs. 2939 ± 317.0 mg/d, $P = 0.01$) and tended to increase DF of B1 (50.7 vs. 40.4 ± 3.7 mg/d, $P = 0.07$). Floury treatment increased DF of B3 (3453 vs. 3000 ± 317.0 mg/d, $P = 0.04$). Fine grinding increased AS of B2 (215 vs. 146 ± 23.8 mg/d, $P < 0.01$), B3 (2671 vs. 2083 ± 289.5 mg/d, $P < 0.01$) and B1 (8.4 vs. −1.4 ± 2.7 mg/d, $P = 0.05$) while floury endosperm increased AS of B3 (2602 vs. 2152 ± 289.5 mg/d, $P = 0.03$). DF and AS of B6 were not affected by treatments ($P > 0.13$). B1 AS was correlated negatively with true ruminal digestibility of organic matter expressed as percentage of intake ($P < 0.01$, r = −0.48) or as kg/d ($P = 0.02$, r = −0.40). Duodenal flow of microbial nitrogen was correlated positively with AS of B2 ($P < 0.01$, r = +0.52), B3 ($P < 0.0001$, r = +071) and B6 ($P = 0.02$, r = +0.41). B-vitamin supply to dairy cows is affected by dry corn particle size and to a lesser extent, by endosperm type.

Key words: dairy cow, B-vitamin, corn grain

T330 Abrupt changes in forage dry matter of one to three days affect intake and milk yield in late lactation dairy cows. J. Boyd*[1] and D. R. Mertens[2], *[1]US Dairy Forage Research Center, Madison, WI, [2]Mertens Innovation & Research LLC, Belleville, WI.*

Our objective was to determine if late lactation cows were susceptible to 1, 2, and 3d changes in forage DM. Forty-four Holstein cows (22 primiparous and 22 multiparous), averaging 155 DIM, 42.5 kg/d of milk, and 597 kg body weight, were used in a study conducted from Jan to Mar 2010. Within each parity, cows were assigned to 1 of 11 blocks based on production and DIM 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 of 1, 2, or 3 d treatments. Each period consisted of a 3-d pre-treatment, 1 to 3d treatment, and a 3-d 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 mimic 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 constant 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. Alfalfa silage samples dried at 55C for 48h obtained 2%-units higher DM than predicted by NIR. Thus, water addition was underestimated, resulting in a 3%-unit change in forage DM instead of the target 8%-unit change that was planned. Data was analyzed using Proc MIXED of SAS with cow within parity-block as a random variable. On d1, DMI was reduced 1.22 ($P < 0.0001$), 0.67 ($P = 0.04$), and 2.06 kg ($P = 0.0001$), for the 1, 2, and 3d treatments, respectively. The amount of feed offered was adjusted based on refusal level, and DMI recovered during the following 1 to 3 d even during Trt phases. Milk yield and components were not affected by treatment ($P > 0.37$). We conclude that abrupt changes in forage DM reduce daily feed intakes, but a change >3%-units in forage DM is necessary to affect milk yields and components for late lactation cows.

Key words: DM changes, silage, feeding

T331 Effects of adding fibrolytic enzymes to diets containing bermudagrass silage harvested at two maturity stages on the performance of lactating Holstein cattle. O. C. M. Queiroz*[1], A. T. Adesogan[1], J. L. P. Daniel[2], J. J. Romero[1], J. H. Shin[1], C. R. Staples[1], and J. E. P. Santos[1], *[1]University of Florida, Gainesville, [2]University of Sao Paulo, Piracicaba, Sao Paulo, Brazil.*

The objective was to examine effects of adding fibrolytic enzymes to diets containing bermudagrass ensiled after 4 or 8 weeks (4-wk or 8-wk) of regrowth on the performance of Holstein cows. Fifty-eight lactating cows (22 ± 4 DIM) were assigned to treatments arranged in a 2 by 2 factorial design. Treatments were diets containing 4- or 8-wk bermudagrass silage without (4-C and 8-C) or with exogenous enzymes (4-E and 8-E). The cellulase-xylanase enzyme was applied at 2.5 g/kg of TMR DM during ration mixing immediately before feeding. Milk production and DMI of individual cows were recorded daily. Milk and feed ingredients were sampled weekly and chemically characterized. The statistical model included treatment, time, parity, and all interactions of these terms. No enzyme by maturity interaction was detected. Dietary treatment did not affect milk yield (lsmean = 38.4 kg/d, SEM = 1.00) or FCM:DMI ratio (lsmean = 2.09 kg, SEM = 0.08). Feeding the 4-wk diet instead of the 8-wk diet tended ($P < 0.07$) to increase DMI (22.6 vs. 21.4 kg/d; SEM = 0.7) and milk fat yield (1.83 vs. 1.71 kg/d, SEM = 0.06). Applying the enzyme increased ($P = 0.02$) lactose concentration (4.84 vs. 4.73%; SEM = 0.04), but did not affect milk protein or fat concentrations (2.70 vs. 2.65%; $P = 0.21$ and 4.41 vs. 4.49; $P = 0.44$, respectively) or milk protein yield ($P = 0.27$). Feeding the enzyme did not improve the performance of the cows.

Key words: fibrolytic enzymes, cellulase, xylanase

T332 Effects of *Bacillus subtilis natto* on intestinal morphology in pre and postweaning dairy calves. Y. Sun, J. Q. Wang*, P. Sun, D. P. Bu, G. C. Luan, and H. T. Zhang, *Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China.*

This study investigated the effects of *Bacillus subtilis natto* on duodenal and jejunal morphology in pre and postweaning calves. Twenty 4 China Holstein calves were divided randomly into 3 groups: control group, fed milk and starter or basal diet only; 2 experimental groups, added *Bacillus subtilis natto* N1 and Na strains cultures respectively at a dose of 1×10^{10} cfu daily. Four calves selected randomly from each group were slaughtered and sampled at weaning, and the remaining calves were slaughtered 44 d after weaning. Results showed that *Bacillus subtilis natto* reduced calves diarrhea incidence. Supplementation of *Bacillus subtilis natto* N1 and Na strains in weaning calves increased villus height and villus height/crypt depth (V/C) in duodenum and jejunum ($P < 0.05$), elevated muscle layer thickness in duodenum and anterior jejunum ($P < 0.05$), but decreased crypt depth in duodenum, anterior jejunum and posterior jejunum ($P < 0.05$). Villus height, V/C and muscle layer thickness in duodenum and jejunum of postweaning calves fed N1 and Na strains were higher ($P < 0.05$) while the crypt depth was lower than control ($P < 0.05$). In conclusion, *Bacillus subtilis natto* may have the potential to prevent diarrhea and improve duodenal and jejunal morphology in dairy calves.

Key words: *Bacillus subtilis natto*, dairy calves, intestinal morphology

T333 Effect of dietary delivery product Force 6 on performances and antioxidant status of high-producing dairy cows. D. Éclache, P. Etienne, and V. Noirot*, *Phodé Laboratories, Terssac, France.*

High producing dairy cows are at risk of oxidative stress. Force 6 (Phodé Laboratories, France), a product containing curcumin and formulated to ensure product delivery and absorption in the gut, has been tested during 6 weeks on 2 groups of 17 Holstein dairy cows, matched in pairs according to the following criteria: parity, milking stage (DIM), dairy production (DP), milk solids content, live body weight and body condition score (BCS). The aim of this trial was to evaluate the effects of the product on dairy production parameters, as well as on the animal antioxidant status. At the beginning of the trial, the average DIM was 97 d and DP was 44.1 kg. The control group was fed non supplemented basal diet (corn silage based; 17% crude protein, 1530 kcal/kg), the treated group received the same basal diet supplemented with 2 g/animal/day of the tested product. Daily individual DP, weekly and daily milk solids contents and somatic cells counts (SCC), as well as body weight gain and BCS were measured. Blood samples were taken on the first day of the trial and then every fortnight, to assess plasma hydroperoxides content, an indicator of free radicals production (d-ROM kit, Dacron, expressed in U.CARR. - Carratelli units). Statistical analysis were performed using a linear model with treatment (n = 2), matched pairs (n = 1 to 17), week (n = 1 to 6) and the interactions matched pair × week and treatment × week as factors. Dairy production parameters measured 2 weeks before the trial and d-ROM values measured on the first day of the trial were used as covariates. Milk solids contents, ADWG and BCS were not significantly different. The treatment, however, improved DP (44.9 kg/day vs. 43.8 kg/day for the control group, $P < 0.05$), and decreased SSC (166,000 vs. 257,000 somatic cells/ml for the control group, $P < 0.05$). Plasma hydroperoxides contents were significantly lower for the treated cows (137.4 U. CARR. vs. 162.6 U. CARR. for the control $P < 0.05$). The increased dairy production and reduction of SCC for high producing dairy cows could be linked to their improved antioxidant status.

Key words: antioxidant status, dairy cow, milk yield

T334 Effects of abomasal infusion of linolenic acid on milk fat synthesis and composition in dairy cows. U. Moallem*[1], D. Vyas[2], B. B. Teter[2], P. Delmonte[3], and R. A. Erdman[2], *[1]Agriculture Research Organization, Bet Dagan, Israel, [2]University of Maryland, College Park, [3]FDA.*

In a recent study, feeding high rates of extruded flaxseed to dairy cows increased the milk C18:3n-3 by up to 2 percentage units (% of FA). However, enrichment of C18:3n-3 in milk fat was negatively correlated with milk fat percentage and yield, and C16:0 yields. We hypothesized that C18:3n-3 suppresses de novo synthesis of C16:0. Therefore, our objectives were to assess the transfer efficiency of abomasally infused C18:3n-3 into milk fat and the interaction with milk fat content and yield, and the proportion of C16:0 in milk fat. Three rumen fistulated multiparous mid-lactation Holstein cows were used in a 3x3 Latin square design, with 14 d experimental periods. Cows were milked twice daily and with treatments applied during last 7 d. Treatments consisted of twice daily (0600 and 1900h) abomasal infusion of: 1) Control - 110 mL water; 2) LFO - 110 mL/d flaxseed oil; and 3) HFO - 220 mL/d flaxseed oil, which provided 52 and 104 g/d C18:3n-3, respectively. Blood samples were collected twice weekly and milk samples were collected during the last 6 consecutive milkings of each period. No differences were observed in DMI, milk, and milk solids yields. However, milk fat and lactose percentages tended to be higher ($P < 0.1$; $P < 0.07$, respectively) in LFO and HFO treatments than in the control. Plasma C18:3n-3 was 2.9 and 4.0 times higher in the LFO and HFO treatments. The C18:3n-3 in milk fat was 9 and 15 higher in the LFO and HFO treatments, (1.89 and 3.30 vs. 0.21 in the control), whereas the C18:3n-3 yields were 8.5 and 16.3 times greater than in the control (26.4 and 50.6 vs 3.1 g/d; $P < 0.01$). The percentage of C16:0 decreased by 10% and 17% in the LFO and HFO compared with the control. There were no differences in C16:0 yields. The transfer efficiency of abomasally infused C18:3n-3 into milk fat averaged 45% for both groups. In summary, abomasal infusion of C18:3n-3 dramatically increased the C18:3n-3 concentration in plasma and milk fat with no effect on milk fat percentage. However, C16:0 percentage in milk fat was decreased in both flaxseed treatments which may indicate on inverse relationship of C16:0 and C18:3n-3 in milk fat.

Key words: flaxseed, milk fat, dairy cows

T335 The time of access to temperate pasture influences rumen pH and NH_3-N concentration in heifers. A. Félix[1], N. Hernández[1], N. Figueredo[2], M. Génova[2], M. Ibarra[2], A. Mendoza[1], M. Aguerre[1], A. Pérez-Ruchel[2], J. L. Repetto[1], and C. Cajarville*[2], *[1]Departamento de Bovinos, Facultad de Veterinaria, UdelaR, Montevideo, Uruguay, [2]Departamento de Nutrición Animal, Facultad de Veterinaria, UdelaR, Montevideo, Uruguay.*

Twenty-four Hereford × Angus heifers (BW = 153 ± 18 kg) were used in a randomized complete block design to determine the effect of time access to pasture (*Lolium multiflorum*, *Trifolium repens*; 19.1% CP, 48.2% NDF DM basis) on rumen pH and NH_3-N concentration. Pasture was daily cut and offered ad libitum as sole feed for 4, 6, 8 or 24 h. After 15 d of adaptation, individual rumen fluid samples were collected through a ruminal cannula, every hour for 24 h (h0 = 0800) and pH and NH_3-N concentration were determined. Results were

analyzed as repeated measures with a mixed linear model. pH was affected by treatment ($P = 0.048$), hour ($P < 0.001$) and treatment x hour ($P < 0.001$). Mean pH values were 6.70, 6.64, 6.47, and 6.30 (SEM = 0.10) for treatments 4, 6, 8 and 24h respectively. The main difference observed was that restricted groups led to higher pH values during fasting periods (20 to 0 h), suggesting lower concentrations of volatile fatty acids or higher buffer availability in relation to OM in the rumen. While pH in treatment 24h reached a minimum of 5.83 at hour 10, in restricted-fed reached minimum values of 5.77, 5.62 and 5.78 between hour 5 and 6 for treatments 4, 6 and 8h respectively (SEM = 0.08), and then increased linearly after hour 13. Minimum pH values did not differ among treatments. NH_3-N concentrations were affected by treatment ($P < 0.055$), hour ($P < 0.001$) and treatment x hour ($P < 0.001$). Mean NH_3-N concentrations were 26.8, 26.5, 28.8 and 30.7 mg/dL (SEM = 1.1) for treatment 4, 6, 8 and 24h respectively. NH_3-N concentrations increased after hour 0 and reached peak values between hour 6 and 7 of 66.0, 56.3 and 58.3 mg/dL (SEM = 2.8) for treatments 4, 6 and 8h respectively and then decreased linearly until hour 14, while in treatment 24h no variations were observed. Minimum NH_3-N concentrations differed among restricted treatments and treatment 24h ($P < 0.001$), being 7.6, 7.9, 9.8 and 19.0 mg/dL for 4, 6, 8 and 24h respectively (SEM = 1.2). Restricting the time of access to pasture significantly influenced dynamics of rumen pH and NH_3-N concentrations, while unrestricted animals had a more stable ruminal environment.

Key words: feed restriction, rumen pH, rumen NH_3-N

T336 The time of access to temperate pasture influences intake and feeding behavior in heifers. A. Félix[1], N. Hernández[1], N. Tortorelo[1], S. Roja[1], M. Aguerre[1], A. Pérez-Ruchel[2], J. L. Repetto[1], and C. Cajarville*[2], *[1]Departamento de Bovinos, Facultad de Veterinaria, UdelaR, Montevideo, Uruguay, [2]Departamento de Nutrición Animal, Facultad de Veterinaria, UdelaR, Montevideo, Uruguay.*

Twenty-four Hereford × Angus heifers (BW = 153 ± 18 kg) were used in a randomized complete block design to determine the effect of number of hours with access to pasture (*Lolium multiflorum*, *Trifolium repens*; 19.1% CP, 48.2% NDF DM basis) on DM intake (DMI), feeding behavior and DMI rate. Pasture was daily cut and offered ad libitum as sole feed for 4, 6, 8 or 24 h from 0800 h (h0). Daily DMI was measured for 10d and DMI rate was registered by weighting the amount of pasture offered and refused every hour for 4 h. Feeding behavior (eating, ruminating, drinking, and others) were recorded every 5 min for 4 h by visual observation. Feeding behavior and DMI rate (analyzed as repeated measures) and DMI were analyzed with a mixed linear model. Mean DMI was 2.03, 2.69, 2.87 and 3.49 kg/day (SEM = 0.19) for treatments 4, 6, 8 and 24h respectively, representing 1.30, 1.78, 1.91 and 2.26% of BW (SEM = 0.12). DMI was lower in the more restricted animals (4 and 6h) than in 24h ($P < 0.001$), but no differences were detected between treatments 6 and 8h, or 8 and 24h. Mean DMI rates were 0.51, 0.54, 0.52 and 0.37 kg/h (SEM = 0.04) for treatments 4, 6, 8 and 24h. During the first hour restricted animals ate more DM than those non restricted (0.90 vs. 0.63 ± 0.05, $P \leq 0.012$), but no differences between treatments were detected from hours 2 to 4. No treatment x hour interaction was detected for behavior activities. Restricted heifers (4 and 6h) had a greater proportion of time eating than non restricted ones ($P = 0.024$), but no differences were observed between restricted groups. Mean proportions for eating were 0.73, 0.76, 0.66 and 0.54 (SEM = 0.05) for treatments 4, 6, 8 and 24h respectively. Eating and ruminating activities were affected by time ($P < 0.001$ and $P = 0.014$, respectively). The proportion of animals eating decreased (0.93 vs. 0.46 ± 0.05, $P < 0.001$) and ruminating increased (0 vs. 0.08 ± 0.02, $P = 0.017$) from hour 1 to 4. DMI rate was affected by treatment ($P = 0.001$), hour ($P < 0.001$) and treatment x hour ($P < 0.095$). It is concluded that time of access to pasture lower than 8 h led to changes in feeding behavior that were not enough to compensate the DMI drop.

Key words: feeding behavior, intake, intake rate

T337 Effect of replacement of conventional corn silage with brown midrib corn silage on behavior and performance of lactating dairy cows. K. W. Cotanch*, H. M. Dann, C. Whitehouse, C. S. Ballard, and R. J. Grant, *William H. Miner Agricultural Research Institute, Chazy, NY.*

Feeding forages with high NDF digestibility to high-producing cows has the potential to increase feed intake and milk yield. However, highly digestible forage-based diets may negatively affect feeding behavior and ruminal fermentation. Fourteen multiparous Holstein cows (6 ruminally fistulated) averaging 196 d in milk were used in a crossover design study with 2-wk periods (10-d adaptation, 4-d collection) to determine the effect of NDF digestibility of corn silage on chewing behavior, ruminal fermentation, total tract digestibility, and lactational performance. Dietary treatments consisted of 1:1 replacement (DM basis) of conventional corn silage (CONV) with brown midrib corn silage (BMR). The total mixed ration (TMR) contained 43% corn silage, 15% grass silage, and 42% corn-soybean based grain mix (DM basis). The NDF content was 37.7 and 42.0%, the physically effective NDF (peNDF) was 35.8 and 39.6%, and 24-h NDF digestibility was 42.3 and 57.0% NDF for the conventional and brown midrib corn silages, respectively. Data were analyzed as a crossover design using the MIXED procedure of SAS. Cows had higher DMI but lower feed efficiency when fed the BMR diet. Diet did not affect milk yield, milk composition, time spent eating, or time spent ruminating. However, cows chewed less per unit of NDF and had a lower mean pH over a 24-h period when fed the BMR diet. Highly digestible forage does not stimulate chewing to the extent that would be predicted based on standard laboratory methods, such as peNDF. Measurement of peNDF may need to be adjusted based on forage NDF digestibility since chewing response is a function of forage particle size and NDF digestibility.

Table 1.

Item	CONV	BMR	SE	*P*-value
peNDF, % of TMR	17.5	18.3	-	-
DMI, kg/d	25.2	27.8	0.7	<0.01
Milk, kg/d	40.6	42.2	3.3	0.26
Milk fat, %	3.62	3.71	0.14	0.30
Milk true protein, %	3.12	3.15	0.10	0.46
Milk/DMI	1.60	1.50	0.10	0.03
Eating, min/d	228	222	10	0.38
Ruminating, min/d	516	498	17	0.12
Eating, min/kg NDF	31	26	1	<0.01
Ruminating, min/kg NDF	70	58	3	<0.01
Ruminal pH	6.08	5.95	0.05	<0.01
Total tract NDF digestibility, %	56.2	61.6	1.3	<0.01

Key words: dairy cow, corn silage, fiber digestibility

T338 Evaluation of protein supplementation strategies for low-starch diets fed to lactating dairy cows. K. W. Cotanch*[1], S. E. Boucher[1], H. M. Dann[1], C. S. Ballard[1], R. J. Grant[1], and K. Fujita[2], *[1]William H. Miner Agricultural Research Institute, Chazy, NY, [2]ZenNoh National Federation of Agricultural Cooperative Associations, Tokyo, Japan.*

The objective of this study was to evaluate the effect of varying concentrations of rumen undegraded protein (RUP) and primary source of RUP [distillers dried grains with solubles (DDGS) or SoyPass (SP)] on ruminal and lactational responses of lactating Holstein dairy cows fed low-starch diets. Sixteen multiparous cows (4 ruminally fistulated) averaging 121 d in milk were fed one of 4 diets in a replicated 4 × 4 Latin square design with 3-wk periods (14 d adaptation and 7 d collection). Diets contained (% of DM) 20% starch, 21% physically effective neutral detergent fiber, and 35.6% RUP (% of crude protein; CP), 38.5% RUP with DDGS, 38.8% RUP with SP, or 41.9% RUP. The diets contained 16.9, 15.4, 17.0, or 16.5% CP with a metabolizable protein balance (g/d) calculated using CNCPS version 6.1 of −60.3, −217, 17.1, and 87.6 for the 35.6% RUP, 38.5% RUP with DDGS, 38.8% RUP with SP, and 41.9% RUP diets, respectively. The data were analyzed as a replicated Latin square design using Proc Mixed (SAS version 9.1) with model effects for diet, period, and replicate. Diet had no effect ($P > 0.05$) on dry matter intake (DMI; 28.2 ± 0.4 kg/d), body weight (732 ± 14 kg), or solids-corrected milk production (43.7 ± 1.2 kg/d). However, milk urea N was least ($P < 0.01$) for cows fed the 38.5% RUP with DDGS diet compared with the 34% RUP, 38.8% RUP with SP, and 41.9% RUP diets (8.8, 12.3, 12.2, and 11.6, SEM = 0.33), whereas milk true protein/CP intake was greatest ($P < 0.01$; 0.33, 0.30, 0.29, 0.30, SEM = 0.01) for the 38.8% RUP with DDGS diet. Ruminal pH (6.05 ± 0.09), total volatile fatty acid concentration (131 ± 2.25 mM), and microbial N (614 ± 19 g/d) were unaffected by diet ($P > 0.05$). The acetate to propionate ratio was depressed for the 38.5% RUP with DDGS diet compared with the 34% RUP, 38.8% RUP with SP, and 41.9% RUP diets (2.57, 2.69, 2.67, 2.78, SEM = 0.04). Efficiency of N use was improved for cows fed DDGS as the primary source of RUP in these low-starch diets, although DMI and solids-corrected milk yield were unaffected by diet.

Key words: rumen undegraded protein, low-starch diets, dairy cattle

T339 Effect of time of access to food on fermentation capacity of rumen fluid in heifers consuming temperate pastures. N. Hernández[1], A. Félix[1], K. Saavedra[1], K. Rosano[1], A. Pérez-Ruchel[2], M. Aguerre[1], S. Brambillasca[2], C. Cajarville[2], and J. L. Repetto*[1], *[1]Departamento de Bovinos, Facultad de Veterinaria, UdelaR, Montevideo, Uruguay, [2]Departamento de Nutrición Animal, Facultad de Veterinaria, UdelaR, Montevideo, Uruguay.*

The objective of this study was to evaluate if the time of access to forage affects the fermentation capacity of rumen fluid in heifers consuming temperate pastures, using the gas production technique. Twenty 4 cannulated heifers (153.1 ± 18.1 kg BW) in a randomized complete block design were housed in individual cages and assigned to one of 4 treatments according to the time of access to fresh forage: 4, 6 and 8h/d (restricted groups), or 24h/d (unrestricted group). Animals within each treatment had forage available (*Trifolium repens - Lolium multiflorum* mix) as sole feed. After 15 d of adaptation, ruminal fluid was taken from each animal 1h after the beginning of the meal and placed at 39°C in flasks with 0.5g of the pasture consumed by the heifers. Gas pressure was measured at 2, 4, 6, 8, 10, 12, 18, 24, 48, 72 and 96h. Cumulative gas production was analyzed by PROC MIXED as repeated measures. Means between treatments were compared by Tukey test for each hour. There were differences between treatments ($P < 0.001$) and hours ($P < 0.001$) without significant interaction treatment x hour ($P > 0.10$). Animals fed all day produced more gas than animals fed 4h until hour 18 ($P \leq 0.04$), for example at hour 12 volumes of gas were 153.84 vs. 188.22 mL/gDM incubated for treatments 4h and 24h respectively ($P < 0.007$). No differences were observed between 6h and 8h treatments ($P > 0.10$). We concluded that unrestricted animals had higher fermentation capacity and suggests that the time of access to food affects the activity of microbial populations. Acknowledgements: ANII for scholarship of the first author.

Key words: in vitro gas production, time access, heifers

T340 Frequency of feed delivery affects feeding behavior of limit-fed dairy heifers. A. M. Greter[1], T. F. Duffield[2], B. W. McBride[3], T. M. Widowski[3], and T. J. DeVries*[1], *[1]Dept. Animal and Poultry Science, University of Guelph, Kemptville Campus, Kemptville, ON, Canada, [2]Dept. Population Medicine, Ontario Veterinary College, University of Guelph, Guelph, ON, Canada, [3]Dept. Animal and Poultry Science, University of Guelph, Guelph, ON, Canada.*

Limit feeding may improve feed efficiency while reducing feed costs and nutrient excretion, but also poses health and welfare concerns. The objective of this study was to determine the effect of feeding frequency on the feeding and competitive behavior of limit-fed growing dairy heifers. Twenty-four Holstein dairy heifers (178.2 ± 9.3 d old) were divided into 6 groups of 4 and exposed to each of 3 treatments using a replicated 3 × 3 Latin square design with 28-d periods. The treatments were providing a high-concentrate ration (containing 16.9% corn silage, 22.1% haylage, 44.1% high moisture corn, and 16.9% protein supplement, DM basis) in a limited amount (1.93% of BW): 1) 1x/d (0800 h), 2) 2x/d (0800 and 1600 h), and 3) 4x/d (0800, 1200, 1600, and 2000 h). The rations were formulated to meet the nutrient requirements of a dairy heifer growing at 0.8 kg/d. There was sufficient bunk space (0.34 m/heifer) for all heifers to feed simultaneously. Feeding behavior was recorded for the last 14 d of each period. Competitive behavior was recorded on d 23, 25, and 27 of each period. Lying time was recorded for the last 7 d of each period. DMI was recorded daily and ADG was recorded weekly. Data were analyzed in a general linear mixed model. DMI was similar between treatments (4.9 kg/d; $P = 0.5$). Daily feeding time was greatest when heifers were fed 1x/d (61.5 min/d, SE = 0.9; $P = 0.01$), followed by when fed 4x/d (51.8 min/d) and then when fed 2x/d (44.5 min/d). When fed 1x/d heifers tended to displace each other more often (4.5 displacements/d, SE = 0.6; $P = 0.08$) than heifers on the 2x or 4x treatments (1.9 and 2.8 displacements/d, respectively). Interestingly, heifers on the 1x/d treatment experienced higher ADG than heifers on the 2x or 4x treatments (0.9 vs. 0.7 kg/d, SE = 0.04; $P < 0.005$). Lying time (802.5 min/d; $P = 0.4$) and the number of lying bouts (11.9 bouts/d; $P = 0.1$) were similar between treatments. These results suggest that although competition at the feed bunk may be greater, when given sufficient feeding space, it may be beneficial to feed limit-fed dairy heifers 1x/d as this treatment improved ADG and increased the amount of time spent feeding per day.

Key words: limit feeding, dairy heifer, feeding behavior

T341 Effect of feeding brown midrib corn silage and dried distillers grains with solubles on bacterial diversity in rumen fluid of dairy cows using bacterial tag-encoded FLX amplicon pyrose-

quencing. H. A. Ramirez Ramirez*[1], L. O. Tedeschi[2], T. R. Callaway[3], S. E. Dowd[4], K. Nestor[5], and P. J. Kononoff[1], *[1]University of Nebraska-Lincoln, [2]Texas A&M University, College Station, [3]Food and Feed Safety Research Unit, USDA-ARS, College Station, TX, [4]Medical Biofilm Research Institute and Research Testing Laboratory, Lubbock, TX, [5]Dow AgroSciences LLC.*

Four ruminally fistulated cows were used in a 4 × 4 Latin square with a 2 × 2 factorial arrangement of treatments to evaluate the bacterial diversity in rumen fluid (RF) of dairy cows fed dual purpose (DP) or brown midrib (bm3) corn silage, and the inclusion of dried distillers grains with solubles (DDGS). There were 4 28 d periods; in each period cows were assigned to one of 4 treatments: DP corn silage + 0% DDGS (CON); bm3 corn silage + 0% DDGS (BMR); DP corn silage + 30% DDGS (CONDG); or bm3 corn silage + 30% DDGS (BMRDG). On d 28 of each period RF samples were taken at 2 and 12 h post-feeding and were analyzed using 16s rDNA bacterial tag-encoded FLX amplicon pyrosequencing (bTEFAP). Two types of bacteria were of special interest and their populations were analyzed by grouping genera according to their known substrate affinity. *Butyrivibrio* sp, *Fibrobacter* sp, and *Ruminococcus* sp were grouped as cellulose digesters (CD); and *Butyrivibrio* sp and *Megasphaera* sp were grouped as bacteria involved in ruminal biohydrogenation of unsaturated fatty acids (BH). Population of CD was similar across treatments representing 8.4 ± 0.69% of the total DNA in the samples. When cows were fed bm3 corn silage, *Fibrobacter* sp tended ($P = 0.15$) to represent a larger proportion of the total bacterial DNA (1.8 vs 2.3 ± 0.28% for DP and bm3). There was a significant forage × DDGS interaction ($P = 0.05$) for *Ruminococcus* sp; DNA of these bacteria represented the largest proportion within the CD group at 5.26, 4.13, 3.34 and 5.03 ± 0.73% for CON, BMR, CONDG and CONBMR, respectively. The BH group was similar among treatments; on average it represented 2.0 ± 0.21% of the total DNA extracted. The ratio of Firmicutes:Bacteroidetes was reduced ($P < 0.01$) by DDGS; the ratio was 0.56 for 0%DDGS and 0.39 ± 0.03 for 30%DDGS. Feeding bm3 corn silage tended to increase the population of the fiber digesting bacteria *Fibrobacter* sp while feeding DDGS decreased the ratio of Firmicutes:Bacteroidetes as determined by the bTEFAP technique.

Key words: bm3, fiber digestion, rumen microbiology

T342 Optimization for isolating ruminal *trans*-11 18:1 hydrogenating bacteria from dairy cow in vitro. D. Jin, J. Wang*, S. Zhao, D. Li, D. Bu, and L. Zhou, *Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China.*

The biohydrogenation of ruminal bacteria has a significant effect on milk fatty acid profile, and *trans*-11 18:1 (TVA) is the major biohydrogenation intermediate. The process of biohydrogenation can be regulated by modulating the metabolism of hydrogenation related bacteria. So far, only partial ruminal hydrogenating bacteria was isolated because of harsh conditions for pure culture. This study was aimed to establish the optimal conditions for enrichment and isolation of ruminal TVA hydrogenating bacteria in vitro. TVA was added into anaerobic mediums with different final concentrations (0, 30, 40, 50, 60 μg/mL). Mixed ruminal microbes were inoculated into mediums for continuous cultivation, samples were collected every 4 h and used for detecting TVA concentration and OD value. In addition, TVA was added into the anaerobic medium to a final concentration of 50 μg/mL, then the cultures were transferred for 6 generations for enrichment. Changes of the bacterial composition during enrichment were analyzed by DGGE profiling. The results showed that concentration of TVA in mediums was significantly decreased at 4 h during continuous incubation and then maintained constancy at 12 h. After incubation for 12 h, degradation rates of TVA were higher than others while initial TVA concentrations were 50 μg/mL and 60 μg/mL, and the final TVA concentrations are 16.1878 μg/mL and 15.0357 μg/mL respectively. Besides, the OD value of the culture initiate increased and reached the highest at 12 h and then decreased. The amounts and types of suspected TVA hydrogenated strains increased most significantly in the 4th generation. Sequencing results for the DGGE bands showed that most of them belonged to *Lactobacillus gasseri* and uncultured bacteria. In conclusion, the suitable TVA adding amount for isolating culture of ruminal TVA hydrogenating bacteria is 50 μg/mL, and the optimal transfer time and transfer generation for enrichment culture are 12h and the 4th generation respectively.

Key words: DGGE, isolation, TVA hydrogenating bacteria

T343 Differential expression of the transcriptome in adipose tissue of first lactation dairy cattle. J. P. McNamara[1], J. M. Thomson*[2], and J. Loor[3], *[1]Washington State University, Pullman, [2]University of Alberta, Edmonton, Alberta, Canada, [3]University of Illinois, Urbana-Champaign.*

Adipose tissue metabolism is an essential factor in establishment of a successful lactation. To continue our investigations into the control of adipose tissue metabolism, we conducted a transcriptomic analysis of adipose tissue of dairy cattle in late pregnancy and early lactation. Our objective was to determine the changes in gene expression in adipose tissue between 30 d prepartum and 14 DIM in first lactation animals, and to determine if changes in expression were related to practical production variables. Animals were Holstein heifers fed the same diet to NRC requirements, and adipose tissue was biopsied at 30 d prepartum and 14 DIM. Total RNA was extracted and used to determine gene expression on a bovine gene array. Genes that code for proteins controlling fatty acid transport were highly expressed including fatty acid binding proteins (FABP4 and FABP5) and lipoprotein lipase. Among those genes increasing in expression were those controlling lipolysis including the ADRB2 (52%) and LIPE (23%). Many genes coding for enzymes controlling lipogenesis decreased, including SREBP (−25%); TSHSP14 (−30.8%), LPL (−48.4%) and ACACA (−63.9%). Another novel finding on control of lipolysis is in the expression of the caveolar proteins, caveolin-1 and caveolin-2), which both decreased in early lactation ($P < 0.02$). This gene expression array analysis in adipose tissue of lactating dairy cattle identifies several key genes that are components of the adaptation to lactation that can be incorporated into models of nutritional efficiency and may be amenable to genetic or dietary manipulation. Further functional analysis of differentially expressed genes revealed changes in synthesis, transport, and metabolism of fatty acids in adipose tissue. The expression values were related to milk production and body fat changes. Other functions revealed were in cell cycle control, immunity, and inflammation. These results confirm some key metabolic control points that can be targeted for further research to define the genotypic and phenotypic control of metabolic efficiency in dairy animals.

Key words: lactation, adipose, transcriptomics

T344 The survival of *Bacillus subtilis natto* in rumen and duodenum of Holstein dairy cows. S. H. Dong, J. Q. Wang*, H. Peng, S. Peng, D. P. Bu, L. Y. Zhou, and H. Y. Kang, *State Key Laboratory*

of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China.

Experiments in vitro and in vivo were conducted to evaluate the survival laws of *Bacillus subtilisnatto* (BSN) in rumen and duodenum of Holstein dairy cows. In experiment 1: BSN spores were added at 10^5/mL to strained rumen fluid or duodenum fluid taken from a healthy dairy cow and incubated in vitro at 39°C. Strained rumen fluid or duodenum fluid with no BSN inoculants served as controls. Changes of BSN spore counts and volatile fatty acid in rumen fluid were monitored at 0, 6, 12, 24, 48 and 72 h. Changes of BSN spore counts in duodenum fluid were monitored at 0, 1, 2, 3, 4, 5 and 6 h. The results of rumen fermentation showed that spores increased in the first 24 h, and then decreased. The survival rate of BSN was 191.3% and 157.1% at 24 h and 72 h, respectively. In addition, BSN increased the concentration of propionate and butyrate in rumen fluid ($P < 0.05$), but reduced the concentration of acetic acid ($P < 0.01$). The results of duodenum fermentation showed that spore counts tended to increase in the first 2 h, and then decreased gradually. The survival rate of BSN was 124.4%, 92.4% and 50.4% at 2, 4 and 5 h, respectively. In experiment 2: 7 cows were randomly assigned to 2 groups. Four cows were infused with 10^{10} spores of BSN into rumen through rumen cannula, but the other 3 cows received no infusion. Rumen fluid, duodenum fluid and feces were collected at 0, 6, 12, 24, 48, 72 h after the infusion. Spore counts increased slightly in the first 6 h, and then decreased gradually in rumen fluid. They continued to decrease in duodenum as well as feces and almost cannot be detected at 48 h after infusion in all of the location. In conclusion, BSN spores have the ability to survive in rumen and alter rumen fermentation. Most of BSN spores are able to survive in duodenum fluid for 4 h. However, the spores cannot permanently colonize in the gastrointestinal tract of Holstein dairy cows.

Key words: *Bacillus subtilis natto*, rumen fluid, duodenum fluid

T345 Milk fatty acid composition of lactating dairy cows fed short and medium chain fatty acids. H. Cui, D. P. Bu, J. Q. Wang*, X. W. Zhao, X. Y. Xu, Y. Sun, P. Sun, and L. Y. Zhou, *Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China.*

The objective of this study was to evaluate the response of dietary short and medium chain fatty acids (SMCFA) (C6:0 to C14:0, plus 50% of C16:0) on milk fatty acid composition. Thirty-six Chinese lactating Holstein cows (150 ± 30 DIM) were used for 8 wks in the experiment. The cows were blocked based on DIM and milk yield (21.43 ± 3.39 kg/d) and randomly assigned to 3 treatments and fed TMR with 1 of 3 dietary fat supplements. The 3 treatments consisted of fat supplements containing increasing amounts of SMCFA replaced LCFA which was imitated to ideal with typical fatty acid in dairy cows milk: 1) LCFA (59% cocoa butter, 16% olive oil and 25% palm oil) (400 g/d), 2) butter fat(400 g/d), and 3) SMCFA (C6:0–6.0%, C8:0- 4.0%, C10:0- 9.0%, C12:0- 10.0%, C14:0- 32% and C16:0- 39%) (400 g/d). Milk samples were collected every 2 wks for fatty acid analysis. Data were analyzed statistically by using PROC MIXED (SAS, 1999). Feeding SMCFA increased the proportion of C < 16:0, C16:0 and saturated fatty acid (SFA) in milk fat ($P < 0.05$) in a linear fashion. Otherwise, dietary SMCFA resulted in concentration of C > 16:0 and MUFA in milk fat decreasing linearly ($P < 0.05$). The concentration of PUFA in milk fat was no significant different between treatments (Table 1). In conclusion, increasing supplement SMCFA replaced LCFA caused the fatty acid composition in milk fat changed respectively.

Table 1. Effect of different type of lipids in milk fatty acid composition (% of total FA)

Lipids	LCFA (400 g/d)	Butter fat (400 g/d)	SMCFA (400g/d)	SEM	*P*-value
<16:0	25.20[b]	26.76[b]	30.17[a]	0.52	0.0001
16:0	29.44[b]	31.62[a]	31.30[a]	0.53	0.0291
>16:0	45.34[a]	41.36[b]	37.91[c]	0.76	0.0001
SFA	65.69[b]	68.88[a]	70.83[a]	0.84	0.0012
MUFA	26.66[a]	22.99[b]	21.98[b]	0.78	0.0008
PUFA	7.17	7.63	6.76	0.26	0.0881

[a–b]Least squares means within a row with different superscripts differ.

Key words: cow, fatty acid profiles, short and medium chain fatty acids

T346 Veal calves deposit nitrogen from solid feed as efficient as nitrogen from milk replacer. H. Berends*[1], J. J. G. C. Van den Borne[1], C. G. Van Reenen[2], and W. J. J. Gerrits[1], *[1]Animal Nutrition Group, Wageningen University, Wageningen, the Netherlands, [2]Livestock Research, Animal Sciences Group, Lelystad, the Netherlands.*

This study was designed to substantiate the contribution of increasing solid feed intake (SF) to protein and energy supply of veal calves. Due to potential interactions between milk replacer and solid feed, occurring either at the level of digestion or post-absorptive, this contribution may differ from that in ruminants exclusively fed on concentrates and roughage. To this end, 48 Holstein Friesian male calves (55 kg, SD: 2.1 kg) were divided over 16 groups of 3 calves each. Groups were assigned to one of 4 solid feed intake levels: 0, 9, 18, or 27 g DM of SF kg $BW^{-0.75}$ d^{-1}. Solid feed consisted of 25% chopped wheat straw, 25% maize silage and 50% concentrates on a DM basis. All calves received 40.7 g DM milk replacer kg $BW^{-0.75}$ d^{-1} during the experimental period. Groups were housed in respiration chambers during the 4-d experimental period, at an average BW of 164 kg (SD: 10.3 kg). Within chambers, calves were housed individually on metabolic cages to allow quantification of nitrogen balance. Data were analyzed using regression procedures with SF intake related parameters as independent variables. Preliminary results show that SF0 calves (exclusively milk replacer) retained 241 kJ kg $BW^{-0.75}$ d^{-1} at an intake of 880 kJ kg $BW^{-0.75}$ d^{-1}. The incremental efficiency with which energy from SF ingested was retained was 0.33 ($P < 0.05$). The incremental efficiency with which digestible energy from SF was retained was 0.53 ($P < 0.05$). SF0 calves retained 0.62 g N kg $BW^{-0.75}$ d^{-1} at an intake of 1.38 g N kg $BW^{-0.75}$ d^{-1}. The incremental efficiency with which N from SF ingested was retained was 0.74. Surprisingly, the efficiency of N retention (% of intake) increased with increasing N from SF by 0.35% per g N ($P < 0.05$). With increasing SF intake, there was a substantial shift in N excretion from urine to feces ($P < 0.05$). In conclusion, results show that in veal calves, efficiency of N utilization from SF (fed on top of a milk replacer diet) is markedly higher when compared with N utilization of milk replacer. Interactions between SF and milk replacer, such as an increased recycling of urea-N, may be involved.

Key words: calf, feed intake, protein and fat retention

T347 Effect of *B2M* haplotype combinations on the expression of FcRn mRNA in mammary gland of dairy cows. X. Hu, J. Wang*, S. Zhao, J. Zhao, and D. Bu, *State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China.*

The Fc receptor (FcRn) is the specific transporter of IgG in mammary gland, which is encoded by FCGRT and B2M. The polymorphism of FcRn would influence the concentration and transportation of IgG in milk. We conducted this study to investigate the association of B2M haplotype combinations with FcRn mRNA expression by Real-time PCR, in hope of provide a basis for further study of the possible regulation mechanism of IgG transportation in mammary gland of dairy cows. The mammary gland samples were collected from 40 healthy Chinese Holstein cows immediately after slaughter (the animals were slaughtered in a permitted way in accordance with the policies of Chinese Academy of Agricultural Sciences) and preserved in liquid nitrogen. Total DNA was extracted from the frozen samples. Specific primers were designed to amplify B2M gene. The SNPs were identified after sequencing. Total RNA was purified from the tissues according to the haplotypes of B2M, and then transcripted reversely into cDNA. The level of FcRn mRNA expression was detected by Real-time PCR. The results showed that there were 3 SNPs in B2M gene. We found a transversion of G to T in SNP1, a transition of T to C in SNP3, and a 2-base deletion in SNP2 (the missing bases were A and T). The 3 SNPs assembled 4 haplotype combinations, which were named H1 (GG-deletion-TT), H2 (GG-AT-TC), H3 (GG-AT-TT), and H4 (GT-deletion-TT) respectively. The expression of FcRn mRNA in H4 was significantly higher than the others ($P < 0.05$), but there were no significant differences ($P > 0.05$) between H1, H2 and H3. We concluded that the haplotype combinations of B2M did produce an effect on the expression of FcRn mRNA.

Key words: B2M, dairy cows, real-time PCR

T348 Effect of feeding *Bacillus subtilis natto* fermentation production on hindgut fermentation and microbiota of Holstein dairy cows. H. Y. Kang, J. Q. Wang*, D. P. Bu, L. Y. Zhou, P. Sun, H. Peng, X. l. Wang, and S. H. Dong, *State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing,China.*

The effects of *Bacillus subtilis natto* fermentation production on hindgut fermentation and microbiota of early lactation Holstein dairy cows were investigated in this study. Thirty-six early lactation Holstein dairy cows were randomly allotted to 3 treatments: no *Bacillus subtilis natto* (CON), 6 g *Bacillus subtilis natto* fermentation production/d (DFM1), 12 g *Bacillus subtilis natto* fermentation production/d (DFM2). All cows were treated with 3 treatments after adaption feeding period of 14 d, and the whole trail lasted for 63 d. Fecal samples were collected directly from the rectum of each animal at 0, 1, 2, 3, 4, 6, 8 wk, after the adaption feeding period. The pH, NH_3-N and VFA concentration were measured, and fecal total DNA was extracted and analyzed by DGGE. The results showed that *Bacillus subtilis natto* fermentation production tended to decrease fecal NH_3-N concentration ($P < 0.1$), but had no effect on fecal pH and VFA. DGGE profile revealed that *Bacillus subtilis natto* fermentation production had some effects on fecal bacteria population. The diversity index of Shannon-Wiener in DFM1 decreased significantly ($P < 0.05$) compared with CON. Fecal *Alistipes* sp., *Clostridium* sp., *Roseospira* sp., *Beta proteobacterium* decreased but *Bifidobacterum* increased after supplementation of *Bacillus subtilis natto* fermentation production. This study demonstrated that *Bacillus subtilis natto* fermentation production has potential to improve hindgut microbiota balance. More researches are needed to describe the mode of action to improve the efficiency of probiotic use.

Key words: *Bacillus subtilis natto* fermentation production, dairy cow, fecal microbiota

T349 Effect of short- and medium-chain fatty acid on milk composition in lactating dairy cows. X. W. Zhao, J. Q. Wang*, D. P. Bu, H. Cui, X. Y. Xu, Y. Sun, L. Y. Zhou, and P. Sun, *Chinese Academy of Agricultural Sciences, Beijing, China.*

Short- and medium-chain fatty acids (SMCFA) (C6:0 to C14:0, plus 50% of C16:0), constitute about 45% of total milk fatty acid (FA) and originate from de novo FA synthesis in the mammary gland. The objective of this study was to investigate the effect of SMCFA on milk composition and its limitation to milk fat. The experiment was conducted for 8wks with 30 6 Chinese lactating Holstein dairy cows (150 ± 30 DIM). The cows were blocked based on DIM and milk yield and randomly assigned to 3 treatments. Cows fed corn silage based TMR were supplemented with 1 of 3 dietary lipids supplements (400 g/d). The 3 treatments consisted of lipids supplements containing mixtures of different ratio of long chain fatty acid (LCFA) and SMCFA: 1) LCFA (59% cocoa butter, 16% olive oil, and 25% palm oil), 2) butter fat (400 g/d), and 3) SMCFA (C6:0–6.0%, C8:0- 4.0%, C10:0- 9.0%, C12:0- 10.0%, C14:0- 32%, and C16:0- 39%). Dry matter intake (16.82, 16.82, and 16.90 kg/d; $P > 0.05$), milk production (24.06, 23.67, and 22.47 kg/d; $P > 0.05$), 4% fat-corrected milk (FCM) (23.94, 23.94, and 24.45 kg/d; $P > 0.05$), milk protein percentage (3.34, 3.38, and 3.52%; $P > 0.05$), milk protein yield (817.30, 783.82, and 815.23 g/d; $P > 0.05$), and milk fat yield (954.33, 964.70, and 1030.62 g/d; $P > 0.05$) were not different between treatments for LCFA, butter fat, and SMCFA, respectively. Whereas milk fat percentage (3.90, 4.16, and 4.45%; $P < 0.05$) were increased in linear level when improved SMCFA content in the diet. Furthermore milk fat percentage reached the peak point coupled with SMCFA. In conclusion, SMCFA supplementation has positive effect in milk fat compared with LCFA, which means SMCFA may promote milk fat secretion in mammary gland in dairy cows.

Key words: Short- and medium-chain fatty acids, milk composition, dairy cows

T350 Effect of feeding *Bacillus subtilis natto* fermentation production on milk production and composition, blood metabolites and rumen fermentation in early lactation dairy cows. H. Peng[1], J. Q. Wang*[1], H. Y. Kang[1,2], S. H. Dong[1,3], P. Sun[1], D. P. Bu[1], and L. Y. Zhou[1], *[1]Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [2]College of Animal Science and technology, Southwest University, Chongqing, China, [3]Faculty of Animal Sciences and Technology, Gansu Agricultural University, Lanzhou, China.*

This experiment was conducted to determine the effect of *Bacillus subtilis natto* fermentation production supplementation on blood metabolites, rumen fermentation, milk production and composition in early lactation dairy cows. Thirty-six multiparous Holstein cows (DIM = 29 ± 6 d, parity = 2.8 ± 1.1) were blocked by DIM and parity and then randomly assigned to 3 treatments (12 per treatment) in a 9-wk trial. Cows in control, DFM1, DFM2 were fed TMR diets supplemented with 0, 6, 12 g of *B. subtilis natto* solid state fermentation production per day per cow separately. Six and 12 g of supplements contained about 0.5×10^{11} and 1×10^{11} spores of *B. subtilis natto* respectively. Plasma nonesterified fatty acids tended to be lower ($P = 0.06$) in DFM1 and DFM2 compared with control cows (639, 633 vs. 685 μmol/L). Ruminal propionate proportion of cows in DFM1 and DFM2 tended to be higher ($P = 0.06$) than control cows (26.3 and 26.9 vs. 23.9 mol/100 mol). There were no significant differences among treatments for DMI, but milk yield was 3.1 kg/d and 3.2 kg/d higher for DFM1 and DFM2 than control cows on average across the 9-wk trial and significant differences

were observed during wk 5 to 9 of the trial, which resulted in 9.5% and 11.7% increases in feed efficiency (kg of milk per kg of DMI). No significant difference were observed in milk yield and feed efficiency between DFM1 and DFM2. Milk fat percentage, protein percentage and yield were not affected by treatment. Milk fat yield tended to be higher ($P = 0.07$) and lactose percentage was significantly higher ($P < 0.05$) for DFM1 and DFM2 (4.93 and 4.95%) compared with control cows (4.80%). The findings suggest that *B. subtilis natto* fermentation production has potential role to improve lactation performance of early lactation dairy cows by altering the rumen fermentation pattern without any negative effects on animal health.

Key words: *Bacillus subtilis natto* fermentation production, dairy cow, milk production

T351 Fermentative and nutritional dynamics of bovine colostrum silage for dairy calves liquid feeding. L. S. Ferreira[1,2], M. C. Soares[1], M. P. C. Gallo[1], M. R. Paula[1,2], and C. M. M. Bittar*[1,2], *[1]University of São Paulo/ESALQ, Piracicaba, SP, Brazil, [2]Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq), Brasília, DF, Brazil.*

The objective of this study was to characterize the fermentative and nutritional dynamics of bovine colostrum fermented under anaerobic conditions 56 d during storage at ambient temperature. Colostrum from the second and third milking was collected, pooled, and stored in plastic bottles, which were filled and lightly pressed before its closure to remove all space with oxygen, thereby creating an anaerobic condition. Bottles were stored in a dark room at ambient temperature and 5 bottles were opened at d 0,1, 2, 3, 4, 5, 6, 7, 14, 21, 28 and 56 after storage, to determine pH, titratable acidity and temperature values. Also, samples were collected for determination of total nitrogen, protein and non-protein fractions by the Kjeldahl method. The pH and the titratable acidity values showed great variation during the storage period, essential for the conservation of colostrum ($P < 0.001$). However, although the pH and titratable acidity has shown great variations during the fermentation process, the colostrum temperature dynamics and values were close to ambient. The non-protein nitrogen fraction presented a high increase during storage ($P < 0.001$) and the true protein values decreased ($P < 0.001$), and presented with very low values after 56 d of storage. The fermentative dynamics observed suggests that colostrum silage has a potential for use as a milk replacer, however the nutritional quality of the resulting product, especially in relation to protein fraction, is inadequate for dairy calves. Strategies for reducing true protein conversion to non-protein nitrogen should be further investigated. Supported by CNPq.

Table 1. Composition and fermentative characteristics of colostrum silage

	Storage days						
Item	0	7	14	21	28	56	SE
pH	6.2	4.6	4.4	4.0	4.1	4.2	0.02
Titratable acidity, % of lactic acid	4.0	17.1	21.5	30.2	35.1	40.1	0.4
Temperature, oC	18.8	18.5	19.0	21.1	21.3	21.0	0.06
Total nitrogen, %	2.9	2.67	2.46	2.27	2.11	2.03	0.04
Non-protein nitrogen, % of total N	1.93	3.49	4.85	6.65	9.58	17.4	0.29
Casein nitrogen, % of total N	45.3	29.0	30.9	19.1	17.4	12.1	0.72
Crude protein, %	18.5	17.0	15.7	14.5	13.4	12.9	0.26
True protein, %	8.4	4.9	4.8	2.8	2.3	1.6	0.3

SE = standard error of means.

Key words: fermented colostrum, protein fractions, colostrum storage

T352 Performance of dairy calves fed "colostrum silage" or milk replacer. L. S. Ferreira[1,2], J. T. Silva[1], G. G. O. Nápoles[1], C. E. Oltramari[1], and C. M. M. Bittar*[1,2], *[1]University of São Paulo/ESALQ, Piracicaba, SP, Brazil, [2]Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq), Brasília, DF, Brazil.*

The objective of this study was to evaluate the performance of male Holstein calves fed bovine colostrum fermented under anaerobic conditions as a replacement to traditional liquid diet. Following birth, 18 male Holstein calves were used in a completely randomized design and assigned to the following treatments: 1) Control: milk replacer (18.5% CP, 22.5% fat, 12.5% solids; Nattimilk, Auster Animal Nutrition) or 2) Anaerobically fermented colostrum (colostrum silage). The animals were housed in individual hutches, with free access to water, starter feed (18% CP; 72% TDN), and 4L of liquid diet (milk replacer or colostrum silage) until weaning which occurred abruptly at the eighth week of life. Colostrum from the second and third milking was collected, pooled, and stored in plastic bottles, which were filled and lightly pressed before its closure to remove all space with oxygen, thereby creating an anaerobic condition. After approximately 45 d of fermentation and at the time of calves feeding, bottles were opened and diluted in warm water in a 1:1 ratio, to ensure acceptance by the animals. The starter feed intake and fecal score were recorded daily and body weight measurements were taken weekly until the eighth week of age. Animals fed colostrum silage presented lower starter intake ($P < 0.07$) during the experimental period, as compared with control animals (238 vs. 412 g/day). As expected, there was an age ($P < 0.0001$) and treatment x age ($P < 0.05$) effect for starter intake, with increasing values throughout the experimental period. However, no effects were observed for average daily gain (0.278 vs. 0.183 kg/day) or body weight (42.3 vs. 40.6 kg for the control treatment and fermented colostrum, respectively). The fecal score was affected by treatments during the wk 2 ($P < 0.05$), with animals fed fermented colostrum showing abnormal and very dry feces (average fecal score = 1.65). Even though the anaerobic fermentation of colostrum may be a good alternative for its storage, feeding it as a liquid feed during all milk-feeding period does not result in adequate animal performance. Financial support provided by CNPq.

Key words: fermented colostrum, fecal score, liquid diet

T353 In situ dry matter degradation kinetics of fennel forage in Holstein cow. M. Chaji*, T. Mohammadabadi, and H. Eghbali, *Khuzestan Ramin Agricultural and Natural Resources University, Molassani, Khuzestan, Iran.*

The objective of this experiment was determination of DM degradability of fennel forage. Dry matter degradability of the samples was measured by in situ technique using 2 fistulated Holstein steers (400 ± 12 kg, body weight). The animals fed a 40:60 concentrate: forage diet. The experimental samples were milled (2-mm screen) and weighed (5 g, DM) into bags (12x19 cm) made of polyester cloth with 52 µm pore size (8 replicates per each treatment). The bag were incubated in the rumen for 2, 4, 6, 8, 16, 24, 48, 72 and 96 h after being soaked in distilled water (38°C) for 10 min. Bags also were washed with cold tap water to estimate the wash-out at zero time. After each incubation time, the removal bags were hand-washed with cold tap water, and then dried in a forced-air oven (60°C, 48 h). The degradable parameters of DM were determined using the equation of $P = a + b (1 - e^{-ct})$. Data of degradable parameters and effective degradability of DM (out flow rate = 0.08 h −1) were analyzed using GLM of SAS in a completely randomized design ($P < 0.05$). Results of the present experiment indicated that the rapidly degradable fraction (a), slowly degradable fraction (b) and fractional degradation rate (c) of DM of fennel forage was 0.29+0.035, 0.4+0.038 and 0.099+0.024, respectively. Potential of degradability and DM effective degradability of fennel forage was 0.68 and 0.61.

Key words: fennel forage, degradability, in situ

T354 The effect of exogenous phytase on ruminal degradation of inositol phosphate in dairy cows. J. Sehested*[1], D. N. Braks-Pedersen[1], V. Glitsø[2], L. K. Skov[2], and P. Lund[1], *[1]Department of Animal Health and Bioscience, Aarhus University, Tjele, Denmark, [2]Department of Feed Applications, Novozymes A/S, Bagsvaerd, Denmark.*

The effect of exogenous phytase on inositol phosphate degradation in the rumen of 4 lactating Danish Holstein dairy cows with ruminal, duodenal and ileal cannulas was investigated in a 4 × 4 Latin Square design with 4 dietary treatments (level of exogenous phytase) and 4 periods (21 d). The cows were offered a total mixed ration (TMR) with a total phosphorus (P) content of 3.8 g/kg dry matter (DM) and a high proportion of dietary P in inositol phosphate (1.7 g P/kg DM). The TMR was composed of (% of DM): Beet pulp (30), grass silage (26), rape seed cake (20), maize silage (17), cane molasses (5) and maize feed meal (2). The TMR was supplemented with one of 4 concentrations of exogenous phytase (phytase units/kg DM): CONTROL (0), LOW (2000), MEDIUM (4000), or HIGH (6000). Preliminary data show, that addition of exogenous phytase to the feed ration significantly increased ruminal degradability (%, $P < 0.001$, SEM = 1.82) and reduced duodenal flow (g/d, $P < 0.001$, SEM = 0.38) of myo-inositol hexakisphosphate (InsP6) compared with CONTROL (75%; 6.7 g/d), whereas there was no difference between LOW (92%; 2.1 g/d), MEDIUM (95%; 1.3 g/d) and HIGH (96%; 1.2 g/d). Ruminal pH, rumen degradability of NDF, and rumen NDF kinetics were not affected by treatment. The present study indicated that ruminal degradation of inositol phosphate was increased by adding exogenous phytase to the diet. The results indicated that max ruminal inositol phosphate degradation was obtained by adding 2000 phytase units/kg DM.

Key words: inositol phosphate, phytase, phosphorus availability

T355 Effect of sample processing on in situ organic matter degradability of distillers grains. M. L. Drewery*[1], J. E. Sawyer[1], N. M. Kenney[1], W. E. Pinchak[2], and T. A. Wickersham[1], *[1]Texas A&M University, College Station, [2]Texas AgriLife Research, Vernon.*

Determination of ruminal OM degradability is important when evaluating feedstuffs. Precise quantification of nutrient availability is important when formulating rations. Wet distillers grains (DG) have a high moisture content that challenges conventional sample processing methods. Our objective was to quantify the effect of sample processing on measures of rate and extent of OM degradation of wet DG samples. Three ruminally cannulated steers were given ad libitum access to a ration (15% CP) containing 38.5% corn, 28% hay, and 28% dried DG. Samples of DG from each plant were divided and a portion was frozen at −20°C while the remainder was dried at 55°C in a forced-air oven for 96 h. Dried samples were ground to pass a 2-mm screen. Five g of each sample was placed in Dacron bags, pre-incubated in tepid water, placed in a weighted mesh polyester bag, and incubated in the rumen for 4, 6, 12, 24, 48 and 72 h. Samples were rinsed in cold water and dried at 60°C. Organic matter was measured and fractionated into A, B, and C pools. Degradation rate of the B fraction was calculated as the slope of the natural log of N remaining against time. Rate of passage was set at 3%/h. The A fraction was larger ($P < 0.01$) for frozen than dried samples, 43.5 and 33.1%, respectively. In contrast, the B fraction was less ($P < 0.01$) for frozen (42.9%) than dried samples (52.6%). The C fraction was not significantly different ($P = 0.16$) between frozen (13.6%) and dried (14.4%). Similarly, the difference in the degradability of the B fraction was not significant ($P = 0.71$) for frozen than dried samples 5.38 and 5.57%/h, respectively. However, estimated degradability was observed to be greater ($P < 0.01$) for frozen than dry samples 69.2 and 65.4%, accordingly. Our observations suggest sample processing affects the fractionation of OM from DG, but not estimates of OM degradability.

Key words: distillers grains, degradability, organic matter

T356 Effect of tannins on in vitro ruminal degradability of purple prairie clover (*Petalostemon purpureum*) harvested at the two growth stages. L. Jin*[1,2], Z. Xu[1], A. D. Iwaasa[3], Y. G. Zhang[2], M. P. Schellenberg[3], T. A. McAllister[1], and Y. Wang[1], *[1]Agriculture and Agri-Food Canada, Lethbridge Research Centre, Lethbridge, AB, Canada, [2]Department of Animal Science, Northeast Agricultural University, China, [3]SPARC-AAFC, Swift Current, SK, Canada.*

An in vitro study was conducted to assess the effects of maturity and tannins on the ruminal degradability of purple prairie clover (PPC; *Petalostemon purpureum*).Whole PPC plants were harvested from 3 pastures at the vegetative (VEG) and full-flowering/early seeding (FL) stages. Ground whole plant samples were placed into ANKOM F57 filter bags that were then incubated with a mixture of ruminal fluid and buffer in glass digestion jars in 3 DAISYII fermentors. Ruminal fluid was collected from steers fed forage (barley silage/grain/alfalfa hay) diet. ^{15}N labeled ammonium sulfate was included in the inoculum to assess microbial protein synthesis and feed colonization. Filter bags that contained the samples collected from the same pasture at the 2 growth stages were incubated in a same unit. Half (2) of the jars in each unit were supplemented with polyethylene glycol (PEG), yielding a 2 × 2 arrangement in each unit. Two bags were retrieved from each jar at 0, 1, 2, 4, 8, 12, 24, 48 and 72 h of incubation. All bags withdrawn were washed under running tap water until the water was clear, dried, and analyzed for DM, N and ^{15}N. Plants harvested at the VEG stage had higher ($P < 0.001$) true dry matter degradability (TDMD), total N degradability (TND) and potential degradable fraction (b) of DM and N than that harvested at FL stage. The rapidly degradable fraction (a) of DM was higher ($P < 0.001$) in VEG than in FL, whereas the same fraction of N was higher ($P < 0.01$) in FL than in VEG. Inclusion of PEG increased ($P < 0.01$) the rate at which b is degraded (c) for DM only, but no growth stage by PEG interaction was found for DM degradation parameters. Inclusion of PEG increased ($P < 0.01$) TND and the potentially degradable fraction of N of PPC harvested at the FL, but not at the VEG stage. Overall, the results indicated that PPC harvested at the VEG stage is more degradable in the rumen than that harvested at the FL stage, but it seemed that the high tannins concentrations had only inferiorly detrimental impact on PPC degradability.

Key words: purple prairie clover, tannins, ruminal degradability

T357 Effect of exogenous fibrolytic enzymes on dry matter in situ digestibility of two *Brachiaria* grasses. J. H. Avellaneda-Cevallos[1,2], O. D. Montañez-Valdez*[3], D. Romero-Garaicoa[1], R. Luna-Murillo[1], J. Bravo-Loor[1], and M. Peña-Galeas[1], *[1]Unidad de Investigacóin Científica y Tecnológica. Facultad de Ciencias Pecuarias. Universidad Técnica Estatal de Quevedo, Quevedo, Ecuador, [2]Jefatura de Investigacóin. Carrera de Pecuaria.Escuela Superior Politécnica Agropecuaria de Manabí Manuel Félix López. Campus Politécnico, Sitio El Limón, Calceta, Manabí, Ecuador, [3]Centro Universitario del Sur de la Universidad de Guadalajara, Ciudad Guzmán, Jalisco, México.*

The effect of an exogenous fibrolytic enzymatic compound on ruminal pH and in situ digestibility of 2 *Brachiaria* hays, *B. mulato* and *B. decumbens*, cut at 28 and 56 d was evaluated. Four ruminally cannulated steers (400 ± 15 kg body weight) were randomly assigned to a replicated 4 × 4 Latin square with 2 different squares for balancing carryover effects. Both squares had 4 steers and squares were conducted simultaneously. Each experimental period consisted of 11 d of adaptation to diets and 4 d of experimental measurements. The ruminal cannulas measured 7.5 cm center diameter (Bar Diamond, Parma, ID). Steers were housed in individual dry lot pens and offered the experimental diets twice a day at 0700, 1800 h for 90% of intake to allow no refusal. The fibrolytic enzyme preparation containing xylanase and cellulase activities (Fibrozyme, Alltech Inc., Nicholasville, KY, USA). The treatments were: T1) *B. mulato* and *B. decumbens* of 28 d with enzyme; T2) *B. mulato* and *B. decumbens* of 28 d without enzyme; T3) *B. mulato* and *B. decumbens* of 56 d with enzyme; T4) *B. mulato* and *B. decumbens* of 56 d without enzyme. Nylon bags were incubated with samples of hay with a size of 2 mm in the rumen at 0, 12, 24, 48 and 96 h and the DM and OM remaining at each incubation time was fitted to the nonlinear regression model using NLIN procedure of SAS and the pH was measured from the liquid ruminal to 0, 3, 6, 9 and 12 h were analyzed using MIXED procedure of SAS. The in situ digestibility of dry matter and ruminal pH, was not change by the application of the compound enzymatic exogenous ($P \geq 0.05$). We can conclude that the use of this enzymes do not affect the digestion of the dry matter of the hay of *B. mulato* and *B. decumbens* cut at 28 and 56 d.

Table 1. In situ digestibility of DM for the experimental materials

	T1[1a]	T1	T2[b]	T2	T3[2a]	T3	T4[b]	T4
Component	EZ+	EZ-	EZ+	EZ-	EZ+	EZ-	EZ+	EZ-
In situ digestibility								
96	69.73	73.73	66.62	66.50	72.69	72.13	61.72	62.52
48	68.79	69.39	61.07	60.66	65.98	68.28	55.40	54.65
24	57.18	57.55	49.58	50.09	57.66	57.74	44.59	43.45
12	44.87	44.22	37.81	38.65	43.77	48.02	33.51	33.24
0	29.68	29.91	25.57	25.55	28.44	28.99	20.14	21.79

[1]*Brachiara mulato* with or without enzyme. [a] 28 or [b] 56 d.
[2]*B. decumbens* with or without enzyme.

Key words: *Brachiaria*, enzymes, digestibility

T358 Method evaluation for determining digestibility of rumen undegraded amino acids in blood meal. S. E. Boucher*[1], S. Calsamiglia[2], M. D. Stern[3], C. M. Parsons[4], H. H. Stein[4], C. G. Schwab[5], K. W. Cotanch[6], J. W. Darrah[6], and J. K. Bernard[7], *[1]Kemin AgriFoods North America Inc., Des Moines, IA, [2]Universitat Autònoma de Barcelona, Bellaterra, Spain, [3]University of Minnesota, St. Paul, [4]University of Illinois, Urbana, [5]Schwab Consulting LLC, Boscobel, WI, [6]William H. Miner Agricultural Research Institute, Chazy, NY, [7]University of Georgia, Tifton.*

To evaluate various methods for estimating digestibility of rumen undegraded AA in blood meal (BM), 5 BM samples (2 bovine, 3 porcine) were obtained. One bovine sample was heated at 125°C for 2 h to generate an additional bovine sample and one porcine sample was heated at 110°C for 2 h (n = 6). Samples were ruminally incubated in situ for 16 h in 3 lactating cows fed a 55% forage diet. Rumen undegraded residues (RUR) were pooled by sample and analyzed for AA. Digestibility of AA in the RUR was determined via the mobile bag technique (MBT) in dairy cows, precision fed cecectomized rooster assay (CRA), modified 3-step procedure (MTSP), and homoarginine assay (HA; estimates available Lys). For the MBT, 0.8 g of each RUR was weighed into 24 polyester bags, soaked in a pepsin/HCl solution for 2 h, and introduced into 2 duodenally cannulated cows. Bags were collected from the feces and undigested residues were analyzed for AA. Digestibility of AA was calculated by disappearance. To calculate standardized AA digestibility using the CRA, RUR were tube fed to 4 birds per sample, and total excreta collected for 48 h and analyzed for AA. For the MTSP, 5 g of each RUR were weighed into 2 polyester bags and incubated (38°C) sequentially in a pepsin/HCl solution for 1 h then a pancreatic solution for 24 h in Daisy^{II} incubator bottles. Digestibility of AA was calculated by disappearance. For the HA method, RUR were guanidinated and analyzed for Lys and HA content. Percent Lys converted to HA was calculated. The REG procedure of SAS was used for data analysis. R^2 values for Lys digestibility using MTSP, CRA, and HA procedures compared with the MBT in cows (independent variable) were 0.89, 0.62, and 0.05, respectively, and the R^2 values for total essential AA (EAA) digestibility using MTSP and CRA compared with MBT were 0.89 and 0.92, respectively. Using MBT in dairy cows as a reference, it appears that HA method is not a good approach to determine available Lys in BM, CRA was adequate to determine digestibility of total EAA in BM, and MTSP is a good approach to estimate digestibility of both Lys and total EAA in BM.

Key words: blood meal, rumen-undegraded protein, mobile bag technique

T359 In vitro modification of ruminal and post ruminal metabolism by lignosulfonate and polysaccharide protected microminerals. M. Ruiz-Moreno*[1], E. Seitz[1], M. D. Stern[1], and J. Garrett[2], *[1]University of Minnesota, St. Paul, [2]Quali Tech Inc., Chaska, MN.*

Ruminal and postruminal availability of trace minerals is affected by chemical nature and presence of chelating agents such as lignin derived phenolic compounds. The aim of this study was to evaluate effects of lignosulfonate and polysaccharide-protected minerals on in vitro rumen fermentation, ruminal and post ruminal partition of Cu, Zn and Mn. Eight dual flow continuous culture fermenters were used during 2 consecutive 10-d periods in a 2 × 2 factorial arrangement of treatments. A synthetic diet consisting of 38% cellulose, 34% starch, 20% powdered whey, 5.3% vegetable oil and 2.5% sugar provided substrate for microbial metabolism. Sulfur was added as $NaSO_4$ or S-bound lignosulfonate to a final concentration of 0.75% of DM. Lignosulfonate was added at 0 (LIG0) or 5% (LIG5) of DM. Copper, Zn and Mn were added as $CuSO_4$, $ZnSO_4$ and $MnSO_4$ or as polysaccharide protected Cu, Zn and Mn (SQM protected minerals, Quali Tech Inc.; SQM- or SQM+, respectively) to a final concentration of 16, 56 and 71 ppm of DM, respectively. At the end of each period, solid and liquid fractions from fermenters outflows were subjected to pepsin-pancreatin enzymatic digestion. Apparent and true OMD (%) were not affected by treatments ($P > 0.05$). Addition of LIG5 decreased ($P < 0.05$) daily flow of non NH_3-N, efficiency of microbial protein synthesis, total VFA and molar proportion of acetic acid, but increased ($P < 0.05$) propionic, valeric and caproic acid while SQM+ decreased molar proportion of propionic acid. Addition of LIG5 increased ($P < 0.05$) ruminally soluble Cu and Mn, while SQM+ reduced ruminally soluble Cu. Concentration of bacterial Cu and Zn increased with SQM+ in absence of lignosulfonate ($P < 0.05$). Addition of LIG5 resulted in higher enzymatic release of Zn from solids outflow but lower from bacterial pellets ($P < 0.05$). Mean, minimum and maximum fermentation pH were higher ($P < 0.05$) with LIG5. Addition of lignosulfonate induced major changes in ruminal fermentation. Protected minerals decreased rumen soluble Cu and increased bacterial Cu and Zn without affecting predicted post ruminal release of minerals.

Key words: protected minerals, rumen, lignosulfonate

T360 Factors affecting estimation of spoilage indices in silage 2: Effects of amount of silage evaluated and type of container. N. Cavalcanti[1,2], J. Leite[1,2], L. G. Paranhos*[1], O. C. M. Queiroz[1], K. G. Arriola[1], and A. T. Adesogan[1], *[1]University of Florida, Gainesville, [2]Federal University of Pernambuco, Recife, Pernambuco, Brazil.*

Aerobic stability is a measure of the shelf life of silage and an indirect measure of the likelihood of undesirable microbial activity, which predisposes to heating, nutrient depletion and growth of pathogenic organisms. Different methods are used for this assay and this likely affects the outcome. This project aimed to examine effects of container type and amount of silage evaluated on the aerobic stability of corn silage. Three different amounts of corn silage, 1, 2, or 3 kg were packed at the same density (550 kg/m3) into 20 L plastic buckets (PB) or 20 L styrofoam containers (SC) in quadruplicate. Wireless temperature sensors were placed in the center of the silage mass in each container and set to record temperatures every 30 min for 14 d. Ambient temperature was similarly measured. Aerobic stability was estimated as the time (h) before silage and ambient temperature differed by more than 2°C. Maximum and minimum temperatures and an instability index estimated as the area under the temperature curve during the aerobic exposure period were recorded. The experiment had a ran-

domized complete block design and a 2 (container type) × 3 (amount of silage) factorial treatment arrangement. The statistical model contained silage amount and container effects and the interaction. Minimum temperature was greatest for 1 kg forage in SC and for 3 kg silage in PB (amount x container interaction, $P = 0.02$). Using SC resulted in greater aerobic stability (168.9 vs.79.9 h; $P < 0.01$) and greater minimum temperatures (2°C difference) compared with using PB. Using 3 kg of silage resulted in greater maximum temperature (37.4 vs. 29.0; $P < 0.01$), greater temperature range (20.3 vs. 11.2°C; $P < 0.01$), and greater area under the temperature curve compared with using 1 kg ($P < 0.01$). These data showed that container type and amount of silage evaluated influence the aerobic stability result.

Key words: aerobic stability, corn silage, methodology

T361 Infusion of marker solution into intact digesta for measurement of the ruminal clearance of volatile fatty acids. J. C. de Resende Júnior*, J. L. P. Daniel, F. da C. Meireles, M. B. Moreira, and R. F. de Lima, *Universidade Federal de Lavras.*

The removal (clearance) of volatile fatty acids (VFA) of the reticulorumen occurs by absorption through the wall or passage to the omasum. This study aimed to validate a new technique for infusion of marker solution into intact ruminal digesta comparing with another technique which has known efficiency for measurements of the ruminal clearance of VFA. Four cows were allocated to 4 treatments in split plot design, aligned in a 2 × 2 factorial arrangement which was diet and method of infusion of markers applied concurrently in 2 periods of 18 d. The 4 combinations were: forage diet and infusion of markers into intact (ID) or evacuated digesta (ED); forage plus concentrate and infusion of markers into intact or evacuated digesta. Four liters of markers solution containing Cr-EDTA associated with valeric acid were added to the ruminal digesta. Rumen fluid samples were serially collected and analyzed for pH, VFA concentration and Cr. The fractional clearance rate of total VFA was estimated by the exponential decay rate of the valerate concentration over time. The clearance of VFA by passage to the omasum was assumed to be equivalent to the decay in ruminal Cr concentration and the fractional clearance rate of absorption was estimated by difference. The fractional rates of total clearance (ID = 37.8%/h; ED = 30.5%/h) and absorption (ID = 26.0%/h; ED = 21.1%/h) of VFA did not differ between techniques ($P = 0.30$ and $P = 0.52$, respectively), demonstrating that the infusion technique into ID is comparable to the infusion technique into ED. The fractional rate of passage of the fluid phase (ID = 11.8%/h; ED = 9.4%/h), however, was lower ($P = 0.06$) when the marker solution was added into the evacuated digesta, probably reflecting the destabilization of the rumen environment during the evacuation and the largest volume of fluid observed in animals with evacuated digesta. It is concluded that the infusion of marker solution into intact digesta with homogenization performed by ruminal motility is effective and seems to be the better choice for the VFA ruminal clearance determination because it allows measurements under more normal physiological conditions.

Key words: acidosis, measurement of metabolizable energy, ruminant stomach

T362 Adjustment of in vitro rumen fermentation protocol for testing products based on rumen pH regulation and the impact of Acid Buf. S. Taylor*[1], E. Pennala[2], and J. Apajalahti[2], *[1]Celtic Sea Minerals Ltd., Cork, Ireland, [2]Alimetrics Ltd., Espoo, Finland.*

Investigating the mode of action of buffering materials by in vitro rumen fermentation is restricted because protocols normally use strong buffers to compensate for the lack of acid absorption from the system. Optimization of buffer strength and volume, and the amount / type of feed enables the mimicking of acidosis and the testing of products designed to impact on this challenge. Simulation protocol: The simulation used 1 g (DM) feed composed of 50% grass silage, 40% barley meal and 10% soy. The buffer based on bicarbonate and phosphate (Agriculture Handbook, Vol 379, USDA 1970) was diluted with 0.9% NaCl as indicated below. The study with 12 replicates was inoculated with 5% of fresh, strained rumen fluid from a cow on a high energy diet and continued for 12 hours at 37°C. Anaerobic techniques were applied throughout. The treatments were: undiluted buffer and this diluted to 1:2 and 1:4 in constant volume (40 ml) A treatment with 1:4 diluted buffer + 50 mg of Acid Buf/40 ml was included. Total gas production, pH, and short-chain fatty acids (SCFAs) were determined at various time points. Cumulative methane production and bacteria were analyzed at the end. SCFAs and methane were analyzed by GC and bacteria by flow cytometry. Dilution of the buffer allowed acidity to increase, which led to suppression of bacterial growth and metabolism. Addition of Acid Buf in the fermentation with the 1:4 diluted buffer significantly reduced the drop of pH and maintained higher bacterial activity. Methane to acid ratio (ml/mM) was lower than with the weaker buffering

Table 1. Results

	Buffer 1:1	Buffer 1:2	Buffer 1:4	Buffer 1:4 + Acid Buf
Gas production at 12 h (mL)	102[a]	86[b]	44[d]	60[c]
pH, 4 h	6.83[a]	6.42[b]	6.00[c]	6.10[c]
pH, 12 h	6.73[a]	6.15[b]	5.31[c]	5.69[b]
SCFA, 12 h (m*M*)	68[a]	67[a]	52[b]	65[a]
Acetate, 12 h (m*M*)	29[a]	24[b]	16[d]	21[c]
Propionate, 12 h (m*M*)	20[a]	19[a]	13[c]	17[b]
Methane 12 h (mL)	4.3[a]	4.1[a]	1.9[c]	2.9[b]
CH4/SCFA (mL/m*M*)	6.3%	6.1%	3.6%	4.5%
Bacteria (cells/mL)	8.9E+0.9[a]	6.1E+09[b]	3.3E+09[d]	4.5E+09[c]

Numbers with the same superscript are not significantly different ($P = 0.05$).

Key words: acidity, rumen, simulation

T363 Impact of different sources of hydrolysable and condensed tannins on rumen fermentation and methane production in vitro. F. Hassanat* and C. Benchaar, *Agriculture and Agri-Food Canada, Dairy and Swine Research and Development Centre, Sherbrooke, Qc, Canada.*

Tannins added to animal diet may generate positive impact on energy and protein utilization in the rumen. The objective of this study was to examine the impact of different sources and levels of condensed and hydrolyzable tannins on rumen microbial fermentation in vitro (24-h batch cultures). Condensed tannin extracts from Acacia (AT; *Acacia mearnsii*; 82% DM) and Quebracho (QT; *Schinopsis balansae*; 90% DM) and hydrolysable tannin extracts from Chestnut (ChT; *Castanea sativa*; 75% DM) and Valonia (VT; *Quercia vallonea*; 71% DM) were used. In vitro incubations (repeated 4 times) were conducted in a completely randomized block design using a control (CTL; 0%) and each source of tannin at 2, 5, 10, 15 and 20% of total mixed ration DM. Each

treatment was tested in quadruplicate. Differences between treatments and CTL were declared significant at $P \leq 0.05$ using Dunnett's comparison test. Gas production (GP) was reduced at ≥5% of AT, while at 2% or more, QT produced less gas than CTL. At ≥5% concentration, both AT and QT reduced total volatile fatty acids (VFA) and CH_4 concentrations. No effect was observed on acetate (C_2) proportion at any level of AT or QT while propionate (C_3) proportion was slightly increased at ≥ 10% of AT or QT, resulting in lower C_2:C_3 ratio. Addition of ChT at ≥5% reduced GP, CH_4 and VFA concentrations compared with CTL. Proportion of C_2 increased when ChT was supplied at ≥10% while no effect of ChT was observed on C_3 proportion or C_2:C_3 ratio. Supplying VT at ≥2% reduced GP while a level of VT ≥5% was required to decrease CH_4 concentration. Total VFA concentration was reduced only at ≥10% of VT while C_2 proportion was increased at ≥2% VT and no change was noted for C_3 and C_2:C_3 ratio. Proportions of isovaleric, and valeric and ammonia concentration were decreased at all levels of tannin sources added, indicating reduced protein degradation. At low concentrations (2–5%), tannins have the potential to reduce CH_4 production and ruminal protein degradation without deleterious effects on fermentation.

Key words: in vitro fermentation, methane, tannins

T364 Changes in ruminal bacterial community composition following feeding of silage inoculated with a commercial silage inoculant. R. Mohammed*[1,2], D. M. Stevenson[1], K. A. Beauchemin[2], P. J. Weimer[1], and R. E. Muck[1], *[1]USDA-ARS, Madison, WI, [2]AAFC, Lethbridge, AB, Canada.*

Some silage inoculants yield an increase in milk production, possibly through altering the rumen microflora. We hypothesized that alfalfa silage treated with a commercial inoculant (*Lactobacillus plantarum*, LP) would alter rumen bacterial community composition (BCC) compared with silage without inoculant (Ctrl). Eight rumen-cannulated Holstein cows were allotted to 2 diets (Ctrl- or LP-treated silage) in a double crossover design with 4 28-d periods. Diets were formulated to contain (per kg DM) 280 g NDF and 162 g CP, and contained (g/kg DM): alfalfa silage, 509; corn silage, 206; high-moisture shelled corn, 214, soy hulls, 47; plus minerals and vitamins. Ruminal digesta were collected just before feeding on the last 3 d of each period, and were separated into solid and liquid phases. Microbial DNA was extracted from each phase, amplified by polymerase chain reaction (PCR) using domain-level bacterial primers, and subjected to automated ribosomal intergenic spacer analysis (ARISA) for comparison of BCC. Correspondence analysis of the 266 peaks in the ARISA profile across the 192 samples revealed that the first 2 components contributed 6.8% and 4.2% to the total variation in the profile. Data points representing the liquid and solid phases clustered separately, indicating that these phases differed in BCC. Treatment effects were not apparent from the ARISA profiles. However, the relative population size (RPS) of LP, determined by quantitative PCR, was greater in treated silage compared with the Ctrl ($P < 0.01$). Data points corresponding to certain individual cows clustered separately, and the most distinctive bacterial communities were those associated with milk fat-depressed cows. The RPS of one bacterial species, *Megasphaera elsdenii*, was greater in fat-depressed cows. However, mean RPS of *M. elsdenii* did not differ between the treatments. The results indicate that a silage inoculant can affect rumen bacterial composition beyond elevating the population of the specific microbial inoculant.

Key words: rumen, silage inoculant, microbial populations

T365 Effect of a dietary antioxidant with different substrate on rumen fermentation in vitro. Y. Wang*[1,2], J. Wang[1], M. Vazquez-Anon[2], H. Cao[2], G. Zanton[2], and J. Liu[1], *[1]Institute of Dairy Science, Zhejiang University, Hangzhou, P. R. China, [2]Novus International Inc., St. Louis, MO.*

The objective of the study was to evaluate the effect of a dietary antioxidant (AOX; AGRADO® Plus, Novus International) on rumen fermentation with different dietary ingredients as substrate in vitro, in the absence or presence of 500 mg/kg AOX. Data were analyzed as a completely randomized design using the MIXED procedure. Neither substrate nor AOX had significant effect on rumen pH. Inclusion of different substrates significantly affected gas production, organic matter digestibility, and total VFA ($P < 0.05$), where corn appeared to have highest values, while cotton seed had lowest ones, compared with extruded soybean and DDGS. Extruded soybean had higher NH_3-N than corn ($P < 0.05$), and cottonseed and DDGS were intermediate in NH_3-N levels. AOX had no significant effect on gas production, organic matter digestibility, NH_3-N, or total VFA production. However, addition of AOX significantly increased the molar proportion of propionate ($P < 0.05$), and tended to decrease the molar proportion of acetate ($P = 0.10$). Different substrates had similar anti-oxidative status in the rumen ($P > 0.05$). AOX significantly increased the total antioxidant capacity ($P < 0.01$), but did not change other antioxidant biomarkers (superoxide dismutase, malondialdehyde, glutathione peroxidase, and hydrogen peroxide). Except for *Fibrobacter succinogenes*, the population of *Ruminococcus flavefaciens*, *Ruminococcus albus*, fungi, protozoa and *Butyrivibrio fibrisolvens* were significantly affected by substrate treatment ($P < 0.01$). Addition of AOX increased *Ruminococcus albus* population ($P < 0.05$). There was no significant interaction between substrate and AOX for fermentation patterns, oxidative status or rumen microflora. It is concluded that different substrates significantly affected the fermentation pattern and microflora, but not for anti-oxidative status in the rumen. Addition of AOX improved the total anti-oxidative status, increased the molar proportion of propionate and *Ruminococcus albus* population, regardless of substrate type.

Key words: antioxidant, anti-oxidative status, rumen fermentation

T366 Effect of dietary roughage and sulfur concentration on hydrogen sulfide production from corn-based diets containing dried distillers grains. E. Seitz*, A. Carpenter, M. Ruiz-Moreno, M. D. Stern, and G. I. Crawford, *University of Minnesota, St. Paul.*

An in vitro rumen fluid incubation was conducted using differing dietary concentrations of roughage (R) and sulfur (S) in a 3 × 2 + 2 factorial arrangement of treatments during 4 consecutive 24-h periods. Isonitrogenous dietary treatments included a corn-based control diet with no distillers grains (DG), 9% R, and 0.18% S (CON); a high R treatment with 27% R, 40% DG and 0.50% S (HRHS), and 6 treatments arranged in a 3 × 2 factorial with 3 S concentrations (0.3, 0.4, and 0.5%; LS, MS, HS, respectively), and 2 R concentrations (3 and 9%; LR and MR, respectively). Grass hay served as the roughage source and S concentrations were achieved through combination of 2 DG with differing S concentrations. Rumen fluid adapted to each treatment was mixed with saliva in a 1:1 ratio (10 mL each) and incubated with 0.2 g substrate DM in crimp-sealed, 50 mL serum bottles (n = 24; 3 reps/trt) at 39°C. At 5 and 24-h post-incubation, gas production was measured and a subsample of headspace gas was analyzed for hydrogen sulfide (H_2S). Final pH was measured at the end of each 24-h incubation. These results indicate that DG inclusion generally increased

batch culture pH, and compared with CON, the MS and HS treatments had higher total μg H_2S and μg H_2S/mL gas.

Table 1. Effect of dietary roughage and sulfur concentration

Parameter	CON	LRLS	LRMS	LRHS	MRLS	MRMS	MRHS	HRHS	*P*-value
Final pH	5.44[a]	5.55[ab]	5.65[be]	5.62[bc]	5.67[ce]	5.66[be]	5.81[d]	5.95[f]	<0.0001
Total H_2S (μg)	28.3[a]	51.1[ad]	81.9[bd]	77.9[bd]	57.2[acd]	89.4[bd]	113.3[b]	93.1[bc]	0.01
Total gas (mL)	38.9[a]	35.9[bd]	35.0[bc]	37.8[ad]	35.8[bd]	37.1[acd]	37.0[acd]	33.4[b]	0.01
μg H_2S/mL gas	0.7[a]	1.4[ac]	2.3[bc]	2.1[bc]	1.6[ac]	2.4[bc]	3.0[b]	2.8[b]	0.005
NH_3-N (mg/100 mL)	4.2	3.9	3.8	5.1	3.8	4.5	4.7	5.1	0.52

[abcdef]Means in the same row with uncommon superscripts differ ($P < 0.05$).

Key words: hydrogen sulfide, in vitro, rumen

T367 Effects of hops on rumen fermentation and bacterial populations using the rumen simulation technique. N. Narvaez*[1], Y. Wang[1], Z. Xu[1], T. Alexander[1], S. Garden[2], and T. McAllister[1], *[1]Agriculture and Agri-Food Canada, Lethbridge, Alberta, Canada, [2]John I. Haas Inc., Washington DC.*

A rumen simulation technique (Rusitec) experiment was conducted to assess the effects of supplementation of 3 varieties of hops on rumen fermentation and rumen bacterial communities. The treatments were Control (no hops) and 3 hop varieties (Cascade, CAS; Millenium, MIL and Teamaker, TM). Two RUSITEC with 8 vessels each were used. Each vessel was initially inoculated with rumen solids and liquids from cattle fed a barley silage-barley grain diet and fermenters were fed 10 g of a barley silage-barley grain diet daily. Hops extract (800 μg/mL) was added so as to have 2 replicate fermenters per variety. Microbial protein synthesis (MN) was estimated using ^{15}N labeled ammonium sulfate and principal ruminal bacteria were quantified using real-time polymerase chain reaction (qPCR). Addition of all hop varieties reduced ($P < 0.001$) total gas and CH_4 production per g of truly digested dry matter (TDDM). True DM disappearance was reduced ($P < 0.05$) by CAS and MIL but only MIL reduced ($P < 0.001$) neutral detergent fiber disappearance (NDFD). Productions of volatile fatty acids (VFA) and MN were unaffected by hops, but the acetate:propionate (A:P) ratio was decreased ($P < 0.001$) with all hop varieties. Proportions of 16S rDNA gene of *F. succinogenes* and *S. bovis* were decreased ($P < 0.05$) with addition of MIL and TM whereas *S. bryantii* was increased ($P < 0.001$) by CAS. The proportion of *Archae* marker gene in solid fraction was also reduced ($P < 0.05$) by all 3 hops. The decreased methane production by hops is likely due to their effects on altering rumen microbial community by reducing methanogens and cellulolytic bacteria and reducing A:P ratio of the VFA. Inclusion of hops in ruminant diet may have potential to reduce methane production and thereby improve feed efficiency.

Key words: hops, rumen bacteria, rumen fermentation

T368 Effect of nitrate, sulfate, monensin, and corn gluten feed on in vitro ruminal methane production. C. Davis[1], S. Ghimire*[1], T. Wiles[1], Z. Wen[2], M. A. McCann[3], and M. D. Hanigan[1], *[1]Department of Dairy Science, Virginia Polytechnic Institute and State University, Blacksburg, [2]Department of Biological Systems Engineering, Virginia Polytechnic Institute and State University, Blacksburg, [3]Department of Animal and Poultry Sciences, Virginia Polytechnic Institute and State University, Blacksburg.*

Two in vitro studies were conducted using hay and total mixed dairy ration (TMR) as substrates to evaluate the effect of nitrate and Monensin on methane production. Study 1 was conducted to compare the effectiveness of different doses of nitrate and Monensin on methane production, and study 2 tested the effects nitrate, sulfate, and corn gluten feed (CGF). Four levels of nitrate (0, 2.5, 5, and 7.5% of DM) and 2 doses of Monensin (0, and 4 mM) were tested for each diet in study 1. Two doses of nitrate, 2 doses of sulfate (0 or 4% of DM each), and the absence or presence of CGF in the diet (22% of DM) were tested in study 2. In study 1, nitrate was added without lowering the TMR protein level. Treatments were isonitrogenous in study 2. Each study was replicated 3 times and contained one bottle for each treatment to measure methane production and a second bottle to measure total gas production. Bottles were inoculated with 20 mL of strained rumen fluid plus 60 mL of McDougall's buffer. Ruminal fluid was collected from 2 nonlactating, Holstein cows, one on hay and the other on a lactating cow ration. Hay substrate was used for the hay diets and TMR for the TMR diets. Bottles were incubated for 48 h at 39°C. Total gas production was measured at different time intervals after incubation by water displacement and methane production was measured by displacement after removal of CO2 using sodium hydroxide. Cumulative methane production was greater ($P < 0.05$) for the TMR diet. Monensin, sulfate, and CGF did not have significant effects on methane production ($P > 0.05$). Nitrate reduced methane production in both studies. In study 1, the reduction as compared with the controls was 16.92%, 28.03%, and 30.43% for hay and 29.41%, 35.95% and 41.53% for TMR at concentrations of 2.5, 5, and 7.5% of DM, respectively. In study 2, nitrate reduced methane production by 25.74% for hay and 13.23% for TMR. Total gas production was reduced when nitrate was present ($P < 0.05$) in study 1, but the reduction was not significant in study 2. These results suggest that nitrate can be used as a strategy to reduce methane production in cattle.

Key words: dairy cow, ruminal methane, nitrate

T369 Effects of microwave irradiation on ruminal dry matter degradability of canola and corn gluten meal. M. Dehghan-Banadaky[1], H. Khalilvandi-Behroozyar*[1,2], H. R. Khazanehi[3], and N. Vahdani[1], *[1]Department of Animal Science, University of Tehran, Karaj, Tehran, Iran, [2]Department of Animal Science, University of Urmia, Urmia, West Azerbaijan, Iran, [3]Department of Animal Science, University of Manitoba, Manitoba, Canada.*

Microwave energy causes a rise in the temperature within a penetrated medium as a result of rapid changes of the electromagnetic field. This study was conducted to evaluate effects of 900 W microwave irradiation for 4 and 6 min on dry matter degradability of canola and corn gluten meals (CGM) using nylon bag technique. The DM of meals was determined by oven drying of a 1 g sample in triplicate. Based upon this value, sufficient water was added to increase the moisture content of 2 kg of canola meal to 250 g/kg. Two samples (each of 500 g) were subjected to microwave irradiation at a power of 900 W for 4 and 6 min. Dry matter degradability was determined using 3 ruminally fistulated non lactating Holstein cows, fed balanced rations with forage:concentrate ratio of 60:40. Samples were ground to pass 2 mm screen and 5 g was weighted into nylon bags with 50 micron pore size (sample size:surface area was 12.5 mg/cm^2). Duplicates were

incubated for 2,4,8,12,24 and 48 in ventral rumen. Effective degradability (ED) was calculated with NEWAY computer package. CRD design, GLM PROC of SAS 9.1 and Duncan test option was used for data analysis. In the case of canola meal results (Table 1) showed that microwave irradiation decreased rapidly degradable fraction and increased lag time ($P \leq 0.05$). Also, a trend ($P \leq 0.08$) was observed for increasing of potentially degradable fraction and reduction of the rate of degradation of b fraction with irradiation. Increasing the irradiation time, decreased effective degradability of dry matter ($P \leq 0.08$). Microwave irradiation resulted in statistically significant ($P \leq 0.05$) increase in DM ED of CGM in rumen outflow rates of 0.05 and 0.08 h^{-1}. Although treatments were resulted in increased b and reduction of a fraction ($P \leq 0.1$), degradation rate of b fraction also increased ($P \leq 0.12$). Previous reports about heat treatment of CGM revealed that ruminal effective degradability decreased with heat treatment, but our results showed increased DM degradability with irradiation. Further studies about effects of microwave irradiation on ruminal nutrient degradability of CGM, recommended.

Table 1. Rumen DM degradation parameters of untreated and microwave irradiated canola meal

	Control	4 min	6 min	SEM
a (percentage)	27.73[a]	26.59[b]	24.81[c]	0.048
b (percentage)	60.00	61.33	62.40	0.511
c (h^{-1})	0.12	0.11	0.09	0.004
Lag time (h)	1.10[b]	1.68[a]	1.70[a]	0.085
ED (percentage, K = 0.02)	77.37	76.67	74.27	0.559
ED (percentage, K = 0.05)	66.60	65.33	61.97	0.999
ED (percentage, K = 0.08)	59.17	57.63	54.07	1.145

Means within each row with different superscripts are significantly different ($P \leq 0.05$).

Key words: microwave irradiation, protein concentrate, dm degradability

T370 Evaluation of two protein hydrolyzates as a source of soluble protein to foster ruminal microbial growth. A. Aris[1], A. Serrano[1], F. Fabregas[1], J. Polo[3], C. Rodriguez[3], and A. Bach*[1,2], *[1]Ruminant Production, Institut de Recerca i Tecnologia Agroalimentàries (IRTA), Caldes de Montbui, Barcelona, Spain, [2]Institució Catalana de Recerca i Estudis Avançats (ICREA), Barcelona, Spain, [3]APC EUROPE, S.A. R&D department, Granollers, Barcelona, Spain.*

The aim of this study was to determine whether the protein hydrolyzates AproCel and Pepton (APC Europe, Barcelona, Spain) would stimulate rumen microbial growth in comparison to Tryptone, which is the gold-standard of supplementary N for microbes. Ruminal samples from 3 different animals were incubated for 12 h following the Tilley-Terry procedure. There were 4 treatments applied to the ruminal samples: Negative control (CTR), with no N supplement added, positive control Tryptone added at the rate of 2% (TRY) and Pepton (PEP) and AproCel (APR) added at a rate (2.10 and 2.24%, respectively) providing the same amount of N as Tryptone 2%. After incubation, a liquid sample was obtained to determine total volatile fatty acids (VFA) concentrations, pH, and microbial growth (determined by quantitative real time PCR). Data were analyzed with an ANOVA using the treatment as the main effect. Total VFA production was numerically greater in all tubes with N supplementation in comparison to CTR (56.3mM ± 12.24), with this difference being significant ($P < 0.05$) for APR (100.7mM ± 12.24) and Tryptone (128.9mM ± 12.24). Pepton supplementation resulted in an intermediate VFA concentration. Ruminal fluid experienced in all cases a slight increase in pH compared with CTR (6.96 ± 0.03). Pepton (7.20 ± 0.03) showed the greatest increase of pH ($P < 0.05$). The increase in pH indicates that microorganisms used part of the N supplements as a source of energy leading to an excretion of NH_3. Probably the production of NH_3 was lowest with PEP, because this treatment resulted numerically in the least VFA production among the 3 protein supplements, and thus pH would be expected to be greater even in the absence of NH_3. Gram-positive bacteria grew equally among the 3 treatments, whereas gram-negative growth was highly stimulated ($P < 0.05$) by PEP (PEP: 4.52 ± 0.6 ratio to control vs CTR: 1.92 ± 0.6 ratio to control). In conclusion, both APR and PEP, are readily available N sources for microbial protein synthesis. In addition, PEP stimulates growth of gram-negative bacteria to a greater extent than TRY and APR.

Key words: microbial growth, protein hydrolyzate, supplementary nitrogen

T371 Effects of protein protection with orthophosphoric or malic acid and heat in lamb fattening diets. F. Díaz-Royón*, J. M. Arroyo, M. R. Alvir, V. Jimeno, S. Sanchez, and J. González, *University of Politécnica de Madrid, Madrid Spain.*

The objective of this study was to evaluate the efficiency of using acid-heat treated (121°C, 1 h, plus residual oven heat) sunflower and pea meals on diets fed to fattening lambs. Ninety "Entrefino" cross male lambs from three commercial farms (average initial body weight = 14.6; 15.3, and 13.3 kg) were randomly assigned to five diets with different levels of protein and acid treatment, and fattened to an average body weight at slaughter of 25 kg. The control diet (C; CP =18%) contained conventional soybean, sunflower and pea meals. In three of the treatment diets, orthophosphoric acid-protected meals (TM) replaced conventional sunflower and pea meals (CF; CP=18%) and soybean meal was progressively remove (SMF; CP=16.7% and STF; CP= 15.6%). In the last diet (SMM; CP= 16.7%) malic acid substituted ortophosphoric acid. Wheat straw (roughage source) and concentrate were offered. Eighteen lambs, 3 animals per pen, allocated to 6 pens, were assigned to each diet. Data were analyzed using a factorial analysis with initial body weight as covariate and farm of origin as block. Treatments were compared through the following contrasts: C. vs. CF, SMF, STF; CF vs. SMF, STF; SMF vs. STF; C. vs. SMM; SMF vs. SMM). Average daily gain (ADG), carcass yield (CY), dorsal fat (DF) and kidney pelvic fat (RPF) were analyzed by animal. Intake and feed conversion (FC), were analyzed by pen. There was no diet effect on any parameter observed which suggests that when protected proteins are used, it is possible to work with 15.6% CP (DM basis) reducing the need to include vegetable protein meals. Lambs on SMM had higher ADG (15.2%; P= 0.042), and better CY (1.3%; P= 0.037) than on SMF. Improved efficiency can be attributed to greater protection by malic acid (Arroyo, 2007) or a higher propionic acid production as result of a shift in rumen fermentation in response to malic acid inclusion.

Key words: acid-heat treatment, fattening lamb, protein protection

T372 Identification of several novel fungal species in feed samples from the southeast United States. J. D. Chapman*[2], Y. Q. Wang[1], and N. E. Forsberg[1], *[1]OmniGen Research, Corvallis, OR, [2]Prince Agri Products, Quincy, IL.*

Fungi grow freely on preserved feeds. Concerns about the presence of fungi include their production of mycotoxins, their invasive (mycotic)

potential and their metabolism of nutrients. Despite years of work in this area, the full spectrum of fungi which grow on silages and the implications of their growth have not been fully established. The goal of this study was to identify unknown fungi found growing on a balage sample in Georgia and on a corn silage sample in Florida. Samples of fungi-contaminated feeds were recovered and inoculated onto Sabouraud culture plates. Pure cultures were selected from the plates and DNA extracted from each. The ITS-1 domain was amplified by polymerase chain reaction (PCR) using pan-fungal primer sequences. PCR products were electrophoresed on agarose and the fragments corresponding to the ITS-1 fragment were excised, purified then sequenced. Four fungi were identified of which 3 were relatively unknown. The 4 included *Aspergillus clavatus* (a dark green-black fungus), *Coccidioides immitis* (a pale blue fungus), *Gibberella zeae* (also known as *Fusarium graminearum*; a red fungus), and *Neosartorya fischeri* (a white fungus). Based on the published abilities of these species to secrete mycotoxins and/or to cause invasive mycosis, each holds potential to adversely affect animal health. *A. clavatus* secretes a broad spectrum of mycotoxins including alanyltryptophan, cytochalasin E, kotanin, nortryptoquivaline, and patulin. *C. immitis* is a Level-III pathogenic fungus, resides principally in the Southern US and is responsible for Valley Fever. Reports of mammary *C. immitis* infections in dairy cattle exist. *G. zeae* secretes a variety of mycotoxins including deoxynivalenol, an important immunosuppressive toxin. Finally, *N. fischeri* secretes aflatoxin, fumetrimorgans and verrucologen. *C. immitis* has been reported to cause spasms and cramps in sheep and swine. Collectively, these observations further demonstrate the potential for adverse effects from feeding spoiled silages. Additional studies are needed to identify the specific effects of ingestion or inhalation of these and other feed-borne fungi.

Key words: dairy, fungi, silage

T373 Evaluating the inclusion of Met and Lys to mechanically extracted soybean meal with soy gums on the ruminally-undegraded Met and Lys content. C. A. Macgregor*[1], L. O. Tedeschi[2], and T. K. Miller-Webster[3], *[1]Grain States Soya Inc., West Point, NE, [2]Texas A&M University, College Station, [3]West Virginia University, Morgantown.*

Mechanically-extracted soybean meal (MES) with fresh soy gums (MESG) was compared with MESG with added dl-Methionine and Lysine (MESG-ML) to evaluate the impact of the added Met and Lys on the ruminally-undegraded Met (RUM) and Lys (RUL) using the in situ technique. Dacron bags containing the treatments (TRT), MESG or MESG-ML, were incubated in the rumen of 3 lactating cows for either 4 or 8 h (6 bags/cow/TRT/time) using the simultaneous removal method. Cows were 12, 45, and 222 DIM and milk production was 35.8, 41.3, and 24.4 kg/d, respectively. Met and Lys in the MESG-ML were added to soy gums simultaneously by means of 2 variable augers and mixed into the soy gums in an in-line mixer before soy gums were applied onto the MES at time of manufacture. Met content of MESG and MESG-ML was 0.65 and 0.70% DM and Lys content of MESG and MESG-ML was 2.67 and 2.72% DM, respectively. The RUM and RUL remaining in the Dacron bags at 4 and 8 h were reported as percent of the original sample DM. The statistical analysis was performed as a factorial arrangement (2 TRT × 2 incubation times) in a complete randomized block design, assuming cows as random factors. For Lys, there was no interaction between TRT (MESG vs. MESG-ML) and incubation time ($P = 0.7824$; 2.106 vs. 2.185% at 4 h and 1.707 vs. 1.805% at 8 h, respectively). As expected, the RUL was greater at 4 than at 8 h ($P < 0.0001$; 2.15 vs. 1.76%, respectively). The MESG-ML had a significantly greater RUL than MESG ($P = 0.0145$; 2.0 vs. 1.91%). Similarly, there was no interaction between TRT (MESG vs MESG-ML) and incubation time for Met ($P = 0.7834$; 0.536 vs 0.578% at 4 h and 0.445 vs 0.491% at 8 h, respectively), the RUM at 4 h was greater than at 8 h ($P < 0.0001$; 0.557 vs 0.468%, respectively), and treated MESG with dl-Methionine had greater RUM than control MESG ($P < 0.0001$; 0.534 vs 0.491%, respectively). Our analyses indicated that enriching MESG with dl-Methionine and Lysine using the method described above can increase the content of these 2 amino acids in the ruminally-undegraded protein pool.

Key words: amino acid, gums, soybean meal

T374 Effect of ghrelin on bovine myogenic differentiation. D. Montoya-Flores*[1,2], O. Mora[1], E. Tamariz[1], L. González-Dávalos[1], A. González-Gallardo[1], A. Antaramian[1], A. Shimada[1], A. Varela-Echavarría[1], and J. L. Romano-Muñoz[2], *[1]Universidad Nacional Autónoma de México, Querétaro, Querétaro, México, [2]Instituto Nacional de Investigaciones Forestales, Agrícolas y Pecuarias, Colón, Querétaro, México.*

Ghrelin is an acylated hormone, reported to influence food intake, energy metabolism, and reproduction, among others. Ghrelin may also stimulate proliferating myoblast cell differentiation and multinucleated myotube fusion. The aim of this work was to study the effect of human ghrelin (hGHRL) and human ghrelin fragment 1–18 (hGHRL1–18) on myoblast differentiation, measuring the effect of different concentrations on myogenic differentiation by analyzing myogenin expression at the mRNA and protein level. Two types of cells were tested, the cell line i28 obtained from mouse skeletal muscle and primary cultures of bovine myoblasts. Ghrelin and its N-terminal fragment hGHRL1–18 were used at concentrations of 0, 0.01, 0.1, 1, 10, and 100 nM. Treatments were applied to pre-confluent cultures and were maintained during 4 d. Myogenic differentiation of i28 cells was positively affected by hGHRL and hGRHL1–18, starting at a concentration of 0.1 nM ($P < 0.01$). On the other hand, only concentrations of 10 and 100 nM of hGHRL stimulated bovine myoblast differentiation. These results could be attributed to the presence of the mRNA for GHS-R1a and CD36 receptors, in both i28 cells and in bovine myoblasts. Hence, hGHRL might be useful in beef cattle production by promoting muscle differentiation.

Key words: ghrelin, bovine, myogenic differentiation

T375 Essential oil and rumensin affect ruminal fermentation in continuous culture. D. Ye*[1], S. K. R. Karnati[1], J. L. Firkins[1], M. L. Eastridge[1], and J. M. Aldrich[2], *[1]Ohio State University, Columbus, [2]Provimi-North America, Lewisburg, OH.*

The combination of Rumensin and essential oil could be beneficial for ruminal fermentation by suppressing protozoa and their associated methanogens, while maintaining normal rumen function. The objective of this study was to determine the effects of feeding Rumensin and Cinnagar (essential oil from cinnamon and garlic) in diets on ruminal fermentation characteristics. Four continuous culture fermenters were modified to retain protozoa (slower stirring and a special filter apparatus) and maintained at a liquid dilution rate of 7%/h and solids dilution rate of 5%/h in 4 periods of 10 d each (7 d of adaptation) in a 4 × 4 Latin square design. Four dietary treatments (fed in one meal per day) were arranged in a 2 × 2 factorial: (1) Control diet, 40 g of a 50:50 concentrate: forage (ground alfalfa hay) diet (40% NDF, 17% CP) containing no additive; (2) Rumensin at 11 g/909 kg of DM; (3) Cin-

nagar at 0.0043% (DM basis); and (4) combination of Rumensin and Cinnagar. There were no effects ($P \geq 0.36$) of treatment on concentrations of NH3-N or total VFA. Rumensin (main effect, no interaction) decreased ($P < 0.05$) molar percentages of acetate (62.6 vs. 64.4%) and valerate (1.78 vs. 1.86%); decreased acetate: propionate ratio (2.69 vs. 3.04) but increased ($P < 0.05$) propionate (23.3 vs. 21.3%) and isovalerate (1.94 vs. 1.67%). Rumensin increased ($P < 0.05$) the protozoa generation time (27.6 vs 21.6 h). Cinnagar tended ($P = 0.11$) to increase isovalerate (1.77 vs. 1.67%) and decrease the protozoa counts (14.9 vs. 18.5 × 10^3/mL). Rumensin and Cinnagar tended ($P = 0.06$) to interact for methane production (29.0, 22.4, 22.0, and 36.9 mmol/d, respectively). Under the conditions of our study, we did not detect an additive response for Rumensin and Cinnagar to decrease protozoal counts or methane production.

Key words: Rumensin, essential oil, continuous culture

T376 Energy value of co-products of bioethanol production: comparison between triticale grain and triticale DDGS. B. Liu and P. Yu*, *University of Saskatchewan, Saskatoon, Canada.*

The objectives of this study was to compare triticale grain and triticale DDGS on total digestible component nutrient and energy values, estimated using the NRC-2001 summary approach. The triticale grain and triticale DDGS samples were obtained from 3 years. The results showed that triticale DDGS had lower ($P < 0.05$) tdNFC (29.5 vs. 70.1%DM) and higher ($P < 0.05$) tdNDF (12.0 vs. 6.9%DM), tdCP (30.0 vs. 13.3%DM) and tdFA (5.5 vs. 0.5%DM). Triticale DDGS was also lower ($P < 0.05$) in TDN (76.9 vs. 84.5% DM). However there were no significant differences ($P > 0.05$) in DE1X, DE3X (3.34 in triticale DDGS vs. 3.42 Mcal/kg DM in triticale grain), ME3X (2.94 in triticale DDGS vs. 3.01 Mcal/kg DM in triticale grain), NEL3X (1.89 in triticale DDGS vs. 1.92 Mcal/kg DM in triticale grain) for dairy and NEm (2.99 in triticale DDGS vs. 3.06 Mcal/kg DM in triticale grain) and NEg (1.36 in triticale DDGS vs. 1.41 Mcal/kg DM in triticale grain) for beef cattle. The results suggested triticale DDGS as an alternative to triticale grain in dairy and beef diets.

Key words: bioethanol co-products, energy values, triticale dried distillers grains with solubles

T377 Molecular spectral features of functional groups mainly associated with lipid biopolymer in co-products (DDGS) from bioethanol production. P. Yu* and D. Damiran, *University of Saskatchewan, Saskatoon, Canada.*

To date, there is no study on bioethanol processing-induced changes in molecular structural profiles of lipid biopolymer in DDGS products. The objectives of this study were to (1) determine structural changes that were mainly associated with lipid biopolymer in the co-products that occurred on a molecular level during bioethanol proceesing; (2) quantify the asymmetric and symmetric CH3 and CH2 functional groups, carbonyl ester group and lipid unsaturated groups spectral intensities as well as their ratios, and (3) illustrate the multivariate analyses as a research tool for rapid characterization of biopolymer molecular structures in complex a plant-based feed system. The hypothesis of this study was that bioethanol processing changed the molecular structure profiles in the co-products as opposed to original cereal grains. These changes are highly related to lipid nutrient utilization in animals. The results showed that bioethanol processing had significant effects ($P < 0.05$) on the functional groups spectral profiles which are mainly related to lipid molecular structure in the co-products. The bioethanol processing decreased ($P < 0.05$) the CH3-(a)symmetric to CH2-(a)symmetric ratio, changed ($P < 0.05$) the spectral features of carbonyl C = O ester group and lipid unsaturated group. The results indicated that bioethanol processing changed lipid biopolymer structural conformation and the different types of cereal grains had different sensitivity to the bioethanol processing. The spectral profiles were different between their co-products (wheat DDGS vs. corn DDGS). Different bioethanol plants had different impact on the spectral profiles. The multivariate analyses distinguished the structural differences between the wheat and wheat DDGS and between the corn and corn DDGS. Further study is needed to quantify lipid molecular structural changes in relation to lipid nutrient utilization.

Key words: co-products from bioethanol processing, lipid conformation and nutrient availability, molecular structures

T378 Sheep performance on sorghum or sorghum-soybean silage diets. A. A. Melin[1] and H. M. Arelovich*[2], *[1]Coronel Suárez-Pasman Experimental Station, [2]Departamento de Agronomía-CIC-CERZOS.*

Silages of different species are extensively used in Argentina in a variety of dietary programs. Sorghum (Sor) crop is well adapted to environmental constraints of semiarid areas; however Sor silage is usually low quality. A mixed crop of Sor with Soybean (Soy) is expected to improve silage voluntary DM and protein intake. An assay was conducted to evaluate silage quality and sheep performance when receiving either of 4 silage diets: (1) Grain Sor (GS), (2) Sweet Sor (SS), (3) GS-Soy (85 to 15%) and (4) SS-Soy (85 to 15%). Pure or mixed crops were harvested and processed to a 20–25 mm particle size of green material, to be packed and sealed in 220-kg capacity plastic containers. Twenty Corriedale wethers (51.4 kg IBW) were randomly allocated to individual metabolism stalls. Following a 7-d adaptation period, silages were fed ad libitum on a daily basis previous collection of rejected material at 9 a.m. Feces were collected daily between 11 and 12 a.m. Offered and rejected materials were daily sampled and pooled. Samples were dried at 60°C, ground with a Wiley mill (1 mm) and saved for lab analyses. Diet quality, Daily DM intake (DMI), in vivo DM digestibility (DMD), digestible DMI (DDMI) and Total Protein Intake (TPI) data were analyzed by ANOVA as complete randomized design. Average silage pH was 3.9. Sor type has not affected silage quality, but Soy inclusion improved CP content. Average DMD increased 11% with Soy silages, with a trend for higher DDMI. Higher energy and CP consumption could be achieved by intercropping a minor proportion of Soy in Sor crops for silage.

Table 1.

Item	GS	SS	GS-Soy	SS-Soy	*P* =	CV, %
Diet, %						
DM	25.3	25.1	25.7	25.6	0.894	4.5
CP	5.1[a]	6.5[a]	8.7[b]	8.5[b]	0.0003	6.6
NDF	57.5	58.9	56.7	57.9	0.757	4.6
ADF	32.3	32.3	33.1	34.1	0.503	4.9
Performance						
DMI, g/d	470	459	612	594	0.449	30.5
DMD, %	55.4[a]	57.7[ab]	64.1[b]	63.0[b]	0.041	6.8
DDMI, g/d	262	265	391	374	0.148	28.4
TPI, g/d	30.5[a]	23.5[a]	52.2[b]	51.6[b]	0.008	27.3

DMI= offered DM – rejected DM; DMD= [(DM intake – Fecal output)/ DM intake]; DDMI= DMI*(DMD/100); TPI= DMI*(CP/100).

[ab]Values in the same row differ ($P < 0.05$).

Key words: silage, sorghum, soybean

T379 The effect of sulfuric acid on in vitro gas production parameters of sugarcane top in Arabian sheep. S. Mahmoudi, M. Chaji*, M. Eslami, T. Mohammadabadi, and M. Bojarpour, *khuzestan Ramin Agricultural and Natural Resources University, Molassani, Khuzestan, Iran.*

The objective of this study was to investigate the effect of sulfuric acid (H2SO4) on chemical composition and in vitro gas production of sugarcane top (SCT) by Arabian sheep of Iran. Sugarcane top ensiled with different levels of sulfuric acid (0.9 and 1.8% acid) in laboratory silos for 45 d. Rumen fluid was supplied from 2 fistulated sheep were fed a 40:60 concentrate: forage, and the samples were incubated with 35 mL buffered rumen fluid in 100 mL glass syringes, for 2, 4, 6, 8, 10, 12, 16, 24, 48, 72 and 96 h, at 39°C. Cumulative gas production data were fitted to the exponential equation. The residues of each syringe were dried and used to calculate the cell wall degradation. The obtained data analyzed as a completely randomized design using the general linear model procedure of SAS. The results indicated that the ensiling SCT with 1.8% sulfuric acid caused to increase cell wall degradation, potential of gas production and rate constant in compared with the other treatments (48%, 140.2 mL and 0.04 mL/h, respectively; $P < 0.05$). The highest degradation and gas production at 24 and 72 h after incubation was for ensiled with 1.8% sulfuric acid (39 and 62 mL, respectively; $P < 0.05$). Therefore, the results of the present study demonstrated that ensiling with sulfuric acid improved in vitro gas production parameters of SCT.

Key words: degradation, sugarcane top, sulfuric acid

T380 The effect of urea, molasses and sulfuric acid on in vitro digestibility of sugarcane top by Arabian sheep. S. Mahmoudi, M. Chaji*, M. Eslami, T. Mohammadabadi, and M. Bojarpour, *Khuzestan Ramin Agricultural and Natural Resources University, Molassani, Khuzestan, Iran.*

The objective of this study was to investigate the effect of urea, molasses and sulfuric acid (H2SO4) on in vitro digestibility of sugarcane top (SCT) by Arabian sheep of Iran. Experimental treatments were including: untreated SCT (SCT), SCT ensiled with 10 g/kg DM urea+30 g/kg DM molasses (SCT1), SCT ensiled with urea+molasses+9 g/kg DM sulfuric acid (SCT2) in laboratory silos for 45 d. In vitro digestibility of dry matter (DM) and natural detergent fiber (NDF) was measured by procedure of Tilley and Terry. Rumen fluid was obtained from 2 Arabian sheep were fed a 40:60 concentrate: forage, then was mixed with McDougall buffer in a ratio 1:4, and incubated at 39°C. After 48 h fermentation, 6 mL of HCL (20%) and 5 mL pepsin solution (pepsin in HCL 0.1 N) 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 disappearance of DM were analyzed as a completely randomized design using the general linear model procedure of SAS. The results of this experiment indicated that the SCT2 increased in vitro DM digestibility in compared with the other treatments (44.2, 43.6 and 41.04%, respectively; $P < 0.05$). Sugarcane top ensiled with urea+molasses+sulfuric acid had the highest NDF digestibility (79.77%). Therefore, the results of the present study demonstrated that urea+molasses+ 9 g/kg DM sulfuric acid improved in vitro NDF digestibility value of the SCT.

Key words: sugarcane top, molasses and urea, digestibility

T381 Interactions between nutrient supply and dietary flavors on diet selection by lambs. A. Bach*[1], J. J. Villalba[2], and I. R. Ipharraguerre[3], *[1]ICREA and Ruminant Production-IRTA, Barcelona, Spain, [2]Utah State University, Logan, [3]Lucta, S.A., Barcelona, Spain.*

Thirty-two crossbred lambs (BW = 36.7 ± 4.5 kg) housed in individual pens were used in 3 7-d experiments to investigate 1) the relationship

between protein status of the animals and diet selection based on dietary CP, 2) the interaction between dietary CP and preference for bitter, and 3) the interaction between protein supply and preferences for a caloric and a non-caloric sweetener. In Exp. 1, 16 lambs previously fed a low (LP; 10.9% CP) or a high (HP; 20.4% CP) CP diet for 42 d, received a double choice of the HP and LP diets. In Exp. 2, 16 lambs were offered a double choice of unflavored LP or HP diets or the same diets flavored (0.066%) with a bitter flavor. In Exp. 3, the 16 lambs from Exp. 1 were offered a double choice between an unflavored diet (LP or HP) or the same diet flavored with sucrose (0.2%) or a non-caloric sweetener (0.066%). Data were analyzed using a mixed-effects model with animal within treatment as a random effect, and treatment, time, and their interactions as fixed effects. When offered a choice between HP or LP (Exp. 1), lambs previously fed LP progressively ($P < 0.01$) increased total daily intake, whereas consumption was constant for lambs previously fed HP. On d 1, lambs previously offered HP showed a lesser ($P < 0.05$) preference for LP (23%) than those offered LP (30%), but preference for LP increased to about 50% at d 4, negating thereby differences in consumption between treatments. At the onset of Exp. 2, lambs were unresponsive to flavor; as time elapsed, however, lambs fed LP progressively reduced ($P < 0.05$) preference for the bitter flavor from 53 to 34%. In Exp. 3, lambs previously fed LP diets consumed less ($P < 0.05$) sweetener- than sucrose-supplemented diet, whereas lambs previously offered HP diets consumed more ($P < 0.05$) sweetener- than sucrose-supplemented diet. These results indicate that lambs are able to sense dietary CP content and modulate short-term consumption of flavored feeds based on nutrient requirements.

Key words: diet selection, sheep, flavor

T382 Effect of forage type in the diet on *Ruminococcus flavefaciens*, *Ruminococcus albus* and *Fibrobacter succinogenes* populations in sheep rumen content as determined by real-time PCR.
C. Saro[1,2], M. J. Ranilla*[1,2], and M. D. Carro[1], *[1]Dpto. Producción Animal, Universidad de León, León, Spain, [2]IGM (CSIC–ULE), Finca Marzanas s/n, Grulleros, León, Spain.*

The diet of the host is a major factor influencing the structure and function of ruminal bacterial populations. The objective of this study was to use real-time PCR to quantify the relative abundance of *Ruminococcus flavefaciens*, *Ruminococcus albus* and *Fibrobacter succinogenes* in the solid phase of the rumen of sheep fed 2 different diets. The diets had 70:30 forage:concentrate ratio and contained either alfalfa hay (AL) or grass hay (GR) as forage. Four rumen-fistulated sheep were fed the 2 diets in a crossover design. Rumen content samples (500 g) were collected before and 4 and 8 h after the morning feeding on 2 non-consecutive days, and strained through 2 layers of cheesecloth, and the solid content was thoroughly mixed before sampling. About 20 g of solid content were placed in sterile containers, and stored frozen at −80°C until DNA extraction. DNA was extracted from the samples using QIAamp DNA stool mini kit (Qiagen, Valencia, Spain) and hexadecyltrimethylammonium bromide (CTAB). Concentrations of *R. flavefaciens*, *R. albus* and *F. succinogenes* rDNA were measured by real-time PCR relative to total bacteria amplification. Validated primers specific for genes encoding 16S ribosomal DNA were used, and data were analyzed using repeated measures ANOVA. Relative abundance of *F. succinogenes* was greater ($P < 0.001$) for GR compared with AL, but no differences between diets were detected for *R. flavefaciens* ($P = 0.11$) and *R. albus* ($P = 0.56$). Post-feeding evolution of the 3 cellulolytic bacteria was similar for both diets. At 4 h after feeding the populations were greater ($P < 0.001$) than at 0 h, but they recovered initial values at 8 h post-feeding. The greater values observed at 4 h may be due to the attachment of new bacteria from the liquid phase or other particles and/or to bacteria proliferation on feed particles. *F. succinogenes* was the most predominant of the 3 species at all sampling times, and the only one influenced by forage type, which indicate the ecological and functional significance of this species in sheep receiving forage diets.

Key words: real-time PCR, ruminal cellulolytic bacteria, sheep

T383 The effect of replacing corn bran with water-soaked neem fruit on nutritive value and in vitro gas production characteristics of West African Dwarf sheep.
M. K. Adewumi*, *Department of Animal Science, University of Ibadan, Ibadan, Nigeria.*

Six male West African Dwarf (WAD) sheep (15.6 kg) divided into 2 groups were used in a complete randomized design to evaluate the effect of replacing corn bran with water-soaked neem (*Azadirachta indica*) fruit in a supplementary diet on nutritive value and nitrogen balance. Experimental treatments were (i) control containing 80:10:10 of cassava peels, fullfat soybean and corn bran and (ii) a test diet where corn bran was replaced with the water-soaked neem fruit (w/w). The animals were offered *Panicum maximum* hay ad libitum .The duration of the experiment was 21 d consisting of a 15-d adaptation phase and 7-d data collection phase. Ruminal fluids obtained from the 2 groups of animals were used in an in vitro gas production study to determine gas production characteristics of a standard maize substrate. Gas production was recorded after 24 h of fermentation. Apparent digestibility (g/100 g DM) of DM (56.60 vs. 57.80), CP (32.50 vs. 31.40), ether extract (56.00 vs 49.00) and ADF (63.00 vs. 41.50) were greater ($P < 0.05$) for the control. However, while N intake (g/d) (6.36 vs. 6.38) was similar ($P > 0.05$), nitrogen balance (1.66 vs. 1.37) was greater ($P < 0.05$) for the control. Metabolizable energy (MJ/kg DM) (8.27 vs. 8.36), short chain fatty acids (µml) (0.89 vs. 0.91) and organic matter digested (g/100g DM) (55.79 vs. 56.34) obtained from in vitro gas production were not different ($P > 0.05$) for the 2 diets. Replacement of corn bran with the water-soaked neem fruit increased($P < 0.05$) total gas produced(ml) (83.25 vs. 48.57) but reduced ($P < 0.05$) methane production (mL) (13.00 vs. 2.00).These results showed that replacing corn bran with water-soaked neem fruit has the potential to improve nutritive value and reduce energy loss through methane emission.

Key words: gas production characteristics, nutritive value, West African Dwarf sheep

Small Ruminant: Health, Growth, Extension, and Dairy

T384 Selected condensed tannin-containing plant extracts and their effects on *Haemonchus contortus* larvae. K. J. Stutts*, M. J. Thomas, M. M. Beverly, R. A. Lane, and S. F. Kelley, *Sam Houston State University, Huntsville, TX.*

Several studies have been conducted recently to determine if condensed tannins could be used to augment traditional deworming protocols since many plant extracts have exhibited anthelmintic properties in vitro. The objective of this study was to evaluate the effects of varying concentrations of crude plant extracts from selected condensed tannin containing-forages on motility of infective larvae of *H. contortus*. Extracts from sericea lespedeza (SL), white oak (WO), and black locust (BL) were evaluated in vitro for their effect on *H. contortus* motility. Larvae cultured from fecal samples collected from goats were exposed to one of 4 concentrations of plant extract. Extract concentrations were 2.5, 5, 10, and 20 mg/mL for each plant species. Treatment groups were compared with negative (distilled water) and positive controls (0.55 mg/mL albendazole). Motility was evaluated as an inferred measure of larvae morbidity using a 6 s rule. Motility counts were performed at 2, 6, and 12 h post-inoculation. At 2 and 6 h post inoculation, motility was lowest ($P < 0.05$) for the positive control, the 2 highest concentrations of WO, and the highest concentration of BL. At this time, motility was highest ($P < 0.05$) for the negative control and the lowest concentration of SL. At 12 h post inoculation, motility was lowest ($P < 0.05$) for the positive control, the 3 highest concentrations of WO, and the highest concentrations of BL and SL. At this time, motility was highest ($P < 0.05$) for the negative control and the lowest concentration of SL and BL. These results indicate that the 2 highest concentrations of WO and the highest concentration of BL were as effective in decreasing motility of *H. contortus* larvae in vitro as albendazole within 2 h of inoculation. Within 12 h of inoculation, the highest concentration of SL and BL, and the 3 highest concentrations of WO were all as effective in decreasing motility of *H. contortus* larvae in vitro as albendazole. These results indicate that there is potential for development of these plant species as a component of an anthelmintic regimen.

Key words: goats, parasite control, condensed tannins

T385 Effect of subclinical mastitis and stage of lactation on somatic cell count, composition and plasmin activity of goat milk. R. Shangguan[1,2], L. Spicer[2], C. DeWitt[2], J. Wang[1], and S. Zeng*[1], *[1]Langston University, Langston, OK, [2]Oklahoma State University, Stillwater.*

A total of 91 goat milk samples from individual udders of Alpine does during early, middle and late lactations were collected to investigate the impact of subclinical mastitis induced SCC increase on changes in composition and plasmin (PL) activity in milk. Samples were collected and analyzed for fat, protein, lactose, solids non-fat (SNF) and total solids (TS), SCC and PL activity. Within 3 stages of lactation, all milk samples were sorted into 3 groups based on levels of SCC (low $<2.5 \times 10^6$, middle = 2.5 to 5.0×10^6, high $>5.0 \times 10^6$) and statistically analyzed in a 3 × 3 factorial ANOVA. There were no interactions of level of SCC and stage of lactation on variables measured ($P > 0.05$). Log_{10} (SCC) and percentage lactose in milk were negatively correlated ($r = -0.34$, ($P = 0.001$). Fat, protein, SNF, TS and PL were altered by stage of lactation ($P < 0.05$). PL activity was greatest in early lactation. In conclusion, in high SCC milk, lactose content may be more indicative of SCC level than milk fat, protein, SNF, TS and PL activity during lactation. Stage of lactation is an important factor affecting milk composition and PL activity in goats with infection, and thus a necessary parameter in optimizing goat milk quality in conditions of sub-clinical mastitis.

Key words: dairy goat, subclinical mastitis, plasmin activity

T386 Hematological and spermatological evaluations of Honamli goat in Turkey. M. S. Gulay*[1], A. Ata[1], O. Elmaz[1], M. Saatci[1], N. Mamak[1], B. Dag[2], and A. H. Aktas[3], *[1]Mehmet Akif Ersoy University, Faculty of Veterinary Medicine, Burdur, Turkiye, [2]Selcuk University, Faculty of Agriculture, Department of Animal Science, Konya, Turkiye, [3]Bahri Dagtas Uluslararasi Hayvacilik Arastirma Enstitusu, Konya, Turkiye.*

Honamli goat is distributed throughout the mountains of south-west Mediterranean region in Turkey. This breed is an important breed among the goat breeds of Turkey. However there is no information available on their hematological and spermatological characteristics. Thus, packed cell volume (PCV), plasma protein (PP), hemoglobin (Hg), red blood cell (RBC), white blood cell (WBC), mean corpuscular volume (MCV), mean corpuscular hemoglobin (MCH), and mean corpuscular hemoglobin concentrations (MCHC) from the blood samples and ejaculate volume (EJ), motility (MT), dead spermatozoa (DS), abnormal spermatozoa (AS), spermatozoa concentrations (SC) and acrosomal abnormalities (AA) from freshly collected semen were evaluated from Honamli goats. One to 3 year old female goats (n = 35) were randomly selected from the 7 different farms located in different parts of the Mediterranean region. The does used in this study were 205–220 d in lactation and were on free range feeding with no additional supplements as it is traditionally done for this breed. Blood was withdrawn from the jugular vein into vacationer tubes containing EDTA and evaluated the same day. Sperm from 3 bucks were taken from the 3 different farms by artificial vagina (41–44°C) with the presence of females in estrus. The semen collection procedure was repeated weekly during the mating season for 4 total collections. All animals were healthy with no clinically signs of disease. PCV, PP, Hg, RBC, WBC, MCV, MCH, and MCHC were 22.1 ± 0.45%, 7.5 ± 0.17 g/dL, 8.2 ± 0.23 g/dL, $13.0 \pm 0.4 \times 10^6$ /μL, $5.2 \pm 0.17 \times 10^3$ /μL, 17.5 ± 0.47 fL, 6.6 ± 0.28 pg, and 37.6 ± 1.15%, respectively. EV, MT, DS, AS, and SC were 4.0 ± 1.1 mL, 75 ± 10%, 10 ± 4.0%, 10 ± 5.0%, and $3.25 \pm 1.15 \times 10^9$ /mL, respectively. Sperm with acrosomal abnormalities were 1%. Our results indicated that Honamli goats have smaller red blood cells with higher hemoglobin concentrations than other goat breeds. Moreover, spermatologic parameters of Honamli goats were very suitable for goat breeding.

Key words: hematology, spermatologic parameters, honamli goat

T387 Managing seasonal outbreak of foot rot in sheep flocks. T. Wuliji* and C. Clifford-Rathert, *Lincoln University, Jefferson City, MO.*

Foot rot in sheep flocks during hot, humid and rainy season in Midwest region of the US are on the increase. Foot rot is caused by the synergic activity and infection by bacteria *D. nodosus* and *F. necrophorum* species. In field inspection of a small sheep flock (n = 73), showed that 89% of the flock appeared to be suffering from mild to severe foot rot infection on either one, 2, 3 or 4 feet. Feet were examined for

lesions and assessed for the severity. Sick sheep were hoof trimmed and initially treated with KopperTox and "Purple Wound Spray," and re-examined in 2 weeks. Feet lesions were re-scored and the number of effected feet was recorded. The foot rot lesion scores and number of feet treated at the 2 intervals were analyzed for a Chi-squared goodness of fit test. The results showed a significant ($P < 0.05$) increase in the animals scored for 0, 1, 2 and 4 at the second interval from the first, which means there was improvement in alleviation of the symptoms in the lower score level groups while worsen for score level 3 and 4. The number of feet treated also significantly ($P < 0.05$) decreased at the second examination from the first attendance for all groups except 4 feet infection. Foot lesions from 4 lame sheep were swabbed for bacteria culture. Culture results revealed positive test for *F. necrophorum* and possibly *D. nodosus*. Animals with severe lameness were treated with antibiotic spray (3.9% tetracycline) and most of them responded favorably. However, 20 sheep were culled as result of precaution and management requirement. This case study demonstrated the potential foot rot infection, treatment and labor cost, and early culling of valuable animals by the seasonal foot rot outbreaks.

Key words: sheep, foot rot, *Dichelobacter nodosus*

T388 Comparison of nematode parasite-susceptibility and performance of Boer and Spanish goats supplemented with garlic. R. Zhong[1,2], Z. Wang*[1], A. Goetsch[1], S. Hart[1], and T. Sahlu[1], *[1]American Institute for Goat Research, Langston University, Langston, OK, USA, [2]Northeast Institute of Geography and Agroecology, Chinese Academy of Sciences, Changchun, Jilin, China.*

Twenty Boer (B; 2–7 yr of age) and 20 Spanish (S; 4–6 yr of age) does with their single- or twin-kids (1–4 mo of age) were used to compare nematode parasite-susceptibility and performance of the 2 breeds supplemented with garlic. Initially, all does and kids were treated with a combination of Cydectin (0.8 mg/kg BW), Levasole (11.2), and Valbazen (21.6) on 2 consecutive d to clear existing nematode parasites. The goats were kept in a barn for 7 d and fecal samples from the does were checked for fecal egg count (FEC). Then all does and kids were moved to a pasture known to be contaminated with H. contortus. The goats grazed together for 3 wk before being assigned to 2 treatments for a 98-d experiment. Five does (3 B and 2 S, or 2 B and 3 S) with their kids grazed 8 0.4-ha pastures (68% bermudagrass, 32% other grasses and forbs). Treatments were control (C) and garlic (G), with 4 pastures per treatment. Control does received 200 g/d of concentrate (%: corn 54, SBM 26, molasses 13, dical 1.3, limestone 1.3, trace mineralized salt and vitamin mixes 3.4, $MgSO_4$ 0.7), garlic does received the same amount of concentrate plus 20 g/d of G powder. Kids were weaned on d 32 and removed from the experiment. On d 0, 32, 67, and 98, all goats were weighed and fecal and blood samples collected. Means were separated by LSD. Initial mean FEC was 533 (0 - 8,650) and 440 (0 - 2,050) for B and S does, respectively (SEM = 257; $P > 0.05$). The FEC was not different ($P > 0.05$) between breeds or treatments on any day. Likewise, ADG (−8 and −28 g/d vs 4 and −26 g/d, SEM = 8.0), packed cell volume (25 and 24 vs 25 and 26, SEM = 1.6), FAMACHA score (3.5 and 3.5 vs 3.3 and 3.3, SEM = 0.18), and body condition score (2.4 and 2.4 vs 2.4 and 2.4, SEM = 0.07) of does and ADG of kids (109 and 136 g/d vs 115 and 120 g/d, SEM = 11.0) were similar ($P > 0.05$) for B and S regardless of treatment. In conclusion, nematode parasite-susceptibility appears similar in these 2 common meat goats and garlic supplementation has no effect on internal parasitism under these experimental conditions.

Key words: garlic, goats, internal parasitism

T389 Effect of sericea lespedeza *(Lespedeza cuneata)* leaf meal pellets fed to gastrointestinal nematode infected goats. N. C. Whitley*[1], T. H. Terrill[2], J. E. Miller[3], J. M. Burke[4], K. Moulton[1], L. Townsend[5], J. R. Horton[5], J. French[6], A. K. Cooper[1], and D. S. Kommuru[2], *[1]North Carolina A&T State University, Greensboro, [2]Fort Valley State University, Fort Valley, GA, [3]Louisiana State University, Baton Rouge, [4]USDA-ARS, Booneville, AR, [5]NCDA-UMRS, Laurel Springs, NC, [6]NCDA-UPRS, Reidsville, NC.*

Thirty-six female and castrated male Boer crossbred goats were used at 227 ± 0.4 d of age and 24.0 ± 0.2 kg BW to determine the effect of sericea lespedeza leaf meal pellets (SLP) on gastrointestinal nematode (GIN) parasitism. Goats artificially infected with *Haemonchus contortus* were used when fecal egg counts (FEC) were ≥1000 eggs per gram (epg). Goats were individually penned and fed diets similar in available protein containing 0 (control; commercial alfalfa pellets) or 75% SLP with 18 goats/treatment. Animals were allocated to treatment for similar group d –1 FEC, BW and sexes. Pre-weighed rations were fed once daily to allow for 10% orts. Blood samples for packed cell volume (PCV) and fecal samples for FEC (using the Modified McMasters technique) were collected on d 0, 7, 14, 21 and 28 (d 0 = pen placement and first day of treatment). Orts were measured on sampling dates for estimation of intake; BW was measured on d 0. Data were log-transformed and analyzed using the MIXED procedure of SAS but lsmeans are reported. The FEC were influenced by a treatment by d interaction ($P < 0.02$) in which FEC were similar between treatments on d 0 and were lower ($P < 0.03$) for both treatments at all other sampling dates, and were lower ($P < 0.03$) for 75% SLP treated animals than for control on all other days (control: 5326, 4101, 2715, 2198 and 1858 ± 523 epg and SLP: 5272, 1534, 1376, 1181 and 777 ± 483 epg for d 0, 7, 14, 21 and 28, respectively). There was no influence of treatment on PCV, but there was an influence of d ($P < 0.001$) in which PCV for all animals was lowest on d 0 at 27.8 ± 1.14%, increased to 37.0 ± 1.15% by d 14 and decreased again to 30.9 ± 1.14% on d 28. Intake as a percentage of initial BW was not different between treatments at any time point measured ($P > 0.13$). However, intake for 0% SLP was lowest on d 7 than for any other time point and intake for 75% SLP was highest on d 14 than for any other time point measured ($P < 0.002$; treatment by d). Overall, SLP decreased GIN FEC, supporting the concept of using this pelleted forage-based supplement as a component of a small ruminant integrated GIN control program.

Key words: sericea lespedeza, parasites, goats

T390 Influence of type of pasture and transport stress on microbial loads in meat goats. A. Mechineni, S. Gujja, D. S. Kommuru, T. H. Terrill, G. Kannan*, B. Kouakou, and J. H. Lee, *Fort Valley State University, Fort Valley, GA.*

Livestock transport has been identified as one of the risk factors of microbial contamination in the red meat production. Sericea lespedeza (SL; *Lespedeza cuneata*), a leguminous forage high in condensed tannins, has been reported to reduce gut microbial loads in ruminants. This experiment was conducted to assess the effects of SL grazing and stress associated with transport on microbial load on skin and carcass of meat goats, as well as in their gastrointestinal tracts. In a Completely Randomized Design with split-plot, 30 Spanish intact male kids (6 mo of age; BW = 20.3 ± 3.28 kg) were grazed on either bermudagrass (BG; *Cynodon dactylon*), SL, or a combination of BG and SL pasture for 8 wk (n = 10 goats/treatment). At the end of the grazing period, 5 kids from each pasture were randomly selected, loaded onto a trailer, and then transported to the holding pen at the university abattoir after

driving 3 h. The rest of the kids were directly transported to the abattoir after loading onto the trailer. Animals were held overnight with access to water only before slaughter. Skin swab samples were made on the hind legs immediately after transportation and just before slaughter. Immediately after evisceration, carcass swab samples were taken and rumen and rectal content samples were also collected. Microbial counts in both rectal and rumen contents were not different ($P > 0.05$) among goats grazed on the experimental pastures. Neither pasture type nor transport stress significantly influenced ($P > 0.05$) *E. coli*, total coliform and aerobic plate counts on skin or carcasses. The *E. coli* counts on skin were 0.18 and 0.13 ± 0.091 (mean ± SEM) $\log_{10}$cfu/cm^2 in transport and non-transported groups, respectively. The aerobic plate counts on carcasses were 2.62, 2.91, and 2.41 ± 0.310 (mean ± SEM) $\log_{10}$cfu/cm^2, respectively, in goats grazed on SL, BG and BG plus SL pastures. The results indicate that neither pasture type nor transportation stress appear to significantly influence gut, skin, or carcass microbial loads in meat goats.

Key words: sericea lespedeza, transport, *E. coli*

T391 Gastro-intestinal parasitic infestation in meat goats and its relationships with production traits under a pasture-based performance test in Western Maryland. K. Nadarajah*[1], S. Schoenian[2], D. L. Kuhlers[1], M. D. Carpenter[1], and D. Rankins[1], *[1]Auburn University, Auburn, AL, [2]University of Maryland Extension, Keedysville.*

Variation among meat goats for gastro-intestinal parasitic (GIP) infestation and its relationships with production traits should be explored for selecting goats for resistance to GIP. The objective was to examine between animal variation for GIP infestation and growth performance of bucks participated in a pasture-based performance test in 2009 (n = 60) and 2010 (n = 72), respectively, in Western Maryland. Bucks were managed as a single group on pasture with access to free choice minerals, and were rotationally grazed among 5, 2 acre paddocks. Using SAS, data were analyzed within test-years for fecal egg count (FEC), FAMACHA score (FAM), BCS and growth performance of individual bucks at initial-entry-to-test (IT) and end-of-test (ET). Mean, SD and correlations among traits for IT-weight (IT-WT), IT-FEC, IT-FAM, and IT-BCS and similar parameter estimates for ET-weight (ET-WT), ET-FEC, ET-FAM, and ET-BCS, as well as overall ADG on test were computed. Mean ± SD of bucks on tests in 2009 and 2010 for IT-WT were 21.3 ± 4.8 kg and 20.1 ± 4.5 kg, respectively. For same years, means ± SD of bucks were 1,202 ± 1,614 and 682 ± 1,201 for IT-FEC, 1.82 ± 0.83 and 1.61 ± 0.78 for IT-FAM, and 2.68 ± 0.33 and 2.72 ± 0.40 for IT-BCS, respectively. Means and SD of bucks for ET-WT were 28.1 ± 4.8 kg and 26.3 ± 4.4 kg, for ET-FEC 1,584 ± 1,229 and 400 ± 417, for ET_FAM 2.4 ± 1.1 and 1.57 ± 0.53, and for ET-BCS 2.7 ± 0.4 and 1.6 ± 0.5 in 2009 and 2010, respectively. The mean ADG were 63.5 ± 30.8 g and 54.4 ± 25.8 g for 2009 and 2010, respectively. In both test years, the correlations between IT-FEC and IT-FAM with IT-WT were negative ($P = 0.5$), but IT-WT with IT-BCS was positive ($P < 0.001$). In 2010 test, correlation between IT-FEC and IT-FAM was positive ($P = 0.06$) and correlation between ET-FEC and ET-FAM was positive ($P = 0.08$) in 2009 test. Between variations among bucks for FEC were large. Lack of pedigree information on bucks restricted the estimation of genetic (co)variances from these data. Phenotypic parameters will be used to simulate performance and pedigree data to conduct genetic analyses.

Key words: gastro-intestinal parasite, meat goats, performance test

T392 Gastro-intestinal parasitic infestation and its relationships with growth performance in meat goats on pasture with supplemental grain feeding test at the Kerr Center in Oklahoma. K. Nadarajah*[1], M. Penick[2], D. L. Kuhlers[1], M. D. Carpenter[1], and D. Rankins[1], *[1]Auburn University, Auburn, AL, [2]Kerr Center, Poteau, OK.*

Understanding the relationships between growth performance and gastro-intestinal parasitic (GIP) infestation in meat goats was the objective in this study that should help in selecting goats for resistance to GIP infestation. Data used for this investigation were collected through the buck performance tests at the Kerr Center in Oklahoma in 2009 (n = 58) and 2010 (n = 60), respectively. Bucks on test were grazed on mixed pasture consisting of bermuda, fescue, lespedeza, warm season native grasses and forbs. Bucks also received approximately 340 g of distillers dried grain per head/d and free choice mineral. Using SAS, phenotypic means, SD and correlations among traits of interest were computed within test-years for fecal egg count (FEC), FAMACHA score (FAM) and growth performance of individual bucks at initial-entry-into-test (IT) and end-of-test (ET). Relationships among bucks for performance were estimated for IT weight (IT-WT), IT-FEC and IT-FAM and ET weight (ET-WT), ET-FEC and ET-FAM as well as overall ADG on test. The means ± SD of bucks entered for test in 2009 and 2010, for IT-WT were 22.5 ± 3.4 kg and 23.3 ± 3.5 kg, respectively. In the respective years, the means and SD of bucks for IT-FEC were 976 ± 1,239 and 405 ± 587, and for IT-FAM were 2.6 ± 0.56 and 2.6 ± 0.62. Means and SD of bucks on test in 2009 and 2010, respectively, at ET as follows: for ET-WT 24.6 ± 3.3 kg and 33.7 ± 3.9 kg, for ET-FEC 1,688 ± 2,540 and 1,290 ± 742, and for ET-FAM 2.1 ± 1.2 and 2.75 ± 0.47. Between variations among bucks were large for FEC across test years. The mean ADG in 2009 test was 19.9 ± 30.8 g and the mean ADG in 2010 was 99.8 ± 34.4 g. In 2009 test, correlation between ET-WT and ET-FAM was negative ($P = 0.09$) and ET-FEC and ET-FAM was positive ($P < 0.01$). In both years, correlations between ET-WT and ADG were positive ($P < 0.001$). Lack of pedigree information on individual bucks restricted the estimation of genetic (co)variances from this data. Phenotypic parameters from this study will be used to simulate pedigree and performance data to conduct genetic analyses.

Key words: gastro-intestinal parasite, meat goats, performance test

T393 Lamb immune status (blood IgG, IgM and chitotriosidase activity) during weaning, preliminary results. L. E. Hernandez-Castellano*[1], A. Morales-delaNuez[1], I. Moreno-Indias[1], D. Sanchez-Macias[1], A. Torres[2,1], A. Arguello[1], J. Capote[2], and N. Castro[1], *[1]Universidad de Las Palmas de Gran Canaria, Arucas, Las Palmas, Spain, [2]Instituto Canario de Investigaciones Agrarias, La Laguna, Tenerife, Spain.*

The effect of weaning on some blood immune status-related parameters was investigated using 10 lambs (Canaria dairy breed). Lambs were raised with ewes until they reached 10 kg of live BW with open access to ewe feed. After that, to start the weaning period, lambs were removed from dams and placed in a pen for 6 wk, with free access to starter feed and water. The ewes were milked once a day (morning). During the first week, lambs had access to ewes twice daily (10:00 a.m. after milking, and 17:00 p.m.). During the second week, lambs accessed ewes once a day (17:00 p.m.), and thereafter, the lambs did not have access to ewes. A blood sample was obtained from lambs before the beginning of weaning protocol and subsequently once a week until the end of the experiment. IgG and IgM were measured using a commercial ELISA (Bethyl Laboratories, Montgomery, TX)

and chitotriosidase activity was determined using a fluorescence assay. Blood plasma IgG concentration before the beginning of weaning protocol was 5.14 mg/mL, which was higher than that at wk 4 of weaning protocol (3.93 mg/mL). At wk 6, the IgG concentration increased to values close to the initial ones (6.24 mg/mL). Weaning did not affect the blood plasma IgM concentration, which ranged from 0.64 to 0.76 mg/mL. Weaning did not affect blood serum chitotriosidase activity, which ranged from 2756 to 3292 nmol/mL/h. In conclusion, it would be necessary to improve the knowledge through further research to avoid decreases in blood IgG concentrations in lambs during the critical period in their growth.

Key words: immunoglobulins, chitotriosidase, lamb

T394 Comparison of FAMACHA scores and need for deworming in hair sheep and meat goats grazed together or sheep grazed alone. S. Hart*[1], T. A. Gipson[1], R. Pirtle[2], and W. Cubbage[2], *[1]E (Kika) de la Garza American Institute for Goat Research, Langston, OK, [2]Oklahoma State University Cooperative Extension, Stillwater.*

This study compared FAMACHA scores and need for deworming in hair sheep and goats being grazed together or hair sheep grazed alone. The study involved Boer and Spanish goats and hair sheep crosses of Katahdin, St. Croix, Dorper, Gulf Coast Native and Barbadoes Blackbelly. Treatments were 1) hair sheep grazed alone (88 hd/16.2 ha) or 2) goats and hair sheep grazed together (38 hd of hair sheep and 71 hd of goats/24.3 ha) on tallgrass native range during the summer (average annual precip. 922 mm). Animals were FAMACHA scored (FS) April 30 at the beginning of the study and animals scoring 4 and 5 were treated with moxidectin (MOX; 10 mL). Animals then were FAMACHA scored May 17, June 8, Jul 26, Aug 18 and Sep 20. Animals with FS of 4 were administered either 2.0 g. of copper oxide wire particles (COWP) or 3.4 g of Cayenne pepper (CP). Animals with a FS of 5 were treated with MOX. Animals that were dewormed were fecal sampled for determination of fecal egg counts (FEC) by McMaster procedure and an additional 3 to 6 animals that were not dewormed were fecal sampled. On the hair sheep and goat treatment, goats had higher FS than hair sheep (3.80 vs. 2.63; $P < 0.01$), higher FEC (532 vs. 188 epg; $P < 0.02$) and required more deworming (61.8 vs. 13.5%; $P < 0.001$). Hair sheep grazing alone had a lower FS than hair sheep grazing with goats (2.20 vs. 2.63; $P < 0.01$), lower FEC (50 vs. 188 epg; $P < 0.01$) and required less deworming (2.1 vs. 13.5%; $P < 0$ 0.001). When animals were administered CP, FEC at the subsequent sampling increased by 63%. whereas COWP decreased FEC 36% at the subsequent sampling. Administration of MOX reduced FEC 47% in the subsequent sampling. Hair sheep grazed with goats had lower FS, lower FEC and required substantially less deworming than the goats they grazed with, but sheep grazing with goats required more deworming than sheep grazing alone. COWP was more effective than CP in reducing FEC.

Key words: gastrointestinal nematodes, alternative anthelmintics

T395 Lack of an effect of pelletized diets containing pumpkin seeds on gastrointestinal nematode fecal egg counts in goats. M. Gooden*[1], E. N. Escobar[1], N. C. Whitley[2], D. J. Jackson-O'Brien[3], and H. Taylor[1], *[1]University of Maryland Eastern Shore, Princess Anne, [2]North Carolina A&T State University, Greensboro, [3]Delaware State University, Dover.*

This investigation evaluated the effect of diets containing ground pumpkin (*Cucurbita* sp.) seeds (PS) on an artificial *Haemonchus contortus* infection in goats. Thirty 6 to 8 mo old female and castrated male Boer-crossbred kids at an average body weight of 25.3 ± 4.9 kg were used. Following a 2-week adjustment period in 6-m^2 individual pens with slotted floors, kids were dewormed with albendazole (10 mg/kg) and moxidectin (0.2 mg/kg). After a 21-d dewormer withdrawal period, all kids were orally inoculated 3 times over 5 d with a 3 mL larval inoculum containing 1,450 H. contortus L3. A pelletized 15% crude protein diet was used as the control (C) feed. The treatment diet was formulated with the same ingredients in C diet plus PS. The pelletized treatment diet contained 200 g PS per kg of feed. Two treatment feed levels were used: PS1 had 100 g PS/kg and consisted of PS2 (treatment diet with 200 g PS/kg) mixed equally with the C feed. Weekly, the goats were weighed, fecal samples were taken to determine fecal egg counts (FEC, eggs/g) using the modified McMaster′s technique, and blood samples were collected to determine percentage packed cell volume (PCV). Only goats with FEC ≥200 epg were used for the study, resulting in 9 C, 4 PS1 and 6 PS2 treated animals. Goats were fed the experimental diets for 4 weeks and individual daily feed intake was recorded. Data were analyzed by SAS PROC MIXED. There was no effect of treatment on FEC or PCV; FEC averaged 608 ± 107 for C, 472 ± 134 for PS1 and 780 ± 160 eggs/g for PS2;PCV were C: 27.9 ± 0.5; PS1: 29.8 ± 0.6 and PS2: 28.5 ± 0.8). Average daily feed intake was higher (treatment by week, $P < 0.01$) for the goats eating C diet than PS1 or PS2 for the study′s first 2 weeks only and were similar for the last 2 weeks. Weekly BW was lowest for wk 1 for C but was similar for PS goats over time (treatment by week, $P < 0.05$). In this experiment, PS did not reduce gastrointestinal nematode fecal egg counts in goats, but more research is needed.

Key words: *H. contortus*, goats, fecal egg counts

T396 Comparative efficacies of alternative anthelmintics against natural nematode infection in grazing goats. P. B. Collyer* and E. G. Brown, *Stephen F. Austin State University, Nacogdoches, TX.*

The objective was to determine the efficacy of 3 anthelmintic treatments in East Texas Boer goats. Goats (n = 22) were treated based on sex, age, and initial fecal egg count (FEC). Goats were given a single treatment (TR) that included control (no anthelmintic), Cydectin oral sheep drench (CY, 0.4 mg/kg BW orally), copper wire particles (COWP) in a gel capsule (Copasure, goats <5 mo 1g, goats >5 mo 3 g orally) or cayenne pepper (CP) in a gel capsule (goats <5 mo 3g; goats >5 mo 6g orally). FEC were performed with the FECPAK system. Body weight, FAMACHA score and packed cell volume (PCV) were measured on the day before beginning TR, and weekly for 6 weeks. The obtained measurements were evaluated with a permutation test. COWP reduced nematode eggs ($P < 0.03$) for 2 weeks beginning the second week after TR. CP and CY reduced nematode egg numbers after one week ($P = 0.01$ and 0.03, respectively). FAMACHA scores decreased with COWP after one ($P = 0.01$) and after 3 weeks ($P = 0.03$). FAMACHA scores decreased with CY after 3 weeks ($P = 0.05$). Five weeks post treatment, FAMACHA scores were lower in goats that had been treated with CP compared with the COWP group ($P = 0.04$). Furthermore, COWP TR demonstrated higher FAMACHA scores than the control group after 5 weeks ($P = 0.04$), and also higher FAMACHA scores than CY treated goats after 5 weeks ($P = 0.04$). FAMACHA score and PCV were negatively correlated ($r = -0.31$, $P = 0.01$). Changes in PCV were not evident with any of the treatments. Increase in body weight was seen with COWP after one week of treatment ($P = 0.04$), three weeks ($P = 0.02$), four weeks ($P = 0.02$) and five weeks ($P = 0.02$). Goats treated with CP had an increase in body weight after

4 weeks ($P = 0.04$) and 5 weeks ($P = 0.05$) compared to goats who had received COWP. Results indicate that the onset of FEC reduction with COWP is later and the duration longer, compared to CY and CP, which demonstrated a comparable result in reducing FEC, but shorter in duration. Thus, as an affordable alternative treatment, CP might be considered for a short-interval dosing regimen.

Key words: cayenne pepper, goats, anthelmintic

T397 Effects of immunomodulatory substances added to milk replacer on white blood cell populations during weaning. S. Paez Lama, A. Morales-delaNuez, V. Mendoza-Grimon, L. E. Hernandez-Castellano, D. Sanchez-Macias, N. Castro, and A. Arguello*, *Universidad de Las Palmas de Gran Canaria, Arucas, Las Palmas, Spain.*

To investigate the effect of immunomodulatory substances added to milk replacers on white blood cell populations during the first week of weaning, 21 goat kids (Majorera dairy breed) were randomly allotted into 3 groups. The first group was a control (CON), the second group received a daily dose of 200 mg/kg BW of *Echinacea purpurea* (ECH) and the third group received a daily dose of 20 mg/kg BW of *Polypodium leucotomos* (POL). Goat kids were artificially raised with a milk replacer ad libitum until they reach 10 kg of life BW. After that, animals were enrolled in the weaning protocol. Starter and fresh water were available throughout the weaning period. The first weaning week goat kids received 1 L/d of milk replacer twice daily (morning and afternoon). A blood sample was obtained before starting the weaning protocol and at the end of the first week in heparin containers. Immediately after collection, 50 µL of unclotted blood were added with 5 µL of CD4 (FITC) and 5 µL of CD8 (RPE) monoclonal antibodies (Serotec, Dusseldorf, Germany) and the reaction ran for 15 min at room temperature. After that, 50 µL of Optilyse (Beckman Coulter, Brea, CA) were added and the reaction ran for 15 min at room temperature to lyses red blood cells. Subsequently, 150 µL of saline serum were added to clarify the solution. Fifteen minutes later, the samples were redden using an FC500 flow cytometry device (Beckman Coulter, Brea, CA). An ANOVA (with repeated measures) procedure from SAS was used. Two white blood cell populations were observed clearly, lymphocytes plus macrophages (L+M) and polymorphonuclear (PMN) at both tested times. Control L+M, PMN and CD8 lymphocytes per mL were lower ($P \leq 0.05$) than in preweaning samples but no differences were observed with ECH and POL. Control and ECH CD4 lymphocytes per mL were lower ($P \leq 0.05$) than preweaning samples and POL kids. The addition of immunomodulatory substances would improve the immune status during the weaning in goat kids.

Key words: goat kid, weaning, immunomodulatory

T398 Goat browsing for invasive shrub and internal parasite control. J. C. Warren*[1], D. J. O'Brien[1], C. Heckscher[1], R. Beaman[2], and N. C. Whitley[3], *[1]Delaware State University, Dover, [2]Delaware Department of Transportation, Dover, [3]North Carolina A&T State University, Greensboro.*

The objectives of this study were to determine whether goats were effective in the control of Autumn Olive (AO; *Elaeagnus umbellate*), Multiflora Rose (MR; *Rosa multiflora*), and Japanese Honeysuckle (JH; *Lonicera japonica*) and whether browsing controls internal parasites in goats. 1.95 ha of land was divided into 5 fenced paddocks with 3 treatment (TRT; with goats; 0.45 ha each) and 2 control (CON; without goats; 0.30 ha each) paddocks at the study site, Wrangle Hill (WH). At the University farm site, Hickory Hill (HH), 1.35 ha of mixed grass/legume pasture was divided into 3 fenced paddocks (0.45 ha each). Seventy crossbred meat type goats averaging 745 ± 146 d of age and 39.3 ± 7.2 kg BW from the HH herd were used in the experiment (n = 35/location). Goats at WH were used to browse each TRT for 14 d, after which they were moved to the next TRT. At HH, goats grazed paddocks in the same 14-d rotations concurrently with WH goats. The study lasted 112 d. On rotation days, WH paddocks were analyzed for percentage ground cover and visual estimates were made for AO, MR, and JH using the double DAFOR method; additionally, at this time, for both sites, animal BW and FAMACHA scores were measured and recorded and fecal samples were collected to determine fecal egg counts (FEC) in eggs per gram (epg) using the modified McMaster′s technique. All data was analyzed using the PROC MIXED procedure of SAS. Visual Estimates of both AO and MR were similar between treatments, but JH decreased ($P < 0.01$) in the TRT paddocks compared with the CON over the study period. Browsing goats did not influence groundcover percentage. Goat BW and FAMACHA scores were not influenced by site and averaged 43.2 ± 3.3 kg and 3.1 ± 0.1, respectively. There was a location by d effect with WH goats having lower FEC ($P < 0.05$) than HH goats on d 14 (216 ± 90 and 476 ± 90 epg, respectively), d 42 (33.0 ± 63 and 206 ± 63 epg, respectively), d 56 (45.0 ± 66 and 368 ± 68 epg, respectively), and d 112 (219 ± 83 and 621 ± 82 epg, respectively). In summary, browsing reduced FEC in goats and decreased JH during one grazing season. Multiple grazing seasons may be required to have an impact on AO and MR.

Key words: goat, parasites, invasive shrubs

T399 Gastrointestinal nematode (GIN) resistance and GIN management on small ruminant farms in the mid-Atlantic U.S. D. J. O'Brien[1], K. K. Matthews*[1], E. K. Crook[2], N. C. Whitley[3], B. Storey[4], S. Howell[4], and R. Kaplan[4], *[1]Delaware State University, Dover, [2]Virginia Maryland Regional College of Veterinary Medicine, Blacksburg, [3]North Carolina A & T State University, Greensboro, [4]University of Georgia, Athens.*

The objective was to characterize gastrointestinal nematode (GIN) anthelmintic resistance and parasite control programs on 20 goat and 13 sheep farms in DE (10 farms), MD (10 farms), VA (3 farms), WV (4 farms), and PA (6 farms). Farms were evaluated for GIN resistance to benzimidazole (BZ), ivermectin (IVM), moxidectin (MOX), and levamisole (LEV) using the DrenchRite Larval Development Assay. Fecal samples were collected rectally from at least 10 animals on each farm, placed into labeled zippered bags, and shipped to the University of Georgia for analysis. Completion of a survey to determine previous anthelmintic use and current integrated parasite management methods as part of an overall parasite control program was required of farmers participating. On 100% of farms tested, BZ was ineffective; IVM was ineffective on 79% (26/33) of farms, and MOX was ineffective on 48% (16/33) while LEV was only ineffective on 27% (9/33) of farms tested. Rotational grazing, FAMACHA, fecal egg counts, or mixed species grazing were strategies utilized to help control parasites on 62, 48, 14, and 7% of farms, respectively. The most common anthelmintics previously used by producers was a combination of BZ, IVM, and MOX on 72% of farms. Overall, 90, 79, and 31% of producers had previously utilized macrocyclic lactones (IVM and MOX), BZ and LEV, respectively; 86% of producers had utilized 2 or more classes of anthelmintics, while 17% of producers had utilized all 3 classes of anthelmintics. When asked about frequency of anthelmintic treatments, most participants utilized selective drenching techniques (41%) or used anthelmintics one to 3 times per year (41%). The remaining 17% treated with anthelmintics more than 4 times/year. Results indi-

cate that GIN resistance is a serious problem on small ruminant farms in the mid-Atlantic region, but that producers seem to be trying to utilize some types of integrated parasite control strategies to extend the efficacy of available anthelmintics.

Key words: small ruminants, parasite resistance, FAMACHA

T400 Effects of supplemental dried distillers grains on performance and internal parasites of grazing lambs. C. L. Pickworth*[1], T. L. Felix[1], I. Susin[2], L. M. Shoup[1], and S. C. Loerch[1], *[1]The Ohio State University, Wooster, [2]Universidade de São Paulo, Piracicaba, São Paulo, Brazil.*

Weaned lambs grazing on pasture have high susceptibility to internal parasites which can greatly reduce growth rates and can contribute to lamb mortality. The objective of these studies was to investigate the effects of supplementing weaned lambs grazing orchardgrass pastures with dried distillers grains with soluble (DDGS) or soybean hulls (SH) on parasitism, growth rate, and cost of production. In each experiment, lambs were assessed weekly for 10 wk for parasitism based on FAMACHA eye scores and BW was recorded. Every 3 wk, blood hematocrit and fecal egg counts were determined. Lambs with FAMACHA scores of ≥ 3 were treated with an anthelmintic. Each treatment was replicated in 2 paddocks and data were analyzed as a completely randomized design. In Exp. 1, 62 lambs (26.3 ± 0.1 kg) were allotted to 4 paddocks. The treatments were a control with no supplementation (CONT) or 0.53 kg/head supplemental DDGS (SDG1). The SDG1 lambs had greater ($P < 0.01$) ADG and decreased ($P < 0.01$) anthelmintic costs because fewer lambs were treated (19 vs. 90% for SDG1 and CONT, respectively). In Exp. 2, 96 lambs (25.1 ± 0.4 kg) were allotted to 6 paddocks. The treatments included a CONT, 0.61 kg/head supplemental SH (SSH), or 0.63 kg/head supplemental DDGS (SDG2). The SSH and SDG2 lambs had greater ($P < 0.01$) ADG as compared with CONT lambs (95, 188, and 224 g/d for CONT, SSH, and SDG2, respectively). Both SSH and SDG2 reduced ($P < 0.02$) percent of lambs treated with anthelmintics (31 and 9%, respectively) when compared with CONT (81%). The FAMACHA scores were improved ($P < 0.01$) for SSH and SDG2 lambs than CONT on d 22, 43, and 72. In Exp. 3, 92 lambs (21.0 ± 0.5 kg) were allotted to 6 paddocks. The treatments included CONT, 0.59 kg/head supplemental SH with 0.7% P from monosodium phosphate (SSHP), or 0.54 kg/head supplemental DDGS (SDG3).The ADG was greater ($P < 0.03$) for SDG3 and SSHP than CONT. Only 52% of SDG3 lambs were treated with anthelmintics as compared with 87.5% of CONT or 71.9% of SSHP lambs. In all 3 studies, supplementation of DDGS reduced parasitism and improved weaned lamb growth rates on pasture.

Key words: distillers grains, parasites, lambs

T401 Feeding North American panicled tick-clover containing condensed tannins to growing goats reduces *Haemonchus contortus* infection. N. M. Cherry[1], B. D. Lambert*[1,2], J. P. Muir[1], M. Bullinger[2], J. E. Miller[3], R. M. Kaplan[4], and T. R. Whitney[5], *[1]Texas Agrilife Research, Stephenville, [2]Tarleton State University, Stephenville, TX, [3]Louisiana State University, Baton Rouge, [4]The University of Georgia, Athens, [5]Texas Agrilife Research, San Angelo.*

A major obstacle for goat production, especially in warm humid and sub-humid regions, is gastrointestinal nematodes, specifically *Haemonchus contortus* (HC; barberpole worm). Recent concern over resistance to commercial anthelmintics has led to the search for other ways to suppress HC populations. Condensed tannins (CT) from *Lespedeza cuneata* (sericea lespedeza, SL) have proven effective in suppressing HC but this legume cannot be grown in some edapho-climatic conditions or situations in which aggressive exotics are not ideal. So the search for native legumes that contain equally effective CT while still providing crude protein (CP) continues. In this study alfalfa, SL and a native North American herbaceous legume *Desmodium paniculatum* (panicled tick-clover; PTC) were pelleted into a complete feed that contained 3.94% CT, 18% CP and 2.8 Mcal/kg digestible energy and fed to goats at 3.5% of their body weight. At d 0 average fecal egg counts (FEC) for all infected animals was 2190; by d 14, FEC in kids fed PTC were 2976 and by d 28 FEC were 2665 compared with 4920 and 4560 for infected alfalfa on d 14 and 28, respectively. By d 28 FEC for infected animals fed SL and PTC were not different from each other but were 44% lower than infected animals in the alfalfa treatment. Packed cell volumes throughout the trial were not different among goats fed SL, PTC, or alfalfa. Results indicate that the North American native legume panicled tick-clover has potential as an HC suppressant.

Key words: *Haemonchus contortus*, condensed tannin, panicled tick-clover

T402 Demographic factors of meat goat producers completing an online certification program. T. A. Gipson*, R. C. Merkel, and T. Sahlu, *American Institute for Goat Research, Langston Univ., Langston, OK.*

In 2006, an online training program for meat goat producers was unveiled, consisting of 22 learning modules (http://www2.luresext.edu/goats/training/qa.html). Participants take a pre-test for each module and if a score of 85% or greater is recorded, the post-test is not required. If required, participants may retake the post-test until a passing score of 85% or greater is achieved. For certification, passing scores are required on all 16 required modules and a minimum of 3 elective modules. Demographic data are collected upon enrollment. Participants had the option of not responding to certain demographic questions and those observations were removed from this analysis. As of the end of 2010, 198 of 1,430 enrollees successfully completed the certification program, with 182 from the US and 16 from foreign countries. For those 182 certified in the US, a higher percentage (62%, $\chi^2 = 143.2$, $P < 0.01$) was from the South than from any other region, followed by 22, 12, and 4% from the Midwest, West, and Northeast, respectively. All certified producers reported their gender and there were more males (60% vs. 40%, $\chi^2 = 8.1$, $P < 0.01$) than females. Of the certified, 92% responded to the question on race, and an overwhelming percentage classified themselves as white (89%, $\chi^2 = 686.5$, $P < 0.01$ for equal proportions); however, this is similar to the US population as a whole (89% vs. 80%, $\chi^2 = 0.1$, $P = 0.73$). The response to a question on farm size was 88%; 9% owned <2 ha, 43% 2–8 ha, 14% 9–16 ha, 13% 17–32 ha, 9% 33–65 ha, 8% 66–130 ha, and 4% > 130 ha ($\chi^2 = 162.5$, $P < 0.01$). An 84% of the certified responded to a question on occupation; 78% were part-time farmers and 22% were full-time ($\chi^2 = 53.2$, $P < 0.01$). The response of those certified to a query on herd size was 82%, with 46% owning less than 25 goats, 29% 25–49, 16% 50–99, 6% 100–250, and 3% greater than 250 ($\chi^2 = 103.9$, $P < 0.01$). Demographics indicate that the typical certified participant is a white male living in the southern US and farming part-time with less than 25 goats on 2–8 ha.

Key words: goats, online, training

T403 Variability among enumerators in assigning body condition scores in meat goats. R. C. Merkel* and T. A. Gipson, *Langston University, Langston, OK.*

Body condition score (BCS) is a subjective measure of an animal's condition. In research settings, teams of 3 enumerators determine a true BCS, defined as the median score. The variability among team member scores in determining an animal's true BCS is not well studied. Twenty-four Spanish (28 – 40 wk of age; 26.6 ± 4.43 kg) and 28 predominately Boer (B) blood (24 - 75%B, 4 – 100%B; 33 – 46 wk of age; 33.9 ± 6.99 kg) wethers were allocated to 4 groups having equal breed numbers. Goats were raised on pasture with unlimited access to alfalfa hay with 2 groups consuming either 0.5% or 1.5% BW of a pelleted diet (16% CP, 29% ADF, 60% TDN). BCS (1 = very thin, 5 = obese, 0.25 increments) was taken bi-weekly by the same 3 enumerators with the median value recorded as the true BCS. A total of 1728 observations (576 per enumerator) were recorded. Data was analyzed using repeated measures. The repeatability score was 0.6 ± 0.05. Median BCS and percent of individual scores at the median, respectively, for the BCS given throughout the trial were 2.0, 0.35; 2.25, 1.56; 2.5, 25.0; 2.75, 43.4; 3.0, 20.0; 3.25, 5.9; and 3.5, 3.8 ($\chi^2 = 107.1$, $P < 0.01$). On the same animal at the same time, all enumerators gave the same BCS 37.9 and 2 of the 3 enumerators agreed 56.4% of the time. When only 2 enumerators agreed, enumerators A and B, B and C, and A and C agreed 24.3, 17.7, and 14.4% of the time, respectively. In only 5.7% of animals were all 3 scores different. All scores were either at the median, 0.25 above, 0.25 below, 0.5 above, or 0.5 below (77.4, 10.8, 11.2, 0.23, and 0.46%, respectively; $\chi^2 = 166.2$ $P < 0.01$ for equal distribution). In no instance did an individual score deviate from the median by 0.75 of a score. Results show close agreement in assigning BCS to growing meat goats with 99.4% of scores given by enumerators either at or within 0.25 of the median score. In 94.3% of animals scored by 3 enumerators, at least 2 scores were at the median whereas combinations of 2 enumerators giving the same score ranged from 52.3 to 62.2%. Data confirms that 3 enumerators are preferable to 2 in determining an animal's true BCS.

Key words: body condition score, meat goats

T404 Comparative effect of implants with trenbolone-estradiol or zeranol on feedlot-performance of Katahdin × Pelibuey hair-lambs. B. Ortiz*[1], A. Camacho[1], N. E. Villalba[2], L. R. Flores[1], J. J. Lomeli[1], J. A. Romo[1], and R. Barajas[1], *[1]FMVZ-Universidad Autonóma de Sinaloa, Culiacán, Sinaloa, México, [2]Agricola Ganadera Mojolo, Culiacán, Sinaloa, México.*

The objective of this study was to compare the effect of trenbolone-estradiol and zeranol implants on feedlot-performance of Katahdin × Pelibuey lambs. Thirty-six lambs 3/4 Katahdin × 1/4 Pelibuey (24.23 ± SE 0.67 kg of initial BW) were assigned to 1 of 3 treatments. In groups of 3, lambs were placed in elevated (0.6 m) plastic floor pens (0.9 × 1.9 m). In a completely randomized block design lambs were assigned to next treatments: 1) Feeding with a 95% concentrate corn-canola meal based diet (14.2% CP; 2 Mcal of NEm/kg) without hormonal implant (CTRL); 2) Diet similar to CTRL and implanted with 12 mg of zeranol (one pellet of Ralgro implant; Intervet Schering-Plough Animal Health); and 3) Diet similar to CTRL and implanted with 40 mg of trenbolone acetate and 8 mg of estradiol (2 pellets of Component-TES; ELANCO). Lambs were weighed on d 28 and 49. During first 28 d, lambs implanted with trenbolone-estradiol were 8.5% heavier ($P = 0.02$), gain 27.8% more weight ($P = 0.03$), and had a gain/feed ratio 14% higher ($P = 0.05$) than CTRL. Zeranol was not different from the other 2 treatments ($P > 0.10$). From d-29 to 49, there was not effect of treatments ($P > 0.10$). Over the complete 49-d experiment, lambs implanted with trenbolone-estradiol gain 18.9% more weight than CTRL ($P = 0.04$). Zeranol implant did not show any effect ($P > 0.10$). It is concluded, that trenbolone-estradiol implants are better option than zeranol implants to promote feedlot performance of Katahdin × Pelibuey hair-lambs.

Key words: feedlot-performance, lambs, trenbolone

T405 Influence of zeranol implant on performance of Dorper × Katahdin feedlot lambs. B. Ortiz*[1], A. Camacho[1], N. E. Villalba[2], L. R. Flores[1], J. J. Lomeli[1], J. A. Romo[1], and R. Barajas[1], *[1]FMVZ-Universidad Autonóma de Sinaloa, Culiacán, Sinaloa, México, [2]Agricola Ganadera Mojolo, Culiacán, Sinaloa, México.*

With the objective to determine the influence of zeranol implant on performance of feedlot lambs. A 35-d feedlot experiment was performed. Twenty-four lambs ¾ Dorper × ¼ Katahdin with 29.23 ± SE 0.87 kg of initial weight were used. In groups of three, lambs were placed in elevated (0.6 m) plastic floor pens (0.9 × 1.9 m) fitted with automatic drinker. Animal were blocked by weight, and in agreement with a completely randomized block design were assigned to 1 of 2 treatments: 1) Feeding with a 95% concentrate corn-canola meal based diet (14.18% CP; 2.002 Mcal of NEm/kg) without hormonal implant (CTRL); or 2) Diet similar to CTRL and ear implanted with 12 mg of zeranol. Commercial presentation of Ralgro implant cartridge (Intervet Schering-Plough Animal Health) contains 36 mg of zeranol (12 mg by each pellet). One Ralgro pellet was used to obtain the dosage of 12 mg of zeranol. Lambs were feed ad libitum. Final weight was not affected ($P > 0.20$) by implant (38.8 vs. 40.5 kg). Average daily gain was improved 20% ($P = 0.06$) by zeranol implant 273 vs. 329 g/d for CTRL and Zeranol, respectively. Dry matter intake (1.23 ± SE 0.03 kg/d) was not affected by treatments ($P > 0.20$). Lambs that received zeranol implant showed a feed/gain ratio 25% higher ($P = 0.02$) than non implanted lambs. It is concluded that implantation with 12 mg of zeranol is enough to improve feedlot performance of Dorper × Katahdin feedlot lambs

Key words: feedlot-performance, lambs, zeranol

T406 Seasonal changes in chemical composition of Hungarian raw goat′s milk. L. Varga*, *Department of Dairy Science, Institute of Food Science, Faculty of Agricultural and Food Sciences, University of West Hungary, Mosonmagyarovar, Hungary.*

The aim of this research was to monitor the changes in chemical composition, acidity, and freezing point of raw caprine milk during lactation, from milking to refrigerated storage, on a Hungarian dairy goat farm. The herd involved in the study consisted of approximately 200 goats belonging to a Hungarian native breed. The following sampling locations were selected: (i) individual animals, (ii) milk sampling unit in pipeline, (iii) milk flowing from pipeline into refrigerated bulk tank, and (iv) refrigerated bulk tank. Four samples were taken each time at each sampling location, and samples were collected biweekly over a 7-mo period from May through November. The data was subjected to ANOVA using the general linear model procedure of Statistica data analysis software system, version 9.1 (StatSoft Inc., Tulsa, OK). Significant differences among the means were determined by using Duncan′s multiple comparison test at $P < 0.05$ (StatSoft). A total of 216 sample units were tested. In terms of all the chemical components analyzed, decreased values were found in the samples compared with the average gross composition of goat′s milk. Fat and protein contents

were especially low in the first 5 mo of the study, and the concentrations of these components were not influenced ($P > 0.05$) by the sampling location. Similarly, lactose levels were rather low with values ranging from 4.1% to 4.3% (w/w) all through the study. It is worth mentioning, however, that the raw goat milk samples collected contained no extraneous water and their pH was mostly acceptable. The low freezing points, together with the low lactose contents, suggested that the milk produced by Hungarian native goats must have contained high levels of minerals. In conclusion, because profitability of milk production and processing largely depends on the fat and protein contents of raw milk, the levels of these components need to be increased by genetic improvement and nutrition of goats.This work was supported by the National Development Agency of Hungary (Project No.: TÁMOP-4.2.1.B-09/1/KONV-2010-0006).

Key words: goat milk, chemical composition, freezing point

T407 Examination of microbiological and physicochemical quality of raw materials and end products during manufacture of cheeses from caprine and ovine milk. L. Varga*, *Department of Dairy Science, Institute of Food Science, Faculty of Agricultural and Food Sciences, University of West Hungary, Mosonmagyarovar, Hungary.*

In Hungary, over 99% of the raw milk processed commercially is bovine milk. Only a few thousand tonnes of milk are produced annually by small ruminants. The majority of ovine and caprine milk is processed into various types of cheese, which have gained popularity among Hungarian consumers in recent years. For this reason, the purpose of the present study was to monitor the manufacturing process of semi-hard cheeses made from sheep and goat milk in a small-size cheesemaking factory located in the northwestern part of the country. Raw bulk milks were analyzed for aerobic mesophilic microorganisms, coagulase-positive staphylococci, inhibitory substances, total solids, fat, protein, lactose, solids-non-fat, pH and freezing point. In addition to detection of *Salmonella* spp. and *Listeria monocytogenes*, viable counts of the following microorganisms were enumerated in pasteurized milk and cheeses: coliforms, *Escherichia coli*, yeasts, molds, coagulase-positive staphylococci, and mesophilic sulfite-reducing clostridia. Pasteurized milk samples were also tested for the same physicochemical attributes as raw bulk milk samples. As for cheese samples, total solids and fat measurements were made. The results showed that the overall microbiological quality of raw goat milk was slightly better than that of raw sheep milk; however, total plate counts and coagulase-positive staphylococci counts were rather high in both types of milk. The mean protein content of caprine milk was as low as 2.99%, which should be considerably increased by breeding and feeding methods. By contrast, ovine milk had a mean protein level of 6.94%. None of the raw milk batches processed contained extraneous water because their freezing point was well below −0.520°C in each case. In conclusion, both raw goat and sheep milk were effectively heat-treated and this, together with the proper implementation of manufacturing technology, resulted in high quality and microbiologically safe finished products. This work was supported by the National Development Agency of Hungary (Project No.: TÁMOP-4.2.1.B-09/1/KONV-2010–0006).

Key words: goat milk, sheep milk, cheese

T408 Milk yield and milk composition of ewes fed diets with canola oil or linseed oil. C. P. Nolli*, I. Susin, A. V. Pires, M. O. Maia, E. M. Ferreira, R. S. Gentil, and D. Eysink, *University of São Paulo/ESALQ, Piracicaba, SP, Brazil.*

Sheep rations have a diversity of sources and some ingredients can improve animal growth and product quality. Additionally, vegetable oils can modify milk fatty acid profile and are an alternative to achieve nutritional requirements, especially in early lactation. Thirty 3 Santa Inês ewes (63.9 ± 9.3 kg BW and 12 ± 2 DIM) were penned individually and assigned to a randomized complete block design to determine the effects of adding canola or linseed oil on lactation performance. Ewes were fed a basal diet (13% CP and 54% NDF, DM basis) containing 50% concentrate and 50% coastcross hay. The experimental treatments included control (0% oil, CONT), canola oil (3% oil, CAN) or linseed oil (3% oil, LIN). Ewes were fed the diets from 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, milk production recorded and a sample collected for milk composition analysis. Ewes were weighed for 3 consecutive days at the start and at the end of the experiment. Data were analyzed using the MIXED procedure of SAS and means compared by Tukey Test. No effect was observed on DMI among treatments (2.5, 2.2 and 2.3 kg/d for CONT, CAN and LIN, respectively). Milk production in 3 h (177, 164 and 152 g for CONT, CAN and LIN, respectively), milk fat, milk protein and total solids were not different ($P \geq 0.05$) among diets. Final BW was greater for LIN fed ewes compared with CAN fed ewes (64.9, 63.5 and 69.4 kg for CONT, CAN and LIN, respectively). Adding 3% of canola oil or linseed oil in diets had no detrimental effect on DMI, milk yield and milk composition of ewes.

Key words: lactation, lipids, sheep

T409 The mammary gland of the Canarian dairy goats undergone two different milking frequencies: morphological characterization of the tissular components. A. Suarez-Trujillo[1], J. Capote[2], A. Arguello[1], A. Arencibia[1], N. Castro[1], J. Morales[1], and M. A. Rivero*[1], *[1]Universidad de Las Palmas de Gran Canaria, Arucas, Las Palmas, Spain, [2]Instituto Canario de Investigaciones Agrarias, La Laguna, Tenerife, Spain.*

The morphological characteristics of the tissular components of the mammary gland in Canarian dairy goats were studied. Furthermore, the influence of the milking frequency on the histological composition of the mammary parenchyma was determined. The udders of 9 goats of the 3 autochthonous breeds of the Canary Islands (Majorera, Tinerfeña and Palmera) were milked at different frequencies: right half udder was milked twice a day and left half udder was milked once a day. Two samples of each gland were obtained and histologicaly processed. The samples were photographed randomly choosing different fields, which were processed by morphometric analysis software (Image-Pro plus 4.5). The tissular components measured were the secretor tissue, connective tissue, excretor tissue and vascular tissue. In Majorera goats parenchyma the major percentage of tissue are secretor tissues, and the connective tissue was observed in a higher percentage in Tinerfeña goats than in the other studied breeds. No difference was observed between the 2 milking frequencies. We conclude that the use of once daily milking or twice daily milking does not have consequences on the histological structure of the mammary gland. However, the 3 Canary dairy goats have different tissular percentages, which could explain their distinct milk yield.

Key words: goat kid, mammary gland, milking frequency

T410 Effects of Actigen on peripheral blood immune cells in pigs experimentally infected with porcine reproductive and respiratory syndrome virus (PRRSV). T. M. Che*[1], M. Song[1], R. W. Johnson[1], K. W. Kelley[1], W. G. Van Alstine[2], K. A. Dawson[3], and J. E. Pettigrew[1], *[1]Department of Animal Sciences, University of Illinois, Urbana, [2]Animal Disease and Diagnostic Laboratory, Purdue University, West Lafayette, IN, [3]Research, Alltech Biotechnology Center, Nicholasville, KY.*

This study evaluated effects of Actigen (ACT, a mannan preparation, Alltech, Inc.) on peripheral blood immune cells in pigs infected with PRRSV. Pigs (n = 64, 21 d old), free of PRRSV, were divided into uniform blocks on the basis of initial BW within sex. They were randomly assigned from within blocks to 1 of 4 treatments in a 2 × 2 factorial arrangement [2 types of diet: control (0%) and ACT addition (0.04%); 2 levels of PRRSV: with and without]. Sex and ancestry were equalized across treatments. Pigs were penned individually and considered experimental units. After 2 wk of an 8-wk period of feeding the treatments, pigs were intranasally inoculated with PRRSV or a sterile culture medium (Sham) at 5 wk of age. Subsets of blood leukocytes (n = 8/treatment) were measured by flow cytometry at d 0, 3, 7 postinoculation (PI), and subsequently weekly until d 42 PI. Data were analyzed as repeated measures over time using the MIXED procedure of SAS. The numbers of leukocyte subsets in the infected pigs markedly decreased at d 3 to 7 PI, increased at d 14 to 28 PI and started declining by d 35 PI. Overall, PRRSV infection increased the numbers of total leukocytes ($P < 0.03$), neutrophils ($P < 0.001$), natural killer cells ($P = 0.051$) and several T cell subsets ($P < 0.01$) as compared with Sham. There were significant effects of day ($P < 0.001$) and day x PRRSV interaction ($P < 0.05$) on subsets of leukocytes during the course of study. Dietary ACT increased ($P < 0.05$) the numbers of total leukocytes (16.5 vs. 15.2 × 10^6/mL), B cells (1.7 vs. 1.4 × 10^6/mL), cytotoxic T cells (2.0 vs. 1.7 × 10^6/mL) and γδ T cells as compared with the control. The diet x PRRSV interaction did not affect the numbers of total leukocytes or any subsets of immune cells. Briefly, feeding ACT to pigs results in increased peripheral blood leukocytes, B cells, and T cell subsets which may be beneficial, especially in bacterial co-infections. In addition, changes in subpopulations of immune cells over the experimental period would be a useful index of on-going processes of PRRSV infection and for designing future treatment approaches.

Key words: Actigen, pigs, PRRSV

T411 Effects of dietary multi-carbohydrases on growth performance, nutrient digestibility and blood characteristics in finishing pigs. J. P. Wang*, X. Y. Guo, and I. H. Kim, *Dankook University, Cheonan, Choongnam, South Korea.*

The objective of this research was to evaluate the effect of multi-carbohydrases on growth performance, nutrient digestibility and blood characteristics in finishing pigs. A total of 100 crossbred barrows (initial body weight = 56.2 ± 1.3 kg) were randomly allotted to 1 of 5 treatments by their BW and litters (5 replicate pens per treatment, 4 pigs per pen). Treatments included: 1) CON (barley-soybean basal diet), 2) MIX (CON + 0.05% Mixture(α-galactosidase: β-mannanase = w1:w1), 3) MAN (CON + β-mannanase 0.05%), 4) GB1 (CON + 0.05% enzyme complex) and 5) GB2 (CON + 0.1% enzyme complex). The enzyme complex contained protease 2,601 U/g, amylase 7,716 U/g, cellulase 5,204 U/g, xylanase 799 U/g and α-galactosidase 176 U/g. During the 5 week trial, pigs fed MIX, GB1 and GB2 diets had higher ADG than that of CON treatment group ($P < 0.05$). There were no differences in ADFI and G:F among the treatments. Apparent total tract nutrient digestibility (ATTD) of DM and energy were increased by the MIX, GB1, and GB2 treatments as compared with the CON and MAN treatment ($P < 0.05$). Nitrogen digestibility in GB2 treatment was greater than that of the CON and MAN treatment group ($P < 0.05$). No differences in blood glucose, red blood cells (RBC), white blood cells (WBC), lymphocyte percentage and Immunoglobulin-G (IgG) concentration were observed among the treatments. After the feeding period, meat samples from pigs which reached marketing BW were collected from the slaughter house. No numerical differences were observed in backfat thickness, meat color, pH value and water holding capacity (WHC) among 4 treatments. In conclusion, the addition of α-galactosidase, along with β-mannanase or multi-carbohydrases can improve ADG and nutrient digestibility more than single enzyme supplementation in barley soybean based diet of finishing pigs.

Key words: α-galactosidase, β-mannanase, finishing pigs

T412 Effects of a natural feed additive in comparison to an antibiotic treated group to prevent gram-negative associated diseases in pigs. S. Schaumberger*[1], S. Masching[2], A. Ganner[1], and G. Schatzmayr[1], *[1]Biomin Research Center, Tulln, Austria, [2]Biomin Holding, Herzogenburg, Austria.*

Aim of this study was to prove the positive effect of a feed additive containing a yeast-derivate, a clay mineral and a plant extract on health status (diarrhea incidence) and performance of weaning piglets compared with a positive antibiotic treated group. 90 weaning piglets were chosen from 15 litters and randomly assigned to 3 groups (A, B, C) with 3 replications each. Group A was fed the standard diet without additive; Group B was fed the control diet and additionally received 100 mg Colistin/liter drinking water for the first 21 d of the trial; Group C was supplied with 0.2% of the feed additive over the whole trial period. Incidences of diarrhea were recorded daily. Weight of each single animal was recorded at the beginning, at d 14, 21, 42 and 56. The amount of feed distributed, feeding frequency and mixing ratio were recorded automatically per pen and day. All data generated out of the trial was subjected to statistical analysis by means of PASW 18.0 (formerly SPSS Statistics). On d 56 weight of piglets of group C was improved with a statistical difference of $P = 0.019$ compared with the control group. Daily weight gain (DWG) (d 1 to 56) showed significant differences ($p = 0.007$) between groups A and B and A and C. For feed conversion rate (FCR) and feed intake no statistical differences could be observed, but for group C FCR (1.77) was lower compared to groups A (1.83) and B (1.88). On day 7 single incidences of diarrhea occurred in some pens and lasted for 13 days in varying intensities: group A showed diarrhea for 8 days, group B for 7 days and group C only for 4 days. Conclusion of our study was that a feed additive consisting of specific clays capable of binding endotoxin, yeast derivates binding gram negative bacteria as well as acting anti-inflammatory and plant extracts with pro-inflammatory properties have a synergistic effect in vivo since in our study performance was enhanced and diarrhea incidence reduced.

Key words: piglet, feed additive, performance

T413 Effects of feeding Actigen on ex vivo immune responses of porcine leukocytes. T. M. Che*[1], R. W. Johnson[1], K. W. Kelley[1],

K. A. Dawson[2], and J. E. Pettigrew[1], *[1]Department of Animal Sciences, University of Illinois, Urbana, [2]Research, Alltech Biotechnology Center, Nicholasville, KY.*

An experiment was conducted to evaluate whether feeding Actigen (ACT) to nursery pigs subsequently alters cytokine secretion, gene expression of cell receptors and phagocytic activity of leukocytes. Weaned pigs were blocked on the basis of initial BW within sex. Pigs (n = 6/treatment) were fed the control or 0.04% ACT diet for 2 wk and then euthanized for sample collection. Bronchoalveolar lavage cells (BALC) and peripheral blood mononuclear cells (PBMC) were stimulated in vitro with medium as a control, lipopolysaccharide (LPS; 1 μg/mL), or polyinosinic:polycytidylic acid (Poly I:C; 50 μg/mL) and incubated 24 h. Supernatants were collected for measurements of tumor necrosis factor (TNF)-α, IL-1β, interferon (IFN)-γ and IL-10. Gene expression of mannose receptor (MR), toll-like receptor (TLR) 3 and TLR4 in BALC only was measured using qRT-PCR. Phagocytic activity of BALC and whole blood polymorphonuclear cells (PMNC) were determined by flow cytometry. Data were analyzed as a randomized complete block design using the MIXED procedure of SAS. Dietary ACT increased TNF-α secretion by BALC, in response to in vitro microbial stimulations, as compared with the control (17.4 vs. 12.1 ng/mL; $P < 0.05$). Microbial stimulators increased BALC-produced TNF-α and IL-1β as compared with the control ($P < 0.001$). There was a diet x stimulator interaction for IL-1β ($P < 0.03$), as feeding ACT increased IL-1β production by BALC stimulated by Poly I:C (2.7 vs. 1.5 ng/mL; $P < 0.04$), but not in those cells stimulated by LPS. Cytokines produced by PBMC were not different among the treatments. There was a diet x stimulator interaction ($P < 0.05$) for expression of both MR and TLR4 genes, similar in pattern to the production of IL-1β. The expression of TLR3 gene was not detectable at 24-h postincubation. Dietary ACT enhanced the percentage of phagocytic PMNC as compared with the control (86 vs. 77%; $P < 0.01$). Briefly, these results suggest that ACT appears to have a greater immunomodulatory effect in response to a viral model than in response to a bacterial model. It may bring benefits by enhancing the proportion of phagocytic PMNC.

Key words: Actigen, immune response, pigs

T414 Effects of multiple sources and levels of dietary fiber on apparent total tract dry matter digestibility, growth performance, and concentration of fermentation indices in pigs. A. Woldeghbriel, S. Smith*, T. Barrios, and B. Bishop, *North Carolina Agriculture and Technical State University, Greensboro.*

Two experiments were conducted to investigate the effects of sources and levels of dietary fiber (DF) on apparent total tract digestibility (ATTD), growth performance, and concentration of fermentation indices in pigs. In Exp. 1, 16 barrows averaging 16 kg were randomly assigned to 1 of 4 diets after metabolic crate assignments with individual pig serving as the experimental unit. The pigs had free access to water, but feed allowance was limited to 10% of average body weight, fed twice d-1. The study period was split into 10d of adjustment, and 5d of urine and feces collection. In Exp.2, pigs (n = 96; 16.4 kg) were randomly assigned to 16 pens (6/pen; 2 pen/diet) and fed their respective diets for 70 d. Diets used include: corn-soybean based control (C), and 3 antibiotic-free diets (D1, D2, and D3) each containing 5% sugar beet pulp plus, a 1:2, 1:1, and 2:1 oats to barley ratio as sources of DF, respectively. The diets were isonitrogenous (18% CP) and isocaloric (3.415 Mcal DE/kg) supplemented with vitamins and minerals to meet nutrient requirements. Average daily feed intake and body weight gain of pigs that were fed D2 and D3 were higher ($P < 0.05$) than the C or the D1 feed pigs. Pigs that were fed diets containing higher proportions of oats were more efficient than the remaining groups. Fermentation indices, pH and VFA concentrations in particular were lower ($P < 0.05$) in pigs fed the C diet, and particularly in the distal colon. In general, pigs that were fed antibiotic-free, high-fiber diets performed better than pigs fed the control diet. This study demonstrates the potential benefits of adding different sources and levels of DF to the antibiotic-free diets of growing pigs. However, further work needs to be done to better understand the mode of action of DF from multiple sources and levels of fiber in the diet.

Key words: dietary fiber, growing pigs, antibiotic-free

T415 Addition of bee pollen to the sow feed and effects on body weight of piglets. C. H. Casillas-Gómez*, I. J. Ruíz-García, and J. R. Orozco-Hernández, *Departamento de Cienicas Biológicas, Centro Universitario de Los Altos, Universidad de Guadalajara, Twepatitlan de Morelos, Jalsico, Mexico.*

The first days of the piglets life is spent depending on the quality of the mother's milk to obtain nutrients and growth promoters as well as the immunity system. Multiparous (Pietrain × York + Landrace) sows lodged under commercial conditions were used to assess 3 levels of bee pollen (0, 31, 62, or 93 g/d) in the diet and the impact on the piglet performance before weaning. Piglet cumulative weight gain averaged 4.490 kg, and was affected by the addition of pollen to the sow's diet ($P < 0.05$; 5.116, 4.598, 3.504, and 4.109 kg for 0, 31, 62 and 93 g of pollen/day, respectively). Therefore, the addition of pollen to the sow's diet had a negative effect ($P < 0.05$) on the daily gain of weight (243, 219, 167, 196 g, for 0, 31, 62 and 93 g of pollen/day, respectively). Mortality was quite similar among treatments ($P > 0.05$). Based on the results it could be concluded that with the addition of bee pollen to the sow's diet had an adverse effect on the piglets before weaning.

Key words: bee pollen, sow, piglet

T416 Effects of thermal stress on liver xenobiotic metabolism gene expression in swine. J. A. Madden*, S. C. Pearce, N. K. Gabler, L. H. Baumgard, and A. F. Keating, *Department of Animal Science, Iowa State University, Ames.*

Thermal stress compromises intestinal integrity in growing pigs, resulting in increased circulating endotoxin concentrations and reduced pig performance. Thus, the study objective was to examine the effect of thermal stress on hepatic detoxification metabolism gene expression in growing *Sus scrofa*. Crossbred gilts (n = 48; 35 ± 4 kg BW) were housed in constant climate controlled rooms in individual pens and exposed to 1) thermal neutral (TN) conditions (20°C; 35–50% humidity) with ad libitum feed intake (n = 18), 2) HS conditions (35°C; 20–35% humidity) with ad libitum feed intake (n = 24) or 3) pair-fed (PF in TN conditions [PFTN], n = 6: to eliminate confounding effects of dissimilar feed intake [FI]). Animals were sacrificed at 1 or 7d of environmental exposure. RNA was isolated from the hepatic caudate lobe and RT-PCR used to quantify hepatic xenobiotic metabolism gene expression. Genes investigated were: 1) acyloxyacyl hydrolase (Aoah) – required for LPS deacylation, 2) aromatic hydrocarbon receptor (Ahr) and 3) NF-E2-related factor 2 (Nrf2) – transcription factors that regulate metabolism gene expression, 4) cytochrome P450 isoform 1A1 (Cyp1a1) – member of the cytochrome P450 family of enzymes with a wide substrate range and 5) glutathione S-transferase isoform mu (Gstm) – an enzyme that catalyzes xenobiotic glutathione conjuga-

tion. Compared with the TN pigs, there was no effect of HS on liver Aoah, Nrf2 or Gstm mRNA abundance. In contrast, relative to TN, HS decreased liver Ahr ($P = 0.05$) and Cyp1a1 ($P = 0.12$) mRNA expression on d7. There was also a decrease in both hepatic Ahr and Cyp1a1 mRNA expression over time in HS animals compared with the TN and PFTN pigs ($P < 0.10$). In conclusion, these data suggest that despite thermal stress-induced increased endotoxin concentrations, hepatic detoxification enzyme mRNAs are not upregulated. In fact, both Ahr and Cyp1a1 hepatic expression are decreased and this may indicate liver dysfunction and inadequate detoxification capability

Key words: heat stress, toxicology, liver

T417 Effect of sex and housing density on growth performance, carcass quality, and fatty acid profile of pigs slaughtered at 110 kg BW. J. I. Morales[1], M. P. Serrano[1], L. Cámara[1], J. D. Berrocoso[1], C. J. López-Bote[2], J. P. López[3], and G. G. Mateos*[1], *[1]Universidad Politécnica de Madrid, Madrid, Spain, [2]Universidad Complutense de Madrid, Madrid, Spain, [3]Copiso S.A., Soria, Spain.*

In total, 228 crossbred pigs (61 d of age) were used to study the effects of gender and housing density on growth performance, carcass quality, and fatty acid (FA) profile of the internal fat of m. gluteus medius (GM) in 110 kg BW pigs. There were 2 genders (gilts and barrows) and 2 rearing densities (0.84 and 0.76 m^2/pig) forming a 2 × 2 factorial. Each treatment was replicated 6 times (a pen with 10 or 9 pigs depending on tretament). For the entire experimental period, barrows had poorer (2.63 vs. 2.51; $P \leq 0.01$) F:G ratio than gilts. An interaction between sex and density were observed for ADFI and F:G ratio; both variables were improved in gilts as the space allowance decreased whereas the opposite effect was observed for barrows ($P \leq 0.05$ for the interaction). No differences among treatments were found for carcass yield and pH_{24} h postmortem. Furthermore, density did not affect any of the carcass quality traits studied. Trimmed ham (13.3 vs. 13.0%) and loin (5.96 vs. 5.67%) yield were higher ($P \leq 0.001$) for gilts than for barrows. Treatment did not affect palmitic acid, stearic acid, or polyunsaturated FA concentration in GM fat. However, oleic acid content was higher (43.8 vs. 42.6%; $P \leq 0.05$) for pigs reared at the higher density and linoleic (10.0 vs. 9.3%) and oleic (43.9 vs. 42.4%) acid content were higher ($P \leq 0.01$) for gilts than for barrows. In conclusion, fat from GM from pigs reared at 0.76 m^2/pig had more monounsaturated FA content than fat from pigs reared at 0.84 m^2/pig. Also, fat from gilts had more monounsaturated FA content than fat from barrows. We concluded, that under the conditions of the present experiment, a density of 0.84 m^2/pig for gilts and of 0.76 m^2/pig for barrows is recommended. Sex and space allocation affected the FA profile of pigs slaughtered at 110 kg BW.

Key words: carcass quality and fatty acid profile, housing density, pig performance

T418 Productive performance and carcass quality of gilts and surgically and immune-castrated male pigs from crossbreds of Duroc and Pietrain sire lines. J. I. Morales[1], M. P. Serrano[1], L. Cámara[1], J. D. Berrocoso[1], J. P. López[2], and G. G. Mateos*[1], *[1]Universidad Politécnica de Madrid, Madrid, Spain, [2]Copiso S.A., Soria, Spain.*

The influence of gender [intact females (IF), surgically castrated males (CM), and immune-castrated males (IMC)] and terminal sire line [Duroc (DU) and Pietrain (PI)] on growth performance and carcass quality was studied in pigs from 23.5 to 134 kg BW. The female line used was Large White × Landrace in all cases. Each treatment (3 × 2) was replicated 5 times (a pen with 10 pigs). The CM were castrated at 4 d of age and the IMC pigs were immunized against GnRF at 87 and 137 d of age (34 d before slaughter). Backfat thickness at P_2 and intramuscular fat (ITMF) at Longissumus dorsi were recorded. The IMC and CM had higher (1.08 vs. 1.08 vs. 1.02 kg/d; $P \leq 0.001$) ADG than IF. Furthermore, CM ate more feed (2.59 vs. 2.36 vs. 2.35 kg/d; $P \leq 0.001$) than IMC and IF. Consequently, IMC had better (2.17 vs. 2.40 vs. 2.31; $P \leq 0.001$) F:G ratio than CM, with IF being intermediate. Carcass yield was lower for IMC than for IF and CM (76.4 vs. 78.9 and 78.3%; $P \leq 0.001$). Trimmed ham and loin yields were higher ($P \leq 0.001$) for IF than for IMC and CM. The CM had more (28.6 vs. 26.7 vs. 26.1 mm; $P \leq 0.001$) BF than IF and IMC, and ITMF was lower (3.5 vs. 3.9 vs. 3.7%; $P \leq 0.05$) for IF than for CM, with IMC being intermediate. No differences were found between sire lines for carcass yield but crossbreds from PI had more ($P \leq 0.001$) trimmed ham and loin yields than crossbreds from DU. The ITMF was higher ($P \leq 0.001$) for DU crossbreds than for PI crossbreds. We conclude that IMC were more efficient but had lower carcass yield than CM and IF. Furthermore, IF have better carcass quality than IMC and CM and ITMF content is similar from IMC and CM. Crossbreds from PI sires have better carcass quality but poorer BW gain and meat quality traits than crossbreds from DU sires. Therefore, IMC and crossbreds from DU are preferred for the production of heavy pigs destined to the dry-cured industry.

Key words: productive performance and carcass quality, immune-castration, sire lines

T419 Fatty acid composition of piglet tissues changes during suckling time. M. Sini, A. Nudda, G. Pulina, S. P. G. Rassu, and G. Battacone*, *Dipartimento di Scienze Zootecniche, Università Degli Studi di Sassari, Sassari, Italy.*

Aim of this work was to determinate the fatty acid (FA) evolution in different tissue of piglets during the suckling time. Litters of 3 sows similar for age, parity and breed (L × LW), and inseminated with the same Landrace boar semen, were used. Starting a week after parturition one piglet from each litter was stunned, exanguinated, and eviscerated each week. Brain, liver, and skeletal muscle samples were removed from 4 piglets per sow. Fatty acid (FA) composition of total lipid extract from each tissue was determined by gas chromatography. Concentration of each FA was expressed as percentage of total FA. Data were analyzed with ANOVA to detect difference in FA composition between tissue during the suckling period. The mean of saturated fatty acid (SFA) increased during the sucking time, mainly due to the increase of C16:0 which represent about 50% of the total SFA. The mean values of unsaturated (UFA) and monounsaturated (MUFA) fatty acid and the PUFA-n3 decreased during the suckling time. FA composition differed significantly within tissues during the suckling time. In brain, the SFA decreased during suckling period, whereas SFA increased in liver and muscle. Conversely, UFA and MUFA increased in brain and decreased in liver and muscle. This leads to a significant decrease in relationships MUFA/SFA and SFA/UFA. These results confirm that the FA composition of the fat differed within the suckling time and suggest that the FA source in the diet must be adequate to support the growing piglets requirements.

Key words: fatty acid, piglet, tissues

T420 Opinions of farm versus urban freshman college students on issues involving animal agriculture before and after animal science instruction. E. A. Bobeck*, D. K. Combs, and M. E. Cook, *University of Wisconsin-Madison, Madison.*

Increasingly, incoming university animal science majors have urban demographics with no history of direct contact with farm animals and no or neutral opinion regarding issues facing animal farming. A study was conducted to determine 1) opinions of incoming students on critical issues involving animal farming practices, and 2) changes in their opinions after 4 mo of instruction involving basic principles and issues of animal farming. A class of 114 students was given 2 identical surveys (start and end of semester) with 14 questions regarding demographics and animal use issues. Students marked a continuous scale of 129mm where 1 = agree and 129 = disagree for issue questions and identified their survey with a student-generated identifier (favorite food+superhero). Paired *t*-test analyses were conducted only on students with strictly farm (n = 14) and strictly urban (n = 19) backgrounds who completed both surveys using the same identifier (33/114 students). Before education, students with urban backgrounds were less likely to agree with animal farming issues involving value to society (27.0mm), morality (28.4mm), welfare (53.8mm), humaneness of agricultural practices (61.0mm), and ethics of breeding livestock for valuable traits (29.3mm) than farm students (4.2mm, 7.2mm, 27.2mm, 38.7mm, and 12.4mm, respectively, $P < 0.05$). Urban students were more likely to purchase organic animal products (60.2mm) and animal products based on environmental/ welfare standards (57.5mm) than farm students (99.9mm and 94.5mm, respectively, $P < 0.05$). After education, the opinions of urban students did not differ from farm students for questions involving humaneness of agricultural practices (36.1mm vs. 24.5mm, $P > 0.05$), breeding for valuable traits (16.6mm vs. 10.1mm, $P > 0.05$), and purchase of animal products based on environmental/ welfare standards (72.4mm vs. 91.5mm, $P > 0.05$). Data showed that urban students tend to be neutral with regards to animal farming issues, but when exposed to science-based instruction on animal farming, attitudes change to agree more closely with students with farm backgrounds.

Key words: survey, student opinion, agriculture issues

T421 Connecting lecture to the real world in animal sciences. J. J. Parrish*, J. R. Schindler, and R. L. Monson, *University of Wisconsin, Madison.*

A structured authentic learning experience was devised to connect lecture and the real world in a reproductive physiology course in animal sciences. The course had on-line, podcast lectures (2/week) and a 2 h lab/week. There were 4 lab sections with 73 students total. A cow project was created in which groups of 4 students within a lab section were assigned 1 of 20 cows for the semester. Student groups completed experiences with or without instructors that included: observation of estrus, design and implementation of a timed artificial insemination (AI) scheme, actual AI of their cow, determine potential pregnancy by return to estrus and plasma progesterone levels, and ultrasound for pregnancy 63 d following insemination. The specific goals of the project were to: 1) understand estrus behavior, 2) identify and administer drugs used in timed AI, 3) understand how drugs used in item 2 effect physiological events, 4) make connections between molecular mechanisms of hormone action and physiological events, 5) AI and detection of potential pregnancy in the group's cow, and 6) teach students to handle, interact and develop the skills needed to work with a large domestic animal. Students were assessed in 2 ways. First, an individual essay exam was given in lab to assess goals 1 to 5. A separate question addressed each goal. Second, group reflection on the project was required at the end of the semester but content of that reflection was not specified. The reflection was scored for an overall increase (scale 1 to 5, none to multiple indications of an increase) in understanding of animal physiology and increase in understanding cattle behavior and ability to work with cattle via completion of the project. The average exam score ± SEM was 78 ± 2% and students deemed to have accomplished goals 1 – 5 satisfactorily (>65% exam score) was 82%. When the group self reflection was evaluated, the mean ± SEM score assigned for understanding of physiology and understanding how to work with cattle and their behavior was 4.2 ± 0.2 and 4.8 ± 0.1 respectively. The described cow project was an effective means of connecting lecture material to the real world in a structured authentic learning experience.

Key words: reproduction, cattle

T422 Enhancing the pool of underrepresented minorities in veterinary medicine. O. U. Bolden-Tiller*, *Tuskegee University, Tuskegee Institute, AL.*

The Tuskegee University School of Veterinary Medicine (TUSVM) has trained over 70% of all African American veterinarians in the United States. The Department of Agricultural and Environmental Sciences is home to almost 300 underrepresented minorities (URM) majoring in Animal Sciences, which has long served as a feeder program for TUSVM. A capstone course, Domestic Animal Anatomy (DAA) that is partially taught by TUSVM students, was initiated to enhance student performance in Veterinary Anatomy. The objective of the current study was to determine the impact of DAA on academic performance in veterinary school. Former students enrolled in DAA from 2007 to 2010 who had finished at least one semester of Veterinary Anatomy completed a survey consisting of quantitative items, primarily on a Likert scale, aimed to gauge students′ opinions on the impact of the course on their performance in Veterinary Anatomy. TUSVM students who participated in teaching DAA completed a similar survey aimed to gauge their opinion on how their participation in DAA impacted their performance in veterinary school. Overall, DAA had a positive impact on student performance in Veterinary Anatomy and other veterinary courses. Similarly, TUSVM students who participated in teaching DAA also tended to perform well in veterinary school. There remains a disparity in the number of underrepresented minorities in the field of veterinary medicine. Here we have identified a mechanism that enhances the performance of URM in veterinary school and provides a format for training future veterinarians in undergraduate teaching.

Key words: underrepresented minorities, veterinary medicine, anatomy

T423 Comparison of multiple choice and short essay assessment vehicles on student performance in an upper division animal reproduction course. L. J. Spicer* and M. E. Payton, *Oklahoma State University, Stillwater.*

The primary assessment vehicle in most basic science courses in undergraduate programs is the multiple choice question (MCQ) exam. Regular assessment of students' knowledge, comprehension, and com-

petence is also important for motivating learning. In addition, short essay question (SEQ) exams take longer to grade and grading can be subjective. The aim of this study was to compare student performance on MCQ and SEQ exams. This study analyzed exam performance records from 653 students collected over a 9 year period in an upper division animal reproduction class. Student numbers for each year ranged from 50 to 98. Records from each student included results from 3 exams given during a 15-week semester. Each exam varied between 20% to 80% of either MCQ or SEQ, and results for each question style were summarized as the percentage correct. One-third of the MCQ were true-false questions. The first analysis used the MIXED procedure of SAS to determine if differences in performance scores existed between MCQ and SEQ among exam 1, 2 or 3, using year as a random effect. MCQ scores were not significantly different for the 3 exams, but scores were significantly different for the SEQ. There was a difference ($P < 0.001$) in scores for MCQ and SEQ for exams 1 and 2. However, for exam 3, the difference was not significant ($P > 0.23$). Over all records, Pearson correlations coefficients revealed a significant positive correlation between MCQ and SEQ scores (r = 0.56, n = 1907) and this correlation did not differ among exam 1, 2 or 3. The correlation between MCQ and SEQ was similar regardless of whether SEQ point totals were 32–50 (r = 0.56, n = 796) or 20–30 (r = 0.59, n = 1111). Correlations conducted within year and exam also revealed positive correlations ($P < 0.001$) for all exams and years, but correlations ranged from a low of 0.46 (n = 50) to a high of 0.83 (n = 84). Results indicate that MCQ and SEQ, in general, provide similar student assessment scores, and that student scores in SEQ increase as they become familiar with examination style.

Key words: assessment, exams, undergraduate

T424 Variables that affect academic performance in undergraduate animal science courses. M. M. Beverly, K. J. Stutts, and S. F. Kelley*, *Sam Houston State University, Huntsville, TX.*

The objective of this study was to evaluate the effect of student absenteeism and student characteristics on academic success in undergraduate animal science courses. Data were collected on 2,129 students enrolled in animal science courses at Sam Houston State University during 2 fall and 2 spring 16-week semesters. Data collected included number of absences, gender, classification, major field of study, and final course grade for each student. Least squares means for absences and final course grades were calculated using the mixed procedure of SAS. All main effects and all 2-way interactions were included in the model. Mean number of absences for all students was 3.75 per course. Students were divided into 3 groups based on number of absences in a course during the semester: low (0–2), average (3–6), and high (7 or more). Students with a low number of absences had the highest ($P < 0.01$) mean final course grade (83.6). Students with an average number of absences (79.5) had a higher ($P < 0.01$) mean final course grade than students with a high number of absences (69.5). There was also a significant effect of gender and student classification on final course grade. Female students had a higher ($P < 0.01$) mean final course grade (81.3) than male (77.3) students. In addition, students classified as juniors (80.4) or seniors (81.6) had a higher ($P < 0.01$) mean final course grade than students classified as freshmen (78.2) or sophomores (77.0). Regarding absences, males (4.2) had a higher ($P < 0.01$) mean number of absences than females (3.4), and seniors (3.3) had a lower ($P < 0.01$) mean number of absences than freshman (4.2) and sophomores (4.0). These results indicate that students with a greater number of absences attained a lower final course grade and females outperformed males and upper classmen outperformed lower classmen in terms of final course grade in undergraduate animal science courses. Male students and students classified as freshmen or sophomores were more likely to have a greater number of absences than females or students classified as juniors or seniors.

Key words: undergraduates, attendance, course grades

T425 CyberSheep: Improving student understanding of animal breeding concepts with a virtual sheep flock. K. L. Kessler*[1], R. M. Lewis[2], J. P. Cassady[3], and K. M. Cammack[1], *[1]University of Wyoming, Laramie, [2]Virginia Polytechnic Institute and State University, Blacksburg, [3]North Carolina State University, Raleigh.*

Animal breeding educators have identified the need to develop genetic simulation tools that provide undergraduate students an opportunity to apply course concepts. The CyberSheep program, developed at Virginia Tech, is an online genetic simulation tool in which students manage a flock of sheep for 6 generations within a cooperative breeding scheme. Each generation occurs within a one-week time frame, enabling students to observe consequences of their culling and mating decisions in "real time". Flocks compete to accomplish one of 2 main objectives: 1) maximization of market weights or 2) maximization of flock net worth. Students are also challenged to eradicate a lethal recessive allele. Undergraduate students playing at the University of Wyoming and North Carolina State University were anonymously evaluated before and after the simulation to determine its contribution to their understanding of concepts presented in an introductory animal breeding course. Students were asked to evaluate their level of understanding of fundamental concepts used in CyberSheep, including animal evaluation based on genetic merit and level of inbreeding. Survey scores were analyzed using the GLM procedure of SAS. Based on a 5–point scale, students rated their initial understanding of these 2 concepts at 3.5, coinciding to a moderate level of understanding. Scores rose ($P \leq 0.014$) to 3.8 in the final survey, indicating a slight improvement in understanding of these same concepts with the use of CyberSheep. Greatest improvement was seen in understanding of cooperative breeding schemes with the score rising ($P < 0.001$) from 2.7 to 3.5. Survey scores were not affected by university ($P \geq 0.415$). In general, students were satisfied with their level of learning from CyberSheep with a score of 3.6, and found the simulation to be ′informative′ and ′fun′ with an average score of 3.5 for each. It was concluded that animal breeding students benefited in their understanding of fundamental concepts through the use of CyberSheep.

Key words: animal breeding, education, genetic simulation

T426 Academic preferences of freshman college students in the Department of Animal Industry of the University of Puerto Rico at Mayagüez. G. Ortiz-Colón*, J. M. Huerta-Jiménez, L. del Valle-Mercado, M. Pagán-Morales, and E. Jiménez-Cabán, *University of Puerto Rico at Mayagüez, Mayagüez, PR.*

The student retention in the College of Agricultural Sciences of the University of Puerto Rico at Mayagüez has been under 61% for at least the last 6 years. Within the College of Agricultural Sciences, the situation of the Department of Animal Industry (DAI) is not different. The last reported DAI student retention was only 59.4%. The reasons for this low retention in the DAI have not been previously investigated. We hypothesized that the DAI course work is not fulfilling the students' expectations. Surveys were developed to evaluate the professional interests of DAI freshman students and delivered to those taking the introductory course of Animal Industry. Of the 141 surveyed individu-

als, 68.8% were 18 years old and 56.1% were males. Most (69.8%) of these students had no previous agriculture experience, while only 7.2% had participated in 4H Clubs, and only 5.0% had been Future Farmers of America. Most (84.4%) of the students had not taken a course in agriculture before being accepted into the DAI. Moreover, 53.2% of the students came from urban settings (developments and condominiums). While 35% of the students intend to become veterinarians in the future, only 7.9% would like to become animal scientists and 7.1% expressed a desire to change to other academic programs. When students were asked to choose what species they would like to specialize in, 24.8% chose companion animals, 16.6% indicated wild animals, and 12.4% beef cattle. Because the DAI does not have the animals or facilities to supports course work related to companion animal management and wild animal management, 41.4% of the clientele might be dissatisfied with the curriculum offered by the DAI and this might contribute to the low retention rates observed in this department.

Key words: Hispanic serving institutions, animal science, student retention

T427 Impact of duration of an online animal science nutrition course on student learning assessments. K. D. Ange-van Heugten* and A. Renjifo McComb, *North Carolina State University, Raleigh.*

To determine whether learning assessments differ when the same online course is offered over 5 wk versus 10 wk semesters, Principles of Animal Nutrition was taught twice during the summer of both 2009 and 2010. All offerings had the same instructor and teaching assistant. Both 5 and 10 wk durations in 2009 started with 30 students and finished with 29, while for 2010, both 5 and 10 wk durations started with 35 and ended with 35 students for 5 wk and 31 for 10 wk. Assessments were identical between 5 and 10 wk, but varied between 2009 and 2010. The 2009 5 wk course had 4 students finish with an F grade, 3 of which dropped after final grade distribution. No students in the 10 wk class received an F or dropped after final grades. In 2010, both the 5 and 10 wk class had 1 student finished with an F. Students in the 5 wk course were compared with those in the 10 wk course with and without outliers (late withdrawals). When all students were included (5 wk n = 64 and 10wk n = 60), 2009 and 2010 did not differ. Similarly, when student outliers were deleted, 2009 and 2010 did not differ. When all students were evaluated, 5 wk students had lower exam 1 grades ($P < 0.01$), participation points, quiz and final grades ($P < 0.05$; 82% ± 2.2 vs. 87% ± 2.3). The total number of times logged into the course (65.2 vs. 100.3) and total amount of time (47 h vs. 65 h) were lower ($P < 0.001$) for the 5 wk course. When the 5 wk courses were compared with the 10 wk ones without the outliers, participation points (88% ± 1.0 vs. 91% ± 1.1) and exam 1 grades (81% ± 1.8 vs. 86% ± 1.8) tended to be lower ($P < 0.10$) for the 5 wk course and times logged in (69 vs. 101) and total time online (50 vs. 66 h) were higher ($P < 0.001$) for the 10 wk courses. Five wk students only had 11 d before exam 1 while 10 wk students had 22 d. Final grades were 88.5% for 10 wk and 86.9 for 5 wk, indicating students can be successful regardless of course duration. However, the greater number of late withdrawals in the 5 wk course, less time online and lower scores indicates that learning large amounts of material in the shorter course length is more overwhelming than some students anticipate.

Key words: distance education, course duration, nutrition

T428 Effectiveness of a university introductory course in developing student confidence in horse handling and riding. M. Nicodemus*, *Mississippi State University, Mississippi State.*

Horsemanship is the art of riding and managing horses. These skills are fundamental to those college students wanting a career in the equine industry and so Mississippi State University (MSU) equine students are required to take one horsemanship elective for their degree, which may include ADS 1132 Introduction to Horsemanship. While introductory courses are designed to cover the basics of a subject matter, covering the necessary horsemanship skills for those students going into the equine industry is difficult to accomplish in one semester; and thus, study objectives were to determine the effectiveness of an introductory course in developing student confidence in performing various horsemanship activities. Researcher-developed, 19 question survey instrument focused on horse riding and handling was given both at the start and end of the semester to 42 students taking ADS 1132 at MSU. Each question described a horsemanship activity that students gave a score ranging from 1 to 5 indicating their confidence in performing the activity with 5 reflecting *extreme confidence*. Means (SD) were determined for each question and one-way ANOVA was performed to determine the effect of the course on student confidence in their horsemanship skills ($P < 0.05$). While all questions showed improvement in confidence, only 7 questions demonstrated a significant increase in scores with only 2 of the improved scores focused on riding activities (Table 1; $P < 0.05$). Although most improvements were made in ground handling activities, these skills lay the foundation to more advanced horsemanship activities and are vital to those students going into the field of veterinary sciences in which 50% of the students were applying to veterinary school. Survey results assist in suggesting course development areas and indicate additional horsemanship courses may need to be required for equine students focusing on a career requiring advanced riding skills.

Table 1. Initial and final survey means (SD) of confidence levels on questions with significant score improvements ($P < 0.05$)

Question	Initial	Final
Adv Groundwork: Trained Horse	2±1	4±1
Riding: Trained Horse	3±1	5±1
Riding: Trained Horse w/Behavior Problems	2±1	5±1
Groundwork: Society-Type Breeds	2±1	4±1
Groundwork: European Breeds	2±1	4±1
Handling/Utilizing Tack	2±1	5±1
Mgt/Health Care Activities	3±1	5±1

Key words: horsemanship, introductory equine courses

Animal Behavior and Well-Being 2

304 ASAS Early Career Award Presentation: Working to foster the discovery, sharing, and application of knowledge concerning the well-being of farm animals. A. Johnson*, *Iowa State University, Ames.*

In developed countries there has been intense marketing, social and political interest in farm animal well-being and husbandry procedures. The need for relevant science that can be applied in education, assessment, audits and legislation has escalated. Yet in the US there are minimal farm animal ethologists compared with the more traditional sciences of nutrition, physiology and reproduction. Ethologists have risen to this challenge by working together and across disciplines on farm animal well-being research and extension. This approach creates a more efficient delivery mechanism to share and apply contemporary scientific knowledge. Three central themes have driven my research and extension program (1) maintenance behaviors of farm animals (2) handling and system design for the finisher pig and (3) sow productive lifetime. It is certain that progress in these areas requires collaboration of experts in many disciplines and our efforts in developing handling and system designs for the finisher pig will be highlighted. Three important questions must be addressed in regards to the occurrence of market pigs that become injured, non-ambulatory or die during the marketing process (1) science; what is the etiology of the non-ambulatory pig? (2) economics; it was calculated that transport losses cost the US swine industry $50 to $100 million loss/yr (2009) and (3) legislation whereby if passed these animals would not be allowed into the human food chain resulting in approximately $500 million/loss/yr to the US swine industry alone. Several of our studies have addressed loading gantry design, pre-sorting and raising pigs in large and small pens. Data collected from these studies will provide science back to decision makers and information for extension such as the Transport Quality Assurance program, posters, flyers, media stories and fact-sheets in addition to peer review abstracts and papers. The overall aim of these efforts will be to reduce stressors that impinge on the pig at marketing, reduce transportation losses and maintain the well-being of the pig.

Key words: handling, swine, transport

305 The effect of reactive state on the physiology of dairy cows milked in a novel environment. M. A. Sutherland*[1] and G. A. Verkerk[2], *[1]AgResearch Ltd., Animal Behaviour and Welfare Group, Hamilton, New Zealand, [2]DairyNZ, Hamilton, New Zealand.*

Differences in the way animals react behaviorally and physiologically to a stressor may reflect differences in fearfulness or coping style. The objective of this study was to determine if reactive state affects the physiology of dairy cows being milked in a novel environment. The reactive states of multi-parus cows were assessed using 4 behavioral tests: restraint test, exit velocity, flight distance, and an approach test. After this initial testing, 20 cows were selected and separated into 2 groups: low responders (LR: n = 10) and high responders (HR: n = 10). Cows were milked according to their established routines in a rotary shed and physiological data as well as milk production parameters were collected over 5 consecutive days. On Days 2 and 5, blood samples were collected via the tail vein before and after milking to measure cortisol and oxytocin concentrations, and heart rate monitors were attached to measure autonomic responses during milking. The following week, cows were milked in a novel environment (herringbone parlor within the same farm facility) over 5 consecutive days, and the sampling program was repeated. Data were analyzed using the MIXED procedures of SAS. Pre-milking cortisol concentrations were greater ($P < 0.05$) in HR than LR cows, and cortisol concentrations were greater ($P < 0.05$) when cows were milked in the herringbone compared with the rotary parlor, regardless of reactive state. Pre-milking heart rate was greater ($P < 0.05$) in HR than LR cows, and heart rate was greater ($P < 0.05$) in HR cows in response to being milked in the herringbone parlor than in LR cows. Milk yield was greater ($P < 0.06$) and milking duration longer ($P < 0.05$) for LR compared with HR cows. Average milk flow did not differ ($P > 0.05$) between LR and HR cows, but the milk let-down pattern was affected ($P < 0.001$) by cow reactive state and milking environment. These results indicate that baseline physiological measures differ between cows of differing reactive states, and that a cow′s reactive state will affect the way she responds to a novel environment.

Key words: behavior, dairy, stress

306 The effect of reactive state and training on the behaviour and milk production of heifers during the first week of lactation. M. A. Sutherland*[1] and G. A. Verkerk[2], *[1]AgResearch Ltd., Animal Behaviour and Welfare Group, Hamilton, New Zealand, [2]DairyNZ, Hamilton, New Zealand.*

Differences in the way in which animals react behaviorally and physiologically to new situations may reflect differences in fearfulness or coping style. The objective of this study was to determine if training before calving could modulate the reactive state in heifers during their introduction to milking routines after calving. The reactive state of heifers was assessed pre-partum using 4 behavioral tests: restraint test, exit velocity, flight distance, and an approach test. On the basis of this testing, 40 heifers were selected and denoted as either low (LR: n = 20) or high (HR: n = 20) responders. One month before calving, half the heifers from each group were allocated randomly for training in the rotary milking-parlor over a 2 d period while the other heifers were left undisturbed in the paddock. During the first 5 d of lactation, behavioral and physiological data were collected from all heifers, including behavior during cup attachment, milk yield, milk flow rate, and residual milk volume. Data were analyzed using the MIXED procedures of SAS. Behavior scores during cup attachment (scale: 0 = no hind foot movement, 4 = backward kick with a hind leg) were higher ($P < 0.05$) in trained LR compared with non-trained LR heifers, indicating an increased level of reactivity; but training did not influence scores for behavior during cup attachment in HR heifers. Milk yield did not differ ($P > 0.05$) between trained and non-trained LR heifers, but was lower ($P < 0.001$) in trained HR compared with non-trained HR heifers. The patterns of milk flow-rate differed ($P < 0.01$) between trained and non-trained, LR and HR heifers, with trained HR heifers having the lowest flow rate. Percentage residual milk volume was lower ($P < 0.005$) in trained HR compared with non-trained HR heifers, and tended ($P = 0.07$) to be reduced in trained compared with non-trained LR heifers. Training to the milking parlor negatively affected the behavioral response of heifers to milking and milk production, and this response was further influenced by individual reactive state.

Key words: behavior, dairy, milk production

307 Effect of frequency of feed delivery on the behavioral patterns of dairy cows milked in an automatic system. J. A. Deming*[1],

R. Bergeron[2], K. E. Leslie[3], and T. J. DeVries[1], *[1]Dept. Animal and Poultry Science, University of Guelph, Kemptville Campus, Kemptville, ON, Canada, [2]Dept. Animal and Poultry Science, University of Guelph, Campus d'Alfred, Alfred, ON, Canada, [3]Dept. Population Medicine, Ontario Veterinary College, University of Guelph, Guelph, ON, Canada.*

The primary objective of this study was to determine the effect frequency of feed delivery has on the behavior of dairy cows milked in an automatic milking system (AMS); the secondary objective was to determine if this effect is influenced by lameness. Ninety lactating Holstein dairy cows, kept in a free-stall barn in 1 of 2 pens, each with a free-traffic AMS, were monitored on each of 2 treatments in a cross-over design with 35-d periods. The treatments were delivery of TMR: 1) 1x/d (at 0730h) and 2) 2x/d (at 0730 and 1730h). During the last 7 d of each period standing/lying behavior of the cows were recorded with data loggers, while milking frequency and yield were recorded by the AMS. Cows were lameness scored (scale of 1 = sound to 5 = severely lame) twice each period. Data were analyzed in a general linear mixed model including lameness score as a covariate. There was a tendency ($P = 0.06$) for cows to get milked more frequently when fed 2x/d (2.6 vs. 2.5 milkings/cow/d; SE = 0.08). Cows with higher lameness scores got milked less frequently ($P = 0.02$). Frequency of feed delivery did not affect ($P = 0.6$) milk yield (34.7 kg/d; SE = 1.9). Cows spent 10.9 h/d (SE = 0.2) lying down split into 7.2 lying bouts/d (SE = 0.3); these did not vary ($P = 0.2$) with treatment. Cows with higher lameness scores spent more time lying/d ($P = 0.045$) and had more lying bouts/d ($P = 0.03$). When fed 2x/d, cows milked in the AMS closer in time (SE = 57.9; $P < 0.001$) to feed delivery (milking on average 17.1 min from a feed delivery), while when fed 1x/d cows milked in the AMS at time points much further away from feed delivery (milking on average 264.5 min from a feed delivery). Despite having less of an incentive to remain standing, cows still spent more time standing after milking when fed1x/d (94.7 vs. 86.2 min; SE = 5.8; $P = 0.03$). Cows with higher lameness scores tended ($P = 0.09$) to lie down sooner after milking. The results suggest that frequency of ration delivery has some affect on the behavior of AMS-milked cows; further the results show that, regardless of feeding frequency, these behavioral patterns are affected by lameness.

Key words: automatic milking, behavioral pattern, lameness

308 Effect of yearly climate on milk yield in a sub-tropical environment. J. C. Lees* and J. B. Gaughan, *The University of Queensland, Gatton, Queensland, Australia.*

Heat load is a major cause of milk yield (MY) loss in tropical and subtropical dairy production. In this study the long-term effects of heat load on MY in a sub tropical environment were investigated. Individual daily MY was obtained from 250 Holstein-Friesian cows housed outside over 3 summers (340 d) and 2 winters (119 d). The cows had access to a feed pad and pasture. Ambient temperature (TA), black globe temperature (BG), and relative humidity (RH), were obtained at 10 min intervals from an automated on-site weather station. The effects of TA, BG, RH and THI on daily MY were determined for the herd (N) using Pearson partial correlation analysis (days in milk used as a co-variant). The relationship between daily MY and the climate variables at 0800, 1200, 1600, 2000, 0000 and 0400 h was established. The effects of previous heat load on current MY (d 0) were examined using the mean daily THI for d −1, −2, −3 and −4. Cows were categorised by MY as low (LO < 19kg/d), medium (MD 19 to 27kg/d) or high (HI > 27kg/d) and subjected to the same analysis as N. Increasing THI, BG and TA had negative correlations with MY on a herd basis. Climate data obtained at 0800 h had the highest correlations with daily MY. Whole herd correlations ($P < 0.0001$) between MY loss, TA, BG and THI at 0800 h were −0.39, −0.43, and −0.39 respectively. There were weak correlations ($P < 0.05$) between the climatic variables and MY of LO cows, and consistently strong negative correlations for MD and HI cows. The MY of HI cows had the best correlation (−0.54; $P < 0.0001$) with BG at 0800 h. The relationship between daily MY and mean daily THI was −0.38 for N, −0.10 for LO ($P > 0.05$), −0.31 for MD, and −0.45 for HI ($P < 0.0001$). The relationship between climatic variables on previous days was a better indicator of d 0 MY than on d 0. When lag effects were examined the best correlation for d 0 MY was mean THI on d −2 (−0.54; $P < 0.0001$). This suggests that effects of heat load on MY are cumulative. Heat stress models need to be developed that will account for the impact of cumulative heat load on production and welfare.

Key words: heat load, milk yield, dairy cows

309 Evaluation of two different cooling systems on a Sicilian dairy farm: Physiological parameters and milk aroma. R. Ben Younes[1,3], G. Azzaro[2], I. Schadt[2], G. Belvedere[2], M. Caccamo[2], R. Petriglieri[2], G. Licitra[3,2], and S. Carpino*[2], *[1]INAT, Tunis, Tunisia, [2]CoRFiLaC, Regione Siciliana, Ragusa, Italy, [3]DISPA, Catania University, Catania, Italy.*

Two cooling systems were evaluated on a Sicilian dairy farm, during summer time, with regard to cows' responses in terms of respiratory rates (RR) and rectal temperatures (RT) and milk chemical composition. The effects on milk aroma were also evaluated, because cows′ body temperature might influence milk temperature, oxidation processes and stability as a result. Cows were assigned to 2 groups of 10 animals with similar average days in milk (DIM), milk production and composition. One group was cooled with a sprinkler system (SP) the other was cooled by showers (SH). Both had additional ventilation. Cows initial average values of DIM, milk yield (kg/cow/d), fat (%), protein (%), lactose (%) ± standard deviation in SP were 141 (±88.3), 36 (±10.2), 3.7 (±0.4), 3.2 (±0.1), 4.2 (±0.6), and 139 (±73), 35 ± 6.6), 3.6 (±0.4), 3.2 (±0.2), 4.6 (±0.5) in SH, respectively. Individual milk samples were analyzed for fat, protein and lactose content and RR and RT were measured 6 times with 15 d intervals, beginning at the end of June. At each test day, THI values were calculated. Milk samples of the last 3 test days were additionally analyzed by SmartNose for milk aroma profiles. THI values were 73.3, 79.7, 79.6, 77.8, 74.1 and 72.3 at test d 1 through 6, respectively. Cows cooled with SH compared with SP had significantly higher RT and RR ($P < 0.001$). Measured RT and RR (LSMeans ± SE) in SH and SP were 39.26 ± 0.001, 59.92 ± 0.018 and 38.95 ± 0.001 and 54.84 ± 0.018, respectively. SmartNose analysis highlighted differences in milk volatile composition between treatments. Fat, protein and lactose (%) were not different between groups ($P > 0.05$). These parameters were only affected by test day ($P < 0.001$). Relative humidity with SH might be higher compared with SP and might have increased heat stress of dairy cows. Milk aroma profile was apparently related to RR and RT and oxidation processes might be involved. Further investigations on the effects of cows′ body temperature on milk oxidation processes and stability might be needed.

Key words: cooling systems, heat stress, milk aroma profile

310 Assessment of a web camera to evaluate farm management and cow behavior. G. Licitra[1,2], G. Azzaro[1], R. Petriglieri[1], M. Cac-

camo[1], and J. D. Ferguson*[3], *[1]CoRFiLaC, Regione Siciliana, Ragusa, Italy, [2]DISPA, Catania University, Catania, Italy, [3]University of Pennsylvania, PA.*

The objective of this project was to evaluate the use of a web camera to assess cow behavior and management activities on a dairy farm. Often advisors are requested to provide expert advice to management based on observation of cow behavior from a farm visit. This can be biased as often observations are made from a one-time visit, however to view the farm more frequently may be expensive if the advisor is coming from a distance. Using a web camera or digital videos taken at times throughout the day may provide views of cow behavior and facility use relative to management activities, such as feeding and milking, facilitating a more comprehensive evaluation of the farm avoiding the expense of repetitive farm visits. In addition, as developing countries expand their dairy industry, expert advisors may be contacted in countries with mature dairy industries to provide support and training of local professionals through the internet without a physical visit to the dairy in question. Use of digital media has the potential to expand interaction across regions and enhance training and support of novice dairy advisors and producers. Assessment of cow behavior, cleanliness, body condition, lameness, and facility comfort via web technology was evaluated against assessments made from farm visits. Assessments were made from 2 farms with 2 observers visiting the farm contemporary to an individual viewing the farm(s) via a web camera. Subsequently, observations by all 3 individuals were made using the web camera at different times of the day from separate computers. In general, cow behavior assessments between observers and methods were consistent, but there were differences in assessing BCS between methods and observers and in assessing cleanliness and lameness between methods. The web camera enabled assessment of management activities over successive periods. Results therefore demonstrate that visual assessment of animal behavior and management of a facility may be performed through distant imaging by precluding advisors a visit to the farm in working with dairy producers and local advisors.

Key words: cow behavior, management evaluation, visual assessment

311 Novel techniques for anesthesia during disbudding of calves. K. R. Tapper*[1], J. P. Goff[1], B. L. Leuschen[2], J. K. West[2], and S. T. Millman[1,2], *[1]Iowa State University Department of Biomedical Sciences, Ames, [2]Iowa State University Veterinary Diagnostic and Production Animal Medicine, Ames.*

The objective of this study was to evaluate novel anesthetics to alleviate pain during disbudding. Efficacy was determined by latency for loss of sensation (LS), as well as presence and duration of analgesic effect. Thirty calves were randomly assigned to one of 3 cornual anesthetic treatments: 100% ethanol (E), depot solution of 2% lidocaine suspended in peanut oil (D), or control 2% lidocaine (C). On Day 0, 2 mL/horn anesthetic was injected and LS was measured at 5 min increments using a needle prick test at 4 locations around the horn bud. Calves with sensation at +10 min received an additional 1 mL anesthetic injection. When LS was achieved, calves were disbudded using heat cautery. Presence and duration of analgesic effect were determined using pressure algometry (PA), which quantified mechanical nociceptive thresholds as kilograms of force (kgf) relative to a head withdrawal response. Four landmarks around each horn bud and a non-painful control location were measured hourly for the first 9 h on Day −1 and Day 0, and at 12 h increments on Day+1 through Day+3 post-disbudding. Mean latency for LS was analyzed in SAS version 9.2 using a mixed model. There was a significant difference in loss of sensation at 10 min, such that treatments differed for the number of calves that required an additional injection (E: 6/10 calves; D: 7/10 calves; Control: 2/10 calves, $P < 0.0001$). However, there was not a treatment difference for latency to LS (Latency to LS (min) ± SEM: E 26.40 ± 6.12; D 25.60 ± 4.78; Control 13.50 ± 4.47). PA data were analyzed using PROC GLIMMIX by treatment and trial day. Ethanol did not differ from C at hour +1, but displayed higher pain thresholds thereafter from Day0 through Day+3 (Raw Means, [kgf] ± SEM: Day0 = E 4.4 ± 0.1; C 3.6 ± 0.1; Day+3 = E 4.6 ± 0.1; C 3.3 ± 0.1; $P < 0.01$). Depot did not differ from C for PA response nor for latency to LS (Raw Means [kgf] ± SEM: Day0 = D 3.2 ± 0.1; Day+3 = D 3.0 ± 0.1). In conclusion, longer latency to LS was associated with E and D anesthetics compared with control (C). Ethanol provided superior analgesia compared with C, whereas D did not when pain was measured using PA.

Key words: analgesia, disbudding, pain

312 The effect of pain relief on the physiology and behavior of calves after castration and/or dehorning. M. A. Sutherland*[1,2], B. L. Davis[1], T. A. Brooks[1], and M. A. Ballou[1], *[1]Texas Tech University, Animal and Food Sciences Department, Lubbock, [2]AgResearch Ltd., Animal Behaviour and Welfare Group, Hamilton, New Zealand.*

Calves are commonly castrated and/or dehorned without pain relief once they enter the feedlot. The objective of this study was to determine the efficacy of pain relief to alleviate the pain caused by dehorning and/or castration in 3 mo old calves. This study comprised of 8 treatments (n = 10 per treatment): 1) control handling (SHAM); 2) castration (CAS); 3) dehorning (DH); 4) castration and dehorning (CD); 5) control handling plus analgesia (ANA); 6) castration plus analgesia (CAS+A); 7) dehorning plus analgesia (DH^+A); 8) castration and dehorning plus analgesia (CD+A). Analgesia involved administering local anesthetic around each horn (DH^+A, CD+A, and ANA) and/or into the testes (CAS+A, CD+A, and ANA treatments) before performance of the treatment and a non-steroidal anti-inflammatory drug (NSAID) was administered immediately after. Sequential blood samples were collected to measure leukocyte counts and percentages, and cortisol concentrations. Behavior was recorded using 5 min scan samples. Calves were weighed before and 24 h after treatments were performed. Data were analyzed using the MIXED procedures of SAS. At 360 min, the neutrophil to lymphocyte ratio was lower ($P < 0.05$) in CAS, DH, and CD calves that received analgesia compared with castrated and/or dehorned calves that did not receive analgesia. The integrated cortisol response was greater ($P < 0.05$) in CAS, DH, and CD compared with SHAM calves, but similar in CAS+A, DH^+A, CD+A, and SHAM calves. The frequency of tail wagging was greater ($P < 0.05$) and eating was reduced ($P < 0.05$) in CAS, DH, and CD compared with SHAM calves, but similar among castrated and/or dehorned calves that received analgesia compared with SHAM calves. Body weight decreased ($P < 0.05$) in CAS, DH, and CD calves compared with ANA calves. Administration of analgesia prevented body weight loss in CAS ($P = 0.05$) and DH ($P = 0.07$) calves, but not in CD ($P = 0.31$) calves. The behavioral and physiological changes caused by castration and/or dehorning are indicative that these animals experience pain, which can be reduced by administering a local anesthetic in combination with a NSAID.

Key words: dairy, pain, welfare

313 Physiological and immunological effects of surgical castration and amputation dehorning and the influence of anesthetics and analgesics in Holstein calves. M. A. Ballou*[1], M. A. Sutherland[1,2], B. L. Davis[1], T. A. Brooks[1], C. J. Cobb[1], and L. E. Hulbert[1,3], *[1]Department of Animal and Food Sciences, Texas Tech University, Lubbock, [2]Animal Behavior and Welfare Group, AgResearch, Hamilton, New Zealand, [3]Department of Animal Science, University of California at Davis, Davis.*

Objectives were to determine the physiological and immunological effects of surgical castration and/or amputation dehorning and the influence of anesthetics and analgesics in Holstein calves. Eighty 3-mo old Holstein bull calves were completely randomized to treatments in a 2 × 2 x 2 factorial arrangement with castration, dehorning, and anesthetic/analgesic as the main effects. Peripheral blood samples were collected before and 0.5, 1.5, 2.5, 4, 6, 24, and 72 h after the respective procedure and analyzed for total leukocyte and differential counts. Plasma cortisol and haptoglobin concentrations were also determined. Blood samples collected before and at 0.5 and 24 h after the procedures were analyzed for ex vivo innate immune responses. Both castration and dehorning elevated ($P < 0.01$) total leukocyte counts and neutrophil:lymphocyte ratios, and the administration of anesthetic/analgesic ($P < 0.01$) attenuated the leukocyte responses. Plasma cortisol and haptoglobin responses were increased ($P < 0.01$) following castration and/or dehorning and the combination of the 2 procedures was additive ($P < 0.01$). Anesthetics/analgesics reduced the peak and persistency of the elevated cortisol response ($P < 0.01$), and the haptoglobin concentrations at 24 h after the procedure ($P < 0.01$). Castration and dehorning together tended ($P = 0.09$) to decrease TNF-α secretion 24 h after the procedure, and administration of anesthetic/analgesics alleviated ($P < 0.01$) the response. In addition, anesthetic/analgesics lessened ($P < 0.01$) the suppressed neutrophil oxidative burst observed 24 h after castration and/or dehorning. Dehorning decreased ($P < 0.04$) neutrophil L-selectin expression and administration of anesthetic/analgesics reversed the response ($P < 0.05$). Both castration and dehorning cause distress and suppress innate immune responses. The administration of anesthetic/analgesic alleviated the adverse effects associated with castration and dehorning.

Key words: analgesia and anesthesia, castration, dehorning

314 Effects of pair housing versus limited social contact on the response of dairy calves to separation. L. R. Duve*[1], M. B. Jensen[1], and D. M. Weary[2], *[1]University of Aarhus, Tjele, Denmark, [2]University of British Columbia, Vancouver, British Columbia, Canada.*

There is much variety in the extent of social contact allowed to preweaned dairy calves; some are housed individually with no opportunity for physical contact, some are allowed limited physical contact with calves in neighboring pens, and others are group housed for part or all of the milk feeding period. A former study indicated that calves allowed limited physical contact still established a social bond; however, the strength of this relationship may differ from calves with full social contact. The aim of this study was to test the effect of the level of social contact on the strength of the social relations, as measured by calf responses during a 20 min period of separation (and 10 min after reunion) from their social companion. Twenty-seven pairs of calves were reared from birth until 6 weeks in either individual pens (with limited social contact between bars; L-calves), pair housed (with full social contact; F-calves), or in individual pens for 3 weeks and in pairs for the next 3 weeks (LF-calves). The separation test was conducted in the home pen when the calves were 34d old. Responses measured were the number of steps, time spent not moving, and maximum heart rate (MHR). Data were analyzed with a general linear mixed model (SAS). F and LF did not differ for any measure, but these calves spent more time standing (F: 850 ± 99, LF: 824 ± 104, L: 510 ± 99 s; $P < 0.01$), took more steps (F: 21 ± 2, LF: 20 ± 3, L: 13 ± 2; $P = 0.05$) and spent less time not moving (F: 779 ± 64, LF: 730 ± 68, L: 975 ± 64 s; $P = 0.03$) during the separation and reunion phase of the test, compared with those calves allowed limited social contact. MHR did not differ among treatments during separation ($P = 0.52$), but was higher for F than L (F: 172 ± 6, LF: 162 ± 7, L: 151 ± 6; $P = 0.04$) during the reunion phase (LF-calves did not differ from either treatment). In conclusion, calves housed in pairs from birth or from 3 weeks of age were more active when separated from their companion in the home environment at 5 weeks of age, suggesting that calves raised with full social contact have a stronger relation with their companion than do calves housed with limited contact.

Key words: dairy calves, social contact

315 Lameness, leg injuries and lying times on 122 North American freestall farms. A. K. Barrientos*[1], D. M. Weary[1], E. Galo[2], and M. A. G. von Keyserlingk[1], *[1]Animal Welfare Program, University of British Columbia, Vancouver, Canada, [2]Novus International Inc., St Louis, MO.*

The aim of the study was to describe the variation in lameness, leg injuries and lying behavior on dairy farms in 3 regions of North America: California (CA); North Eastern states (NE; New York, Pennsylvania and Vermont) and British Columbia (BC). Data were collected by the same 2 trained individuals from approximately 40 Holstein herds in each region. One group of high production multiparous cows was monitored on each farm. Cows were gait scored using a 5-point Numerical Rating System where 1 and 2 are considered non-lame, ≥ 3 clinically lame, and ≥ 4 severely lame. Prevalence of knee injuries was recorded based on swollen carpal joints (yes/no). Focal cows (n = 40), randomly selected from the assessment group, were evaluated for hock injuries on a scale of 1 to 3 (1 = healthy and 3 = evident swelling or severe lesion). Electronic data loggers recorded lying behavior of the focal cows at 1-min intervals for 3 d. The analysis was descriptive and all results are presented as means ± SD. Prevalence of clinical lameness averaged 30.8 ± 15.5% in CA, 54.8 ± 16.7% in NE and 27.8 ± 13.9% in BC; severe lameness averaged 3.6 ± 4.2% in CA, 8.2 ± 5.6% in NE and 7.1 ± 5.3% in BC. Prevalence of swollen knees was minimal in CA (0.3 ± 0.6%), but high (23.1 ± 16.3%) in the NE (not scored in BC). Overall prevalence of hock injuries (≥2) was 56.2 ± 21.6% in CA, 81.2 ± 22.5% in NE, and 40.7 ± 26.3% in BC; prevalence of severe injuries (3) was 1.8 ± 3.1% in CA, 5.4 ± 5.9% in NE and 3.5 ± 5.2% in BC. Lying times were similar across regions (10.4 ± 0.8h/d in CA, 10.6 ± 0.9h/d in NE, and 11.0 ± 0.6h/d in BC) but cows within farms varied from, 3.7 to 17.5h/d, 2.8 to 20.5h/d, and 4.2 to 19.5h/d in CA, NE and BC, respectively. These results show considerable variation in lameness and leg injury prevalence among freestall farms in North America. The very low prevalence of these ailments on some farms shows great opportunity for improvement on other farms.

Key words: cow comfort, welfare assessment

ARPAS Symposium: Understanding Meta-Analysis

316 Unsophisticated "cowboy" methods used traditionally to merge results from multiple experiments. F. N. Owens* and A. Hassan, *Pioneer Hi-Bred Int'l, Johnston, IA.*

Meta-analysis, initially used in 1904, is one statistical method for combining results from qualitative studies to develop and test relationships among multiple factors. Most concepts in nutrition and biology preceded or evolved without sophisticated meta-analysis. By checking the consistency of relationships across multiple experiments, often by within-trial regressions weighted by animal numbers in the mean, consensus opinions were reached to be substantiated or refuted by subsequent experiments. Scientific giants of the past (S. Brody, J. T. Reid) observed trends and relationships within masses of data and developed our basic concepts of growth and development. Similarly, the "equivalent body weight" concept presumably was developed by unweighted curvilinear regression. Mean energy values and nutrient analyses for 1,088 feeds in texts by F. B. Morrison were generated manually from 8,981 experiments after "outliers" were removed. Concepts in energy metabolism (the California Net Energy system) and amino acid requirements for growth (the Ideal Protein system) involved compilation of masses of measurements cleverly interpreted and merged by simplistic methods. The field of epidemiology is based on correlations across multiple data sets; its blunders illustrate that that correlations need not reflect cause-effect relationships. Meta-analyses helps to detect the statistical consistency of treatment effects among experiments, to reduce the cost of and need for animals or subjects in future experiments, and to define response curve shapes across diverse genetic and environmental conditions. Most granting agencies now require both α and β errors to be predicted. Though pre-packaged programs are widely available for complex statistical manipulations, scientists must understand both the upsides and the pitfalls involved with complex analyses. By including meta-analysis within publications of original research, misinterpretations by authors, readers, and the public could be reduced.

Key words: merged experiments, meta-analysis, statistical methods

317 Meta-analysis: The good, the bad and the ugly. I. J. Lean* and A. R. Rabiee, *SBScibus, Camden, NSW, Australia.*

Meta-analysis can be a powerful tool to provide a more precise estimate of the effect of treatment or risk factor for disease, or other outcomes, than any individual study contributing to a pooled analysis. It is also possible, and desirable, to examine new hypotheses using the pooled data that could not be readily tested using other forms of study. However, the confidence with which a user can apply these results depends on the conduct of the meta-analysis, the basal data that contribute to a meta-analysis and the biological responses of the treatments and responses under consideration. The role of publication bias and the value of unpublished results are explored. This presentation considers the base data that contribute to a meta-analysis and provides guidelines for presentation of results. Examples of meta-analyses will be used to examine sources of variability or heterogeneity in study results and strengths and weaknesses of different approaches to pooling data. Tools for assessing heterogeneity including the I^2 statistic and use of different funnel plots to assess publication bias are evaluated. The value and limitations of meta-regressions approaches to address causal relationships, especially in nutritional studies is addressed. Flaws in some approaches to the pooling of data will be explored with a view to achieving a greater consistency in approach to meta-analytical studies.

Key words: merged experiments, meta-analysis, statistical methods

318 Relationship between postweaning RFI in heifers and intake and productivity of mid-gestation beef females. A. N. Hafla*[1], G. E. Carstens[1], T. D. A. Forbes[2], J. C. Bailey[1], J. T. Walter[1], J. W. Holloway[2], and J. G. Moreno[1], *[1]Texas A&M University, College Station, [2]Texas AgriLife Research, Uvalde.*

Residual feed intake of growing cattle has been associated with between-animal variation in maintenance energy requirements. The objective of this study was to determine if RFI classification of beef heifers affects DMI and productivity of mid-gestation females. RFI was determined in 2 groups of growing Bonsmara heifers during 2 yr (n = 62 and 53/yr), and heifers with the lowest (n = 12/yr) and highest (n = 12/yr) RFI were retained for breeding. Nineteen second-parity cows from trial 1 and 23 primiparous heifers from trial 2 were used in this study. Cows and heifers were fed a chopped hay diet (ME = 2.11 Mcal/kg DM) in separate pens equipped with GrowSafe bunks to measure individual intake and feeding behavior. BW were measured at 7-d intervals, and BCS and ultrasound measurements of REA and rump fat thickness obtained on d 0 and 77 of the study. No interactions between RFI classification and age were found to be significant. Heifers had lower ($P < 0.05$) initial BW (505 vs 474 ± 9 kg), ADG (0.66 vs 0.47 ± 0.05 kg/d), and initial hip height (132 vs 129 ± 0.95 cm), but similar DMI (10.37 ± 2.66 kg/d) compared with cows. Heifers and cows had similar initial rump fat thickness (1.10 ± 0.32 cm) and BCS (5.1 ± 0.4). Bunk visit (BV) frequency was higher ($P < 0.0001$) in heifers than cows (142 vs 93 ± 7 events/d), but BV duration (174 ± 61 min/d) was not affected by age. Meal frequency was similar for heifers and cows, but heifers had longer ($P < 0.05$) meal duration (427 vs 387 ± 14 min) than cows. Females classified as having low RFI had lower ($P < 0.01$) DMI (9.00 vs 11.6 ± 0.54 kg/d) compared with females with high RFI, but initial BW and ADG were similar during the trial. Likewise, RFI classification did not affect initial or final rump fat thickness or BCS. BV frequency was similar, but BV duration was less ($P < 0.001$) for females with low compared with high RFI. Meal frequency and duration were not affected by RFI classification. Females classified as having low RFI as heifers continued to consume 22% less feed than females classified as high RFI while maintaining the same BW and BCS during the 2nd trimester of gestation.

Key words: residual feed intake, feeding behavior

319 Using a mechanistic nutrition model to identify efficient beef cows under grazing conditions. B. M. Bourg*[1], L. O. Tedeschi[1], A. D. Aguiar[5], F. R. B. Ribeiro[2], J. Genho[3], R. R. Gomez[1], D. Delaney[4], and S. Moore[4], *[1]Texas A&M University, College Station, [2]Texas A&M University, Commerce, [3]Eldon Farms, Woodville, VA, [4]King Ranch, Kingsville, TX, [5]University of Florida, Gainesville.*

The cow/calf phase of production represents a large expense involved in the cost of producing beef, and efficient beef cows use less resource to obtain the same outcome in a sustainable environment. The objective of this study was to utilize a mechanistic nutrition model to estimate ME requirement (MER) of grazing cows based on changes in cow BW and fatness measurements (body condition score, BCS) along with calf age and BW, as well as forage quality and quantity. In addition, energy efficiency index (EEI), which is computed as MER divided by calf weaning BW, was used to rank cows within a herd based on their efficiency of utilizing available forage to meet their maintenance requirements and support calf growth. Data were collected from one herd of approximately 140 Santa Gertrudis cows over a 4-year period, and analyzed per calving interval, conception to weaning. PROC CORR of SAS was used to determine phenotypic relationships between model-predicted peak milk and EEI with cow and calf performance and temperament data (exit velocity or chute score). Moderate significant ($P < 0.05$) correlations of EEI were found (r = 0.51) between year 1 and 2, year 1 and 3 (r = 0.46), year 2 and 3 (r = 0.43), year 1 and 4 (r = 0.39), year 2 and 4 (r = 0.53), and year 3 and 4 (r = 0.57), suggesting that the EEI may be consistently predicted for cows across years. A negative relationship was found between predicted peak milk and EEI, and model predicted values were also strongly correlated ($P < 0.05$) across years. Peak milk and EEI were not correlated ($P > 0.1$) to the collected temperament measures. Relationships between EEI and peak milk with ultrasound fat measures indicated that more efficient cows, with a lower EEI, were leaner, and cows with a higher peak milk were also leaner. Cow BCS was also positively correlated to both EEI and peak milk. Preliminary genetic assessment of EEI and MER, indicated additive genetic heritability (h^2) of EEI and MER of 0.58 and 0.05, respectively. In conclusion, the model's estimation of EEI might be moderately heritable and repeatable across years, and that efficient cows might have greater peak milk and be leaner.

Key words: modeling, efficiency, sustainability

320 Relationship among lifetime measures of body weight and frame size in beef cows. A. C. Echols*, D. A. Fiske, M. L. Wahlberg, and S. P. Greiner, *Virginia Polytechnic Institute and State University, Blacksburg.*

The beef cattle industry has placed increased focus on mature cow size as a result of its influence on production efficiency and profitability. The objective of this study was to evaluate relationships among lifetime measures of growth and frame size for commercial beef females in a pasture-based beef production system in the Appalachian region of the United States. Measurements of BW, hip height (HH), BCS, and calculated frame score (FS) were recorded at weaning (WN), breeding (BR), 2 (2YR), and 4 (4YR) yr of age for 232 Angus-cross females born 2004 through 2008. Mean age at WN, BR, 2YR, and 4YR were 230 (SD = 44), 395 (SD = 25), 805 (SD = 19), and 1745 d (SD = 20), respectively. Body weight at 2YR and 4YR were adjusted for BCS. Frame score at WN was related to FS at BR (r = 0.73, $P < 0.001$), and 2YR (r = 0.47, $P < 0$ 0.001), but not at 4YR ($P = 0.61$). Frame score at BR was related to FS at 2YR (r = 0.67, $P < 0.001$) and 4YR (r = 0.62, $P < 0.001$), and a strong relationship existed between FS at 2YR and 4YR (r = 0.83, $P < 0.001$). Similarly, body weight at WN was correlated to BW at BR (r = 0.76, $P < 0.001$), 2YR (r = 0.56, $P < 0.001$), and 4YR (r = 0.51, $P < 0.001$). Body weight at BR was correlated to 2YR (r = 0.56, $P < 0.001$) and 4YR (r = 0.65, $P < 0.001$). Body weight and FS were related at WN (r = 0.57, $P < 0.001$), BR (r = 0.64, $P < 0.001$), 2YR (r = 0.53, $P < 0.001$), and 4YR (r = 0.48, $P < 0.001$). Frame score and BW differed ($P < 0.001$) by birth yr. Mean FS at WN, BR, 2YR, and 4YR were 4.77 (SD = 0.72), 4.79 (SD = 0.84), 5.08 (SD = 0.80), and 5.47 (SD = 0.66), respectively, and did not differ ($P = 0.34$) over time for the same animal. Hip height and BW peaked at 4YR ($P < 0.001$). While BW and FS are related to the same measures taken at maturity, measurements taken at BR appear to be superior to those taken at WN when used to predict mature size of beef cows.

Key words: beef cow, frame score, mature size

321 A mineral survey of Louisiana beef cow/calf production systems. J. Rowntree*[1], K. Guidry[2], G. Scaglia[2], G. Gentry[2], and L. Southern[2], *[1]Michigan State University, East Lansing, [2]LSU Agricultural Center, Baton Rouge, LA.*

The purpose of this research was to determine the state and regional mineral status of Louisiana forages and beef cattle. Louisiana beef cattle operations (n = 25) were sampled and divided into 7 geographical regions, including the northwest (NW), northeast (NE), central (CE), southwest (SW), south central (SC), Florida parishes (FP) and southeast (SE) regions. Over a 2 year period, water and soil samples were collected from each operation annually, forage samples were collected quarterly in Aug to Sep, Nov to Dec, Feb to Mar and May to June and bovine serum samples were collected twice annually in the fall and spring seasons. The highest ($P < 0.05$) average regional water K and S concentrations were observed in the SE region and water Ca and Mg concentrations were the highest ($P < 0.05$) in the NE, CE and SE regions. Similar to water, soil Ca, Mg and K concentrations in our study, were higher ($P < 0.05$) in the SE compared with all other regions. Soil Cu concentrations were below critical levels in the CE region and all soil Zn concentrations, except the SE region, were lower than reported critical levels indicating soil deficiency. The average forage concentration for each mineral were: Ca (0.42%), P (0.28%), Mg (0.21%), K (1.83%), Na (0.10%), S (0.32%), Cu (8.12 ppm), Fe (323.46 ppm), Mn (254.85 ppm) and Zn (41.29 ppm). In addition, only mean forage Cu concentrations were lower than minimum requirements and regional forage K (NW region), Mg (FP region), Na (CE region) and S (NW and SE regions) concentrations were higher ($P < 0.05$) than other regions. The average regional serum K concentration in the NE region was higher ($P < 0.05$) than all other regions. Average bovine serum mineral concentrations in Louisiana were: Ca (9.02 mg/100 mL), P (13.62 mg/100 mL), Mg (1.92 mg/100 mL), K (21.66 mg/100 mL), Na (303.30 mg/100 mL), S (103.31 mg/100 mL), Cu (0.63 µg/ml), Fe (7.44 µg/ml), Zn (1.28 µg/ml), Mn (8.08 ng/ml) and Se (64.48 ng/ml). Furthermore, of these minerals, serum Mg, Na, Cu and Mn concentrations were lower than critical levels, indicative of deficiency.

Key words: beef cattle, forages, mineral

322 Finishing steers and bulls with high-vitamin E diets: Effect on pH and tenderness of beef. C. Reyes, C. Fuentes, and R. E. Larraín*, *Pontificia Universidad Catolica de Chile, Santiago, Chile.*

Release of glucocorticoids to the blood stream during stress may mobilize energy reserves in muscle. Reduced glycogen depots at the time of slaughter may lead to meat pH-values above 5.8, and meat with elevated pH is less tender. Vitamin E reduced activation of the hypothalamic-hypophysial-adrenocortical axis in farm animals. Thus, the objective of this study was to test if bovines finished with a high vitamin E diet produce beef with lower pH and increased tenderness. Thirty-eight steers and bulls were blocked by sex, then grouped in 16 pens of 2 or 3 animals of similar BW, and randomly assign to one of 2 treatments: a control diet designed to provide 60 IU vitamin E•animal^{-1}•d^{-1} and the control diet supplemented with 2,000 IU vitamin E•animal^{-1}•d^{-1}. Each pen was considered an experimental unit (n = 8). Feed was offered once daily to each pen to provide ad libitum access to feed. Initial and final BW were the average of 2 weights before feeding in consecutive days. After 123 d on feed, animals were transported for about 1.5 h to a local abattoir and harvested approximately 8 h after arrival. Beef pH was measured 48 h post-mortem in the longissimus muscle, using a spear-tip pH meter inserted between the 12th and 13th rib. Tenderness was evaluated in 1 × 1 cm strips, cut perpendicular to the fiber axis, using a Warner-Bratzler shear machine. Factors in the model were sex and treatment, and initial BW was included as covariate. Differences were considered significant when ANOVA had $P < 0.05$. There were no differences in ADG (1.16 ± 0.063 kg/d, $P = 0.49$), carcass yield (55.8 ± 0.4%, $P = 0.56$), pH (5.87 ± 0.09, $P = 0.96$) and WBS (2.17 ± 0.12 kg, $P = 0.54$) between treatments. High mean pH value of beef was due to 3 pens having an average pH above 6.0. All of these pens contained bulls, 2 from the control and 1 from the vitamin E treatment. We concluded that 2,000 IU vitamin E•animal^{-1}•d^{-1} produce no changes in pH and tenderness of beef.

Key words: vitamin E, pH, tenderness

323 Effect of beef cow age and calf sex on model-predicted energy efficiency. M. J. Baker*[1], L. O. Tedeschi[2], D. G. Fox[1], and G. Jacimovski[1], *[1]Cornell University, Ithaca, NY, [2]Texas A&M University, College Station.*

The identification of efficient beef cows under grazing conditions is important to ensure competitiveness and profitability. As the on-farm direct measurement of DMI is cost-prohibitive, a model (Cattle Value Discovery System, CVDSbc) was developed to predict an energy efficiency index (EEI, Mcal/kg) that is based on the predicted ME required (MER, Mcal/d) by the cow or cow + calf within a reproductive cycle divided by the calf weaning weight (WW, kg). The objective of this study was to evaluate the impact of cow age and calf sex on the EEI with or without adjusting WW for cow age and calf sex as per Beef Improvement Federation Guidelines. Data from predominantly Angus x Simmental spring calving cows (n = 37, BW = 628 kg) and monthly forage quality were used. The BW at 28% empty body fat (FBW, kg) was assumed 620 and 520 kg for steer and heifer calves, respectively. The CVDSbc computes MER based on cow and calf characteristics and forage quality, and iterates cow peak milk (PK, kg) until the predicted WW matches the observed WW. The statistical analyses were conducted with PROC GLM and PROC REG assuming cow age and calf sex as fixed factors in a completely randomized design. They were analyzed separately. When WW was not adjusted, the age of cow affected the predicted PK ($P = 0.0644$) in which 2 year-old cows tended to have a lesser PK than 3, 4 and 5 year-old cows (3.79, 5.39, 5.41, and 5.38, respectively), suggesting older cows produce more milk to support a greater ADG of the calves. The cow EEI was greater ($P = 0.049$) for heifer than steer calves (40.4 and 36.6 Mcal/kg, respectively). Similarly, the cow + calf EEI was greater ($P = 0.056$) for heifer than steer calves (42.9 and 39.2 Mcal/kg, respectively). These results were expected; at the same age steers have a greater BW which increases the dilution of the cow's MER compared with the lighter heifers. When WW was adjusted to calf sex, no differences ($P > 0.25$) were observed between age and calf sex on EEI and PK. The correlations between adjusted and unadjusted cow and cow + calf EEI were 0.896 and 0.884, respectively. These results suggest that cow age and calf sex have to be accounted for when comparing cow EEI.

Key words: cattle, modeling, selection

324 Selling prices of Arkansas beef feeder calves as affected by management practices. T. R. Troxel* and B. L. Barham, *University of Arkansas, Department of Animal Science, Little Rock.*

The objective of this study was to determine how management factors affected the selling price of beef calves. Data were collected from January 1 to December 31, 2010 at 14 Arkansas livestock auctions. The

database consisted of 38,346 lots consisting of 79,822 head of cattle representing 19% of the total calves sold. Information was collected by experienced livestock market news reporters and included body condition, castration, horn status, fill, health, and individual or group selling. Each factor was analyzed using GLM procedures using weight as a covariate, and least-squared means were generated. All prices are based on dollars per 45.45 kg of live weight. Body condition affected selling price ($P < 0.0001$) with fat, very thin, fleshy, average, and thin calves selling for $94.40, $98.05, $102.23, $108.36 and $110.11, respectively. Steers sold for $6.31 more ($116.16; $P < 0.001$) than bulls ($109.85), and polled calves sold for $8.03 more ($P < 0.001$) than horned calves. Heifers sold for $102.71. Fill affected selling price ($P < 0.0001$) with gaunt, shrunk, average, full and tanked calves selling for $114.40, $109.65, $106.28, $99.41 and $90.33, respectively. Healthy calves sold for $108.69, which was higher ($P < 0.001$) than dead hair ($98.43), stale ($87.21), sick ($62.48), bad eye(s) ($95.38) or lame ($68.57) calves. Calves that were announced as preconditioned sold for a higher price ($113.57; $P < 0.001$) than healthy calves. The selling prices of calves sold as singles, groups of 2 to 5 head or groups of 6 or greater were $107.81, $110.52 and $112.60, respectively ($P < 0.001$). Cattle classified as calves sold for $110.29, which was higher than cattle classified as yearlings ($104.81; $P < 0.001$). Beef cattle producers can greatly influence the selling prices of calves through managing calf body condition, castration, horns, fill, health and group selling.

Key words: selling price, beef calves, auctions

325 The relationship between climatic conditions and the incidence of calving. T. R. Troxel*[1], M. S. Gadberry[1], D. Hubbell[2], and W. Kellogg[3], *[1]University of Arkansas, Department of Animal Science, Little Rock, [2]University of Arkansas, Department of Animal Science, Batesville, [3]University of Arkansas, Department of Animal Science, Fayetteville.*

The object of this study was to examine the relationship of barometric pressure and maximum and minimum temperature with the incidence of calving. Calving data (2005 to 2009) from the Livestock and Forestry Station (Batesville, AR) and Savoy Research Unit (Savoy, AR) were used. All cows were multiparous, predominately Angus, and natural serviced. Both locations calved in the spring (Jan to Apr) and fall (Sep to Dec). Total calving observations were 1,547. Calving occurred on 54% of the days within the calving season. The climate data from the Fayetteville and Mountain Home, AR weather stations were obtained from the Southern Regional Climate Center, Louisiana State University, Baton Rouge and was used for the Savoy and Batesville research stations, respectively. There was a season by calving observation effect ($P < 0.05$) for all 3 climatic measurements. Spring barometric pressure on day of calving and 1, 2 and 3 d before calving was greater than corresponding non-calving dates ($P < 0.05$), but no differences were detected in the fall ($P > 0.10$). Spring maximum temperature was lower on day of calving and 1 and 3 d before calving than corresponding non-calving dates ($P < 0.05$), but fall maximum temperature was higher d 1 and 3 d before calving than corresponding non-calving dates ($P < 0.05$). Spring minimum temperature was lower on day of calving and 1, 2 and 3 d before calving than corresponding non-calving dates ($P < 0.05$), but fall minimum temperature was higher d 1, 2 and 3 d before calving than corresponding non-calving dates ($P < 0.05$). For spring-calving cows, an increase in barometric pressure and a decrease in maximum and minimum temperature were associated with calving. For fall-calving cows, an increase in maximum and minimum temperature with no barometric pressure relationship was associated with day of calving. This data suggest monitoring weather conditions may provide an indication of calving incidences and possibly prepare producers to monitor cows.

Key words: barometric pressure, temperature, calving

326 Selling price of Arkansas beef feeder calves as affected by phenotypic expression. B. L. Barham* and T. R. Troxel, *University of Arkansas, Department of Animal Science, Little Rock.*

A study was conducted to evaluate the impact of genetic factors on the selling price of beef calves marketed through Arkansas auction barns. Data was collected on 38,346 lots consisting of 79,822 head marketed through 14 auction barns in 2010. Data collection was conducted by experienced livestock market news reporters. Information pertaining to the phenotypic expression of calf genetics included subjective identification of breed, color, and USDA frame and muscle scores. Due to the unbalanced nature of the data set, variables were analyzed individually with calf weight as a covariate, and least squares means were generated. All prices are based on dollars per 45.45 kg of live weight. Breed, color (independent of breed), frame and muscle impacted ($P < 0.001$) feeder calf price. Twenty breed or breed groupings were evaluated. Five breed or breed types received the highest selling prices but were not different from each other ($P > 0.10$) were Angus x Brahman ($111.82), Angus x Herford ($111.70), Angus ($111.36), Charolais x Hereford ($110.48) and Hereford x Angus x Brahman ($110.22). Simmental ($99.90), Brahman ($94.34), and Longhorn/Longhorn cross calves ($71.75) were lower in price ($P < 0.001$) compared with other breeds. Black-white faced calves ($111.74) received the highest selling price ($P < 0.001$) followed by black ($110.23), yellow ($110.09), and yellow-white faced ($109.81) which were not different from each other ($P > 0.10$). Spotted calves ($82.16) received the lowest selling price ($P < 0.001$). The selling prices for large- ($108.81) and medium- ($108.67) framed calves were similar ($P > 0.10$) but were higher ($P < 0.001$) than small-framed calves ($86.71). Price also differed ($P < 0.001$) for muscle scores 1, 2, 3 and 4 ($110.82, $101.88, $78.41 and $53.64, respectively). Beef cattle producers can influence the calf-selling price through genetic selection.

Key words: feeder calves, market price, genetic factors

327 Using ultrasonography to determine reproductive tract development in beef heifers. R. A. Cushman*, L. A. Kuehn, R. M. Thallman, W. M. Snelling, and H. C. Freetly, *USDA-ARS U.S. Meat Animal Research Center, Clay Center, NE.*

Choosing replacement beef heifers is a decision with long-term implications for profitability for the cow-calf producer. If a replacement heifer fails to wean the number of calves necessary to recover her development costs, then she incurs a net loss for the ranch. To avoid such losses, it is imperative to develop technologies that aid in identifying heifers with little chance of weaning 3 or more calves. The first hurdle to reproductive competency is the establishment or reproductive cycles (puberty). No intensive research has evaluated the size of the ovaries or uterus in relation to reproductive status in beef heifers. Therefore, the objective of the present study was to use ultrasonography to measure the sizes of these structures and relate them to reproductive status in yearling crossbred beef heifers (n = 368). At weaning, heifers were moved to a feedlot and placed on a growing ration. At 13.6 ± 0.6 mo of age (range 12 to 15 mo), development of the reproductive tract was evaluated using ultrasonography. Each ovary was measured for length and height and a cross-sectional measurement of the endometrium was taken on the right side, approximately 1 cm

anterior to the uterine body. Antral follicles >3 mm and corpora lutea were counted. Percentages of Brahman, Continental, or British breeds were fitted as fixed covariates. Numbers of antral follicles increased as the percentage of Brahman influence in an individual heifer increased ($P < 0.0001$). There was no breed effect for ovarian size or endometrial diameter. Both ovarian size and endometrial diameter were greater in 15-mo-old heifers than 12-mo-old heifers ($P \leq 0.03$). The percent of heifers that had initiated reproductive cycles as determined by the presence of a corpus luteum at ultrasonography increased as age increased and as percent Brahman decreased ($P \leq 0.001$). The use of ultrasonography to evaluate the ovaries and uterus in yearling beef heifers is a practical tool to aid in determining the reproductive status of replacement heifers. USDA is an equal opportunity provider and employer.

Key words: beef heifer, reproductive tract, puberty

328 Characterization of feeding behavior of abrupt-weaned crossbred heifer calves. A. N. Loyd*[1,4], R. C. Vann[2], J. P. Banta[3], T. H. Welsh Jr.[1], J. A. Carroll[4], and R. D. Randel[5], *[1]Texas AgriLife Research, College Station, [2]MAFES, Mississippi State University, Raymond, [3]Texas AgriLife Extension, Overton, [4]Livestock Issues Research Unit, USDA-ARS, Lubbock, TX, [5]Texas AgriLife Research, Overton, TX.*

Stress experienced by calves at weaning often culminates in poor post-weaning feed intake (FI) and growth performance. Understanding feeding behavior during this time is crucial to successful management of these calves. The objective of this study was to characterize the feeding behavior of calves post-weaning. Brahman x British heifers (n = 48) born in spring 2010 at the Brown Loam Branch Experiment Station in Raymond, MS were abruptly weaned from their dams at 199 ± 18 d of age. Heifers were penned in one of 2 dry-lots and received ad libitum access to a high roughage diet offered in GrowSafe bunks. Feeding behavior was monitored for 24–26 d post-weaning and BW was evaluated weekly beginning at weaning. Data were analyzed using the MIXED procedure of SAS with day as a repeated measure when applicable. The number and duration of daily meal events, the duration of daily head down time, and daily FI increased with time post-weaning ($P < 0.0001$). Body weight was similar for all time points ($P = 0.32$). However, there was great variation in the number of days it took heifers to first approach the feed bunks, eat feed for the first time, eat feed consistently for at least 5 d, and consume enough feed to meet estimated NE_m requirements (Table 1). To account for this variation, the proportion of Brahman influence was included in the statistical model as a covariate. Brahman-influenced heifers were slower to attend the bunks ($P < 0.0001$), begin consuming feed ($P < 0.0001$), consistently consume feed ($P < 0.0001$), and consume enough feed to meet NE_m requirements ($P < 0.03$). However, there was no effect ($P > 0.10$) of breedtype on feeding behavior or FI over the course of the entire feeding period. These data suggest there is considerable variation in post-weaning feeding behavior, of which some is attributable to breedtype. These data also highlight an important consideration when utilizing newly weaned calves in feeding trials, especially those using GrowSafe bunks.

Table 1. Feeding behavior traits of heifers post-weaning

Trait	Mean	SD	Minimum	Maximum
First attendance at bunk (d)	3.9	4.1	0	21
First feed consumption (d)	5.1	5.0	0	26
Consistent feed consumption (d)	8.3	6.2	0	26
NE_m requirement achieved (d)	10.7	4.6	3	21

Key words: feed intake, heifer, weaning

Breeding and Genetics: Genomic Selection and Whole-Genome Association II

329 Use of the Illumina Bovine3K BEAD chip in dairy genomic evaluation. G. R. Wiggans[1], T. A. Cooper*[1], K. M. Olson[2], and P. M. VanRaden[1], *[1]Animal Improvement Programs Laboratory, ARS, USDA, Beltsville, MD, [2]National Association of Animal Breeders, Columbia, MO.*

Genomic evaluations using genotypes from the Illumina Bovine3K BEAD chip became available in September 2010 and made official in December 2010. The approximately 4,000 samples a month submitted for this low cost chip are 79% hair, 10% blood, 10% nasal and 1% semen and tissue, and 93% are from females. To integrate the 3K genotypes into the evaluations, they are imputed from the 2,614 single nucleotide polymorphisms (SNP) used from the 3K chip to the 42,503 used in evaluation. Reliability is discounted to recognize errors associated with imputation. The average 3K genomic evaluation reliability is 5 points lower than for 50K evaluations. The accuracy of imputation is dependent on an animal's relationship to the genotyped population. The average imputed call rate for 3K genotypes is 95.2% and ranges from 71.0% to 97.0%. Animals that have a low imputed call rate are those who have unknown pedigree or no genotyped relatives. Animals tested using the 50K chip have at least one genotyped parent 94.5% of the time, whereas only 84.2% of 3K genotyped animals do. For approximately 8% of 3K genotypes, the sire is determined to be incorrect. If the true sire of an animal is genotyped, it can be identified with > 99% certainty. Other errors such as dam conflicts, unidentified identical twins / split embryos and breed conflicts prevent genotypes from being used. The chemistry used for the 3K chip is different from that of the 50K chip and causes greater variability in the accuracy of the genotypes. Because of this, a 3K specific check was added which excludes approximately 1% of samples. They are rejected because they have a high proportion of conflicts between SNP of the sire/dam and progeny. The performance of SNP also differed between chips, resulting in 272 SNP that were usable on the 50K chip being not usable on 3K. The 3K chip has been successful in extending genotyping to a larger portion of the cow population. The evaluation system has been modified to accommodate the characteristics of the chip. Improvements in accuracy of imputation and other improvements will further improve the accuracy of 3K based genomic evaluations.

Key words: 3K, genomic evaluation, parentage

330 Properties of different density genotypes used in dairy cattle evaluation. P. M. VanRaden[1], M. E. Tooker*[1], K. M. Olson[2], T. A. Cooper[1], G. R. Wiggans[1], and C. P. Van Tassell[3], *[1]Animal Improvement Programs Laboratory, ARS, USDA, Beltsville, MD, [2]National Association of Animal Breeders, Columbia, MO, [3]Bovine Functional Genomics Laboratory, ARS, USDA, Beltsville, MD.*

Dairy cattle breeders have used a 50K chip since April 2008 and a less expensive, lower density (3K) chip since September 2010 in genomic selection. Evaluations from 3K are less reliable because genotype calls are less accurate and missing markers are imputed. After excluding genotypes with <90% call rate and other edits, marker properties were compared for 8,305 animals with 3K, 54,643 with 50K version 1, 2,602 with 50K version 2, and 353 with a higher density (777K) chip. Animals were of 3 breeds, and all 4 chips were from Illumina. Numbers of markers selected were 2,614 from the 3K chip, 42,503 from 50K version 1, 41,019 from 50K version 2, and 632,665 from the 777K. Markers selected each had <20% missing genotypes and <2% parent-progeny conflicts, with proportionally stricter limits for markers with minor allele frequencies <0.5. The selected 3K markers averaged 0.7% missing genotypes vs. 0.4% for the 50K markers. Parent-progeny conflicts averaged 0.07% for the selected 3K markers vs. 0.01% for the 50K markers. Properties of the 777K chip are similar to the 50K chips, but only 38,201 markers that match the 50K chip currently are used. Genomic evaluations were examined for 319 animals that had 3K genotypes in December and then 50K in February. Means were nearly identical (within 1 pound for fat and protein). The 3K evaluations had SD about 96% as large as 50K, in agreement with the 95% expected from the lower published reliability (64 vs. 71% for net merit). The correlations ranged from 0.92 to 0.96 across traits as compared with 0.46 to 0.66 for parent average with 50K. Version 2 of findhap.f90 will improve the 3K correlations to 0.94 to 0.97, improve average reliability by 2%, and improve the percentage of correctly imputed genotypes to 96.3% from 93.8% with version 1. Breeders can increase reliability affordably using lower density to impute higher density genotypes.

Key words: genomic evaluation, imputation, marker density

331 Use of the partial least-squares regression to impute missing markers when some animals are genotyped with low-density SNP platforms. C. Dimauro*[1], S. Sorbolini[1], E. Pintus[1], J. T. van Kaam[2], and N. P. P. Macciotta[1], *[1]Università di Sassari, Sassari, Italy, [2]Associazione Nazionale Allevatori Frisona Italiana, Cremona, Italy.*

In genomic selection direct genomic values (DGV) are predicted by using genotype information provided by high-density SNP platforms. At present, genotyping process is very expensive and problems arise when genomic data extracted from different SNP platforms has to be joined. Recently, several algorithms aimed at imputing marker information not directly collected in some animals, have been suggested. In this work the partial least squares regression (PLSR) imputation method, previously developed by using only simulated data, was tested on a real experiment. Data were from 1,042 Italian Holstein sires genotyped with the Illumina BovineSNP50 BeadChip. Animals were divided in 2 groups. 900 old bulls constituted the training population with all SNP markers considered known. The remaining 142 young bulls were the prediction population where only 3,072 markers, corresponding to the Illumina Bovine 3K BeadChip, were considered known. Efficiency of PLSR imputation method was tested through the mean imputation error rate and the mean imputation accuracy. The first refers to the mean proportion of incorrectly imputed genotypes, the second to the mean correlation coefficient between actual and PLSR imputed genotypes. Moreover, DGV accuracies for milk, fat percentage and protein percentage were evaluated both for original and PLSR predicted data. The ratio between DGV accuracies obtained by using PLSR imputed data and original data was used as synthetic index of goodness of prediction. Results for mean imputation accuracy and mean imputation error rate were 0.70 and 0.18, respectively, whereas the DGV ratios were 0.975 for milk, 0.993 for fat percentage and 0.957 for protein percentage. These results are better than those obtained in a simulated scenario with a more favorable number of animals. Therefore, the PLSR imputation method works better with real than simulated data, thus promising a higher efficiency in SNP marker prediction if the number of genotyped animals increases.

Key words: imputation, genomic selection

332 Reduced dimensionality in GS models through Lassoed supervised principal components. C. Maltecca* and K. A. Gray, *North Carolina State University, Raleigh.*

The availability of high-density SNP panels and sequencing information poses a challenge in genomic data analysis due to highly over-parameterized models. Identification of linear combinations that exhibit large variation through principal components analysis is often employed to reduce model dimensionality. In this work we investigated the use of supervised principal components, an extension of principal components analysis aiming at obtaining a combination of features with both high variance and significant correlation with the outcome. De-regressed breeding values for milk, fat, and protein yield, were obtained for approximately 8,000 US-HOL bulls genotyped with the Illumina 50K chip. For each of the 36,768 SNPs available for the analysis a standardized univariate regression coefficient was calculated. For each value, of a threshold θ ($0 < \theta1 < \theta2... < \theta k$), a reduced data matrix was formed, consisting only of features that exceeded the absolute value θ. For features exceeding θ the first 3 principal components were calculated. Optimal values of θ for each trait were obtained through cross-validation. Soft thresholding employing the correlation of each feature with the supervised PC predictor was used in obtaining a reduced number of features. Subsequent genomic breeding value predictions were obtained through the use of Bayesian LASSO. Values of θ of 3.5, 3.1 and 3.6 were found for milk, fat and protein yield respectively. These values resulted in reduced panels of 1,213, 1,189, and 958 SNPs, respectively. Correlations between GEBVs and BV in a prediction set obtained splitting the data chronologically were of 0.691 (0.712 whole panel), 0.713 (0.743 whole panel), and 0.708 (0.731whole panel), while slopes for the regression of GEBV on BV in the prediction set were of 0.780 (0.765 whole panel), 0.801 (1.125 whole panel), and 0.804 (1.198 whole panel), respectively for milk, fat and protein. For all traits, reduced models recovered more than 90% of the overall information at a fraction of the computing cost.

Key words: genomic selection, supervised principal components, shrinkage estimators

333 FImpute - An efficient imputation algorithm for dairy cattle populations. M. Sargolzaei*[1,2], J. P. Chesnais[1], and F. S. Schenkel[2], *[1]L'Alliance Boviteq, Saint-Hyacinthe, QC, Canada, [2]University of Guelph, Guelph, ON, Canada.*

Imputation consists of approximating the high density (HD) genotype of an individual using information from its lower density (LD) genotype and from the HD genotypes of other individuals, which can be relatives of the imputed individual (family-based imputation) or members of the population at large (population-based imputation). An efficient imputation algorithm and program (FImpute) was developed using family followed by population imputation and optimized for memory and CPU time. The algorithm was first tested on a group of 6,246 Holstein animals genotyped for the 50K panel, which was representative of younger animals recently genotyped in the North America. Only the SNP used in the 3K panel were retained, and 50K genotypes were approximated using information from these SNP and the 50K genotypes of older animals in the North American Holstein population. Overall, the percentages of SNP imputed correctly, incorrectly and missing were 96.8, 1.44 and 1.76%, respectively. As expected the correct call rate was the highest when both parents where genotyped with 50K, but it remained above 90% for 96.2% of animals. A validation study was carried out to assess the effect of using imputed genotypes on GPA accuracy. The realized reliabilities for the GPA of validation bulls (n = 498) were only slightly lower when using imputed genotypes compared with actual 50K genotypes, by a range of 0 to 0.04 depending on the trait. FImpute was also used in the Jersey and Brown Swiss breeds, yielding imputation accuracies high enough to make adequate genomic predictions. When using the 3K panel, most of the imputation accuracy comes from family rather than population imputation. Population imputation would contribute more with a larger LD panel, e.g., when imputing from 50k to 777K. Using both types of imputation, as in FImpute, will nevertheless be required to obtain maximum imputation accuracy. FImpute is now used for imputation from 3k to 50k for official genomic evaluations in Canada.

Key words: imputation, software, validation

334 Estimation of linkage disequilibrium in four US pig breeds. Y. M. Badke*[1], R. O. Bates[1], C. W. Ernst[1], C. Schwab[2], and J. P. Steibel[1], *[1]Department of Animal Science, Michigan State University, East Lansing, [2]National Swine Registry, West Lafayette, IN.*

The success of marker assisted selection depends on the amount of linkage disequilibrium (LD) across the genome. To implement marker assisted selection in the swine industry information about extent and degree of LD is essential, and LD can be used to estimate effective population size. The objective of this study was to estimate LD in 4 US breeds of pigs (Duroc, Hampshire, Landrace, and Yorkshire). To estimate LD, 351 animals from 117 sire/dam/offspring trios were genotyped using the Illumina Porcine SNP60 BeadChip. DNA was isolated from samples (blood or semen) obtained from purebred animals recorded with the National Swine Registry. The number of trios per breed was 30, 26, 29, and 32 for the Duroc, Hampshire, Landrace and Yorkshire breeds, respectively. After excluding SNP for low genotyping rate, failure to meet Hardy Weinberg equilibrium, and minor allele frequency below 5%, an average of 36,421 SNP with an average intermarker distance of 66Kb were used for the analysis. The genotypes were phased and pairwise r^2 was computed. Average r^2 across all chromosomes was 0.36 (sd = 0.028) in Landrace, 0.38 (sd = 0.039) in Yorkshire, 0.43 (sd = 0.036) in Hampshire and 0.45 (sd = 0.041) in Duroc. For markers 1Mb apart, r^2 ranged from 0.13 (sd = 0.037) in Landrace to 0.18 (sd = 0.057) in Duroc and Hampshire. The LD between neighboring markers was $r^2 > 0.3$ for 43% of marker pairs in Landrace, 47% in Yorkshire, 51% in Hampshire and 53% in Duroc. The current average estimated effective population size based on estimated r^2 was 105 for Hampshire, 111 for Landrace, and 125 for both Yorkshire and Duroc. These estimates of LD are lower than previously reported values based on a smaller marker panel, and lower than recently reported estimates for Finnish Landrace and Yorkshire pigs based on the SNP60 BeadChip. Estimates of effective population size in Finnish Landrace and Yorkshire pigs using genotypes and pedigree information were smaller than our estimates. Results of this study are relevant to the US purebred seedstock industry and critical for the design of programs of whole genome marker assisted evaluation and selection.

Key words: swine, linkage disequilibrium, effective population size

335 A major QTL for response to porcine reproductive and respiratory syndrome virus in pigs. N. Boddicker*[1], D. J. Garrick[1], J. M. Reecy[1], R. Rowland[2], M. F. Rothschild[1], J. P. Steibel[3], J. K. Lunney[4], and J. C. M. Dekkers[1], *[1]Iowa State University, Ames, [2]Kansas State University, Manhattan, [3]Michigan State University,*

East Lansing, [4]United States Department of Agriculture, Beltsville, MD.

Porcine reproductive and respiratory syndrome (PRRS) is an important disease in swine production. The objective of this study was to discover the genetic basis of host response to PRRS virus using data from the PRRS Host Genetics Consortium PRRS-CAP project by conducting a genome-wide association analysis. Three groups of 200 commercial crossbred pigs were infected between 18 and 28 d of age with virus isolate NVSL 97–7985. Blood samples and body weights were collected up to 42 d post infection (dpi). Pigs were genotyped with the Illumina Porcine 60k Beadchip. Whole genome analyses focused on viral load (VL = area under the curve for log-transformed RT-PCR based serum virus from 0 to 21 dpi) and weight gain (WG = gain from 0 to 42 dpi). Heritabilities estimated using pedigree information were 28 and 26% for VL and WG, with maternal effects estimates of 14 and 11%. Phenotypic and genetic correlations between VL and WG were −0.25 and −0.34. Associations with SNPs were identified using BayesB of Gensel software. Using Porcine sequence build 10, a 33 SNP region associated with both VL and WG was found on chromosome 4. The favorable correlation between the genomic estimated breeding values for VL and WG for the 33 SNP region was −1.0. The region explained 15.7% of genetic variance for VL and 11.2% for WG. The unfavorable allele for the most significant SNP had a frequency of 0.84 and estimated allele substitution effects were significant ($P < 0.01$) for each of the 3 groups when fitting the SNP as a fixed covariate in ASREML, with estimates of −3.9, −4.7, and-4.8 units for VL (phenotypic SD = 6.9), and 3.0, 1.5, and 1.9 kg (phenotypic SD = 3 kg) for WG. This region explains a substantial proportion of the genetic variance in response to experimental challenge with a specific strain of the virus. The SNPs in this region are in high LD, which makes further fine mapping difficult. This region may provide opportunities to select pigs for PRRS resistance, but validation is required. This work was supported by the PRRS CAP, USDA NIFA Award 2008-55620-19132, the NRSP-8 Swine Genome and Bioinformatics coordination projects, and by the breeding companies that provided pigs.

Key words: swine, PRRS, GWAS

336 Use of sample pooling in a genome-wide association study identifies chromosomal regions affecting incidence of bovine respiratory disease. L. A. Kuehn*, J. W. Keele, E. Casas, S. A. Jones, D. A. King, T. G. McDaneld, T. P. L. Smith, and T. L. Wheeler, *USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE.*

We hypothesize that genome-wide association (GWA) based on high-density SNP arrays can be used to identify chromosomal regions affecting disease incidence using a case/control type approach. However, the large sample size required to map a lowly heritable trait like susceptibility to bovine respiratory disease complex (BRDC) makes the cost of such an effort prohibitive. We applied pooling of lung samples from slaughter animals with severe lung lesions (a proxy for incidence of respiratory disease) as the case group, and lungs from animals with no visible lesions as the control group (n = 1,000 for each group), to evaluate sample pooling as an approach to reduce the cost of GWA experiments on complex traits. Comparison of allele frequency estimates for each SNP was used to identify chromosomal regions influencing BRDC. We prepared 10 pools of equal volume lung tissue cores from 100 animals in each of the 2 groups (20 total pools), and DNA from each pool was genotyped in duplicate. Bead level data was used to estimate allele frequency for each pool and combined within group for comparison between case and control. Distances between pools and their replicates across 775,996 SNP were calculated and used to form a neighbor-joining phylogeny, such that individual SNP have minuscule effect on the resulting phylogeny. Allele frequency differences between case and control groups were conditionally compared using phylogenetic comparative methods, resulting in SNP with genome-wide significant associations ($P < 0.05$) in 7 chromosomal regions on BTA 9, 10, 13, 18, 20, 21, and 26. Two additional regions on BTA 7 and 17 harbor SNP under marginally less stringent correction (false discovery rate, FDR, 1%), while 1 or 2 regions on all bovine chromosomes are significant with a relaxed FDR of 5%. We conclude that the presence of lung lesions at slaughter is influenced by multiple loci, consistent with expectations from the multifactorial nature of BRDC, and that tissue pooling represents an economical means to dissect the genetic influences on this trait.

Key words: bovine respiratory disease, DNA pooling, genome wide association

337 Genetic analysis of dry matter intake in Holstein cows. D. Spurlock*, A. Wolc, D. Elkins, E. Scalese, J. Dekkers, and R. Fernando, *Iowa State University, Ames.*

Improving feed efficiency of lactating cows is gaining increased interest in the dairy industry. One strategy to improve feed efficiency is to select cows that consume less feed per unit of milk produced. However, selection for improved efficiency may contribute to undesirable correlated changes in fitness traits due to reduced feed intake at the onset of lactation. The objective of this research was to describe the genetic regulation of dry matter intake (DMI) in Holstein cows over the first 150 d in milk (DIM) using both quantitative and genomic approaches. Daily feed intake was recorded for 228 primiparous and 172 multiparous Holstein cows using the Calan Broadbent feeding system, and dry matter content of feed was determined weekly. Random regression models were used to estimate genetic parameters for DMI. Maximum heritability of daily DMI was 0.27 at 25 DIM, and declined to a minimum of 0.18 at 120 DIM. The genetic correlation between DMI on different days was close to unity when less than 60 d apart, and declined to 0.83 between DMI at 10 and 150 DIM. For genomic analyses, DMI was averaged over each of 5 monthly intervals. Genotypes were determined for all cows using the Illumina Bovine 50K SNP platform. Genomic regions associated with variation in DMI were identified using method BayesC implemented in the software package GenSel. Jointly, all genetic markers accounted for 26 to 50 percent of phenotypic variance in average DMI for months one, 2, 3 and 5, but only 4 percent in mo 4. Individual markers had relatively small effects. For each month of lactation, the 10 genomic regions explaining the greatest variance in average DMI were identified. Only 3 of these regions were shared between average DMI for the first and fifth month of lactation. Together, these analyses confirm that DMI is a moderately heritable trait, and that its genetic regulation changes with stage of lactation. The genetic correlation of daily DMI is high throughout the first half of lactation, but use of genetic markers may help to minimize undesirable change in DMI during early lactation as a correlated response to selection for improved efficiency.

Key words: dry matter intake, heritability, genomics

338 Genetic markers in bovine chromosome 14 are significant for residual feed intake in steers. A. K. Lindholm-Perry*, L. A. Kuehn, T. P. L. Smith, W. M. Snelling, and H. C. Freetly, *USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE.*

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 for traits associated with feed efficiency. Crossbred steers (n = 1,195) were fed a high-corn diet for 140 d and average daily feed intake (ADFI), ADG, and residual feed intake (RFI) phenotypes were obtained. RFI was defined from the regression of ADFI on ADG and mid-metabolic BW. These animals were genotyped with the Illumina Bovine SNP50 BeadChip and an association analysis of these single nucleotide polymorphisms (SNP) was performed. A 1.6 Mb region at BTA14: 22.3 to 23.9 was identified as having significant association (nominal $P = 0.04$ to 0.0006) with RFI. To develop markers with the maximum ability to discriminate favorable alleles, 70 additional SNP, not present on the BeadChip, were genotyped within this chromosomal region. These new SNP were genotyped on the same animals and tested for association with ADFI, ADG, and RFI. The statistical model included fixed effects of year and location; covariates of age, heterosis, and breed percentage; and a random polygenic effect. Ten markers were nominally significant within this region for RFI, the most significant of these were clustered between 23.3 to 23.5 Mb. After conservative correction for multiple testing, one marker at 23.30 Mb remained significant. Many of these markers were also significant for ADG, although none were significant after correction. Alleles with positive effects on ADG correspond to negative effects on RFI, suggesting a marker effect of increased growth without increased feed intake. These markers may be useful as prediction tools for animals that utilize feed more efficiently; however, potential impact of these markers on additional production traits will need to be assessed.

Key words: beef cattle, feed efficiency, genomics

339 QTL-by-feeding period interaction for residual feed intake in crossbred steers: a genome selection approach. O. N. Durunna*[1], D. J. Nkrumah[2], S. S. Moore[1], and Z. Wang[1], *[1]University of Alberta, Edmonton, Alberta, Canada, [2]Pfizer Animal Genetics, Kalamazoo, MI.*

Most feeding trials are conducted within a single feeding period but growing cattle are fed across different feeding periods. It is important to understand whether different feeding periods contribute to differential performance of the QTLs that are associated with residual feed intake (RFI) in growing steers. Our objective was to determine whether similar QTLs associated with RFI in steers are detected during the fall and winter-feeding periods. Feeding trials were conducted over 7 years using crossbred steers fed a finisher diet during the fall (P1) or winter (P2). The number of steers evaluated in P1 and P2 were 319 and 532, respectively. Feed intake was measured with the GrowSafe system, and RFI calculated by linear regression. Genotyping was done using the Illumina BovineSNP50 Beadchip. Genome selection was implemented using a Bayesian approach in Proc QTL using 1407 evenly spaced markers from 40653 SNP. 5000 permutations were used to determine thresholds at 1% and 5% for each group. Group of steers fed in each feeding period was analyzed separately. No QTL was detected on chromosomes 13, 24, 25 and 27 in P1 while QTLs were absent on chromosomes 14 and 22 in P2. More QTLs were observed in the second feeding period than the first feeding period but there was no difference in the number of QTLs that were significant ($P > 0.05$) between the 2 groups at 1% or 5% thresholds. Majority of the QTLs had opposite effects from one feeding period to another. The results indicate that feeding period may contribute to the differential performance of QTLs associated with RFI, therefore it is suggested that effective application of makers in MAS or genome selection should consider their effects in all feeding periods.

Key words: QTL-by-environment interaction, residual feed intake, beef steers

340 Identification of genomic markers for feed efficiency in purebred Simmental, Angus and crossbred steers. N. V. L. Serão*[1], A. D. Markey[1], M. Pérez-Enciso[2], D. B. Faulkner[1], J. E. Beever[1], and S. L. Rodríguez-Zas[1], *[1]University of Illinois at Urbana-Champaign, Urbana, [2]Universitat Autònoma de Barcelona, Barcelona, Catalonia, Spain.*

The identification of genomic markers associated with feed efficiency in cattle is expected to help in understanding the role of genes, pathways and regulatory elements and accelerate the genetic improvement for this trait of utmost economic importance. The purpose of this study was to identify genomic markers associated with variation in feed efficiency. Genotypes of 703 steers were obtained using the Illumina Bovine SNP50 BeadChip. In total, 2,494 markers found on bovine chromosomes 6 were considered. The indicator of feed efficiency residual feed intake (RFI) was computed based on dry matter intake adjusted for average daily gain and mid-test metabolic weight. A model including the fixed effects of individual SNPs, breed (5 levels; Angus (AN), 3/4 AN, 1/2 AN 1/2 Simmental (SM), 3/4 SM and SM), diet (5 levels), breed-diet interaction, days on feed (covariate) and the random effects of harvest group within contemporary group (27 levels) and additive polygenic effect (pedigree including 3,786 animals) was used to identify SNPs associated with RFI. Maximum likelihood parameter estimation and fixed effects testing were implemented using Qxpak v 5.03. After multiple test adjustment, SNPs were deemed statistical significant at $P < 0.001$. From the 47 SNPs associated with RFI at $P < 0.01$, 7 were associated at $P < 0.001$. Among the 7 SNPs, 2 are harbored on gene regions. SNP rs41870471 is located on the intronic region of Ankrd17, a gene known to affect growth, metabolism, muscle, and aging in mice. SNP rs43451062 is located on the intronic region of Prss12, a member of the trypsin family of serine proteases associated with neurological processes. Breed by Diet interaction had a significant ($P < 0.05$) association with RFI for 6 of the top 7 SNPs. The exception was the model including rs41663978, which exhibited a significant effect of Diet on RFI. SNP rs43451062 had the highest allele substitution effect (1.90 ± 0.01), whereas rs29017713 showed the lowest (0.16 ± 0.01). The incorporation of these markers in genomic selection strategies is expected to accelerate the genetic improvement of feed efficiency.

Key words: residual feed intake, SNP, Association analysis

341 Prediction of genomic estimated breeding values for temperament at weaning in *Bos indicus* crossbreds using Bayesian Inference. L. L. Hulsman*[1], S. O. Peters[2], J. O. Sanders[1], A. D. Herring[1], C. A. Gill[1], and D. G. Riley[1], *[1]Department of Animal Science, Texas A&M University, College Station, [2]Department of Animal and Range Sciences, New Mexico State University, Las Cruces.*

Temperament in cattle influences animals handling and carcass traits. Genetic selection can modify this trait. The objective of this study was to predict GEBV for weaning temperament in crossbred cattle using Bayesian analysis of partitioned data sets for training and validation. Calves (n = 698) were from 13 full-sib embryo transfer Nellore-Angus F_2 families and 4 half-sib families sired by the same bulls in central Texas. Temperament was subjectively assessed by 4 evaluators, where

1 indicated docile and 9 indicated extremely nervous or wild. The average score was used as phenotype. All calves were genotyped using the BovineSNP50 assay (Illumina Inc., San Diego, CA). Markers with call rates <0.9, minor allele frequency <0.05, and Hardy-Weinberg Equilibrium proportions rejected at $P < 0.05$ were removed. Analyses were conducted with 34,980 markers using BayesC procedures. Effects of SNP were random in a mixture model with an inclusion fraction (1 - Π) of 0.001. Fixed effects included birth-year-season, breed of dam, family, and sex. Training was done (1) once using all animals in training, (2) 4 times using the progeny of all but one sire, (3) once using only embryo transfer F_2 progeny, and (4) once by random assignment. Each analysis had GEBV predicted; breeding values were also predicted using an animal model. The average of each animal's GEBV when included in training was compared with the predicted GEBV when included in validation. Each calf was included 5 or 6 times in training and 1 or 2 times in the validation. Correlation (r) between averaged GEBV and predicted GEBV was 0.56. For the best 10% of males, GEBV from Bayesian analyses were re-ranked as compared with traditional prediction (r ranged from −0.64 to −0.32; $P < 0.05$). Generally, GEBV for the best calves ranked similarly (r ranged from 0.24 to 0.84), regardless of their inclusion in training or validation. Re-ranks among analyses could be due to data set size, marker structure, or both.

Key words: Bayesian inference, genomic estimated breeding value, temperament

Companion Animals Symposium: Promoting Companion Animal Biology and Research in Animal Sciences

342 Reaching out: Opportunities for developing companion animal biology. C. L. Morris*, *Omaha's Henry Doorly Zoo, Omaha, NE.*

During the last century, Animal Science programs throughout the United States have provided outstanding leadership in scientific inquiry and education regarding livestock production. Changing demographics, including diversity of student populations in the past few decades, along with companion animal industry needs have highlighted the demand for advancement and development of Animal Science program opportunities. Along with demographic changes, career goals and interests of Animal Science students also have shifted. Fewer students are seeking traditional careers in livestock animal production and pursing opportunities in the areas of genomics, companion animals, exotic animals, and specialized interests in topics including behavior and animal welfare. As the US population of pet dogs and cats exceed the number of children in households, and with more than 175 million guests visiting US zoological institutions annually, growing opportunities in the pet and exotic animal industries are on the rise. These animal industries are evolving rapidly in areas such as nutrition, education, behavioral husbandry and training, conservation, outreach, shelter management, and small business management. With growing demand of these industries seeking well-trained professionals, Animal Science departments are charged with developing curricula that appropriately train students for careers in these fields. Currently, few universities have the professional staff with the breadth of expertise to provide teaching and outreach opportunities to students seeking these career directions. These changes in student demographics and educational goals provide exceptional opportunities for Departments of Animal Sciences to promote outreach opportunities and advanced technology education transfer when teaching staff are limited. Therefore, the objectives of this symposium will be to explore the important role of teaching and outreach in the area of companion and exotic animal biology and to discuss potential opportunities to expand teaching, outreach, and research through alternative methodology and technology in academics to reach industry needs.

Key words: companion animals, exotic animals, teaching and outreach

343 Wants and needs: What students want may not be what the current comparative animal industry needs. K. D. Ange-van Heugten*, *North Carolina State University, Raleigh.*

Companion animals are the top commodity preference of study for incoming freshman (Fr) in many North American animal science (ANS) departments. For example, incoming ANS Fr at NCSU are surveyed yearly about their species preference and 2010 data (n = 120) indicate the following as their first preference: companion animal (58%), equine (29%), beef cattle (3%), dairy cattle (3%), marine mammal (2%), swine (2%), sheep (1%), goats and lab animal (0), other (2%). These freshmen were 83% female and 92% want to be a veterinarian. Similarly, when 2 2011 companion animal courses (1 Fr level, n = 120; 1 senior level, n = 51) were surveyed they indicated that the primary determinants for their career were as follows in decreasing order of preference: discipline area, daily work with animals, species specific work, salary, flexible hours, and location. Within the senior course, 92% of the students indicated that they want their future career to involve companion or exotic species. The multibillion dollar companion and comparative animal industries need many specialists with the popular areas of veterinary medicine and behavior being minorities. Sources report the 10 most critical hiring criteria for employers as: communication, integrity, teamwork, interpersonal skills, work ethic, motivation, flexibility, analytical, computer, and organization skills. In contrast, students want: opportunity to advance, job security, benefits packages and friendly coworkers. In the current economy, job security, benefits and coworker choice are not reliable and many employers feel that new graduates lack communication, management and business etiquette skills. Thus, hiring agencies focus on personal skills and are less interested in species or veterinary preferences. Companion animal educators should emphasize that many vital comparative animal career paths exist in addition to veterinary or comparative species professions. In fact, work in other areas can be incredibly lucrative and vital for the industry. In addition, students need to sharpen their management skills while appreciating the critical difference between communicating with their peers and employers.

Key words: companion animal, education, industry

344 Cat and mouse: Utilizing technology and science to reach students. N. A. Dreschel*, *Pennsylvania State University, University Park.*

From simple applications such as blogs, video and the use of course management systems, to complete courses offered online, the availability of resources for companion animal instruction have increased tremendously. The benefits of using technology include improved student interaction, an ability to engage students with different learning styles, and an ability to reach nontraditional student audiences. An online general education animal science course examining the relationship of "Pets in Society" uses a variety of technologies to instruct both traditional, residential animal science students and nontraditional distance learners. Distance-learning students bring a wealth of experience and insight to an integrated course. Choosing appropriate and meaningful technology is important in instructional design. Examples of instructional techniques such as "rollover" animations, narrated PowerPoints, video interviews and online discussion forums will be presented. Technology used or created for online courses can also be transferred to in-class or "hybrid" courses, as well as to extension formats such as eXtension. Challenges in teaching with technology include the time needed to develop technology, faculty and student comfort with using technology, modifications of technology to meet the needs of students with disabilities, and institutional constraints on the ability to offer courses online. The variety of new technology available can be overwhelming; however, presents great opportunities for engaging and teaching students in both traditional and online environments.

Key words: teaching, technology, companion animals

345 Research and outreach: Blending the basic and the applied. L. K. Karr-Lilienthal*, *University of Nebraska-Lincoln, Lincoln.*

The opportunities to complete undergraduate research related to companion animals are limited. Assisting with traditional animal research projects can allow for students to develop a better appreciation for

how research is conducted and expand their interest in graduate school programs. However, universities with companion animal research programs are few. Opportunities to match students with industry partners to gain experiences are critical. Students may have opportunities to assist with research at pet food companies, zoos, or animal assisted therapy programs. Utilizing undergraduate students in community outreach programs provides an opportunity for students to develop critical skills required for employment, but also provides companion animal faculty with research opportunities. A variety of creative activities can be utilized to improve student learning and gain experiences outside of the classroom. Examples of successful programs include student organized dog training courses, service learning projects through humane societies or animal rescues, student involvement in feral cat control programs, and student assistance with spay/neuter programs. These activities can support student learning outcomes as well as provide a valuable community services. Measuring the impacts of these activities on student learning and life skills as well as community implications will be critical to evaluation of the success of the programs. Undergraduate research activities are a meaningful way to provide students with learning opportunities. Extension or outreach programs allow for opportunities for students to develop leadership skills. Undergraduate students serving as instructors in 4-H and other youth programs can provide both an impact on the education of the youth involved, but also develop a deeper understanding of materials to be taught. Undergraduate students can be involved in teaching health care, nutrition, and other topics related to companion animals to youth audiences. Utilizing classroom research can aid in more accurate assessment of program goals and the ability of the program to reach its learning outcomes.

Key words: undergraduate education, companion animals, outreach

346 Biodiversity is life: Teaching conservation biology with zoos and aquariums. R. L. Krisher*, *National Foundation for Fertility Research, Lone Tree, CO.*

Student interest in the conservation of exotic and endangered species is at an all-time high. In fact, more people visit zoological institutions each year than attend all professional sporting events combined. Increased access to video programming about exotic species, and improved access to travel abroad opportunities, has motivated many college students to become passionate about animal conservation as a career choice. Enrichment of traditional Animal Science academic programs with formal coursework to meaningfully fill this void and provide opportunities to Animal Science students in this area has been challenging. To fully understand the multifaceted, complex responsibilities related to conservation of species, topics related to ecology, taxonomy, conservation biology, population genetics, physiology and management of exotic species in a captive setting must be addressed and integrated. Zoos are now an essential part of worldwide conservation strategies, and captive breeding programs are an integral part of this mission. Thus, in addition to fundamental responsibilities such as nutrition and veterinary care, zoos must address reproduction and even assisted reproduction in a directed way. Research conducted in zoos has played a meaningful role in advancing care and maintenance of captive species. Methods to exhibit these species have also improved dramatically, along with attention to environmental enrichment to enhance animal wellbeing and positively impact visitor experiences. However, the ethics of maintaining captive animals must always be explored and addressed. Finally, the public education mission and impact of zoos cannot be overstated. Overseeing all of these activities are worldwide and national organizations of significance. For students to understand and appreciate these many perspectives of a zoo operation, development of critical thinking skills is highly effective to achieve the course objectives; students that are able to speak and write intelligently on current topics pertaining to animal conservation, and students able to create and defend their own informed opinions on the modalities employed in captive animal holding and conservation.

347 The future of companion animal biology in academics. A. Fischer*, *University of Illinois, Urbana.*

As companion animal programs continue to become established components of Animal Sciences departments, the diversity of topics addressed will expand. Likely targets for growth include the fields of human-animal relationships, and applied companion animal welfare. Academic interest in human-animal relationships is growing, as evidenced by recent initiatives to promote research on the human-animal bond and to quantify the benefits of sharing our lives with companion animals. We can expect continued collaborations across a variety of disciplines, such as psychology, sociology, anthropology, and law. In the field of applied companion animal welfare, specifically in animal sheltering, we have seen an increase in data-driven initiatives aimed at increasing adoptions and decreasing euthanasia across the country. We can expect to see a continued integration of applied research in animal sheltering operations, and an increasing number of professional positions for our graduates in the areas of animal advocacy, policy, and management.

Key words: companion animal, academics, careers

Contemporary and Emerging Issues Symposium: Emerging Animal Welfare Issues

348 Does high production increase the occurrence of health problems in dairy cows? K. D. Vogel*, *Department of Food and Animal Science, University of Wisconsin-River Falls, River Falls.*

Over the past 30 years, individual dairy cow production has increased substantially. The production efficiencies gained through genetic selection, improved nutrition, and changes in management practices has come largely through advances in scientific knowledge of animal breeding, physiology, metabolism, and nutrition. Historically, the primary goal of this research was increased animal productivity through increased milk secretion. Although the goal of maximal production was never malicious, but actually quite the contrary, increasing societal concern has arisen regarding the health and welfare of modern high-producing dairy cows. Some have hypothesized that modern production levels may be taxing the metabolic and physiologic capacities of dairy cows, resulting in increased incidences of lameness, mastitis, infertility, and mortality. However, the underlying factors in cases of lameness, mastitis, infertility and mortality vary widely. Recent studies have consistently identified not one, but multiple, underlying factors that culminated in the one common health problem under investigation. Multiple studies have identified genetic selection, management, nutrition, and environment as influential factors in the incidence of health and welfare issues in modern, high-producing dairy cattle. It appears that an interaction of all of these factors dictates the health and welfare state of the dairy cow. The need exists to integrate the current body of knowledge related to dairy cattle health and welfare to identify common contributors to the incidence of the most prevalent production-related diseases. Data suggest that production diseases are not resultant of milk production level alone, but production level does appear to be a risk factor in the development of health problems in dairy cows. Ultimately, the interaction of genetic predisposition, management, and environment dictate the development of the majority of production related health disorders observed in the modern dairy cow. Remediation of production related health issues requires the consideration of all factors included in the interaction.

Key words: dairy, production, welfare

349 Potential solutions for reducing lameness in dairy cows. N. Cook*, *University of Wisconsin, Madison.*

Lameness control is fundamental to the management of the modern confinement housed dairy herd. It is the most important condition impacting a cow's well-being, and it affects everything she does in her day, from resting, to eating, socializing and milking. Foot lameness is dominated by infectious lesions such as digital dermatitis and foot rot (phlegmon), and by lesions of the claw horn, such as white line disease and ulceration of the sole. Infectious hoof disease can be effectively controlled through good nutrition, improved foot hygiene and by the effective use of hoofbaths to clean and disinfect the foot on a regular basis. Copper sulfate, formalin and zinc compounds are the most commonly used disinfectants and all appear efficacious. However, more attention needs to be paid to the design and location of the hoofbath, to optimize its use within individual farm circumstances. Claw horn lesions may be triggered through poor feeding and poor transitions at calving time. However, white line disease is exacerbated in facilities with poor flooring that creates risk for trauma, wear and concussion. Strategic use of rubberized surfaces and improved concrete finishing greatly impacts the incidence of this disease. Increased standing time per day on hard surfaces appears to increase the risk for sole ulcer. Dairy facilities need to be designed so that both lame and non-lame cows can achieve at least 12 h of rest per day. This can be achieved with deep loose-bedded stalls with sand bedding, sized to accommodate the resting area of the cow, with freedom to front lunge in the stall without obstruction. Group sizes need to be matched to parlor size and throughput, to minimize time out of the pen to less than one hour per milking, and stocking rates need to be controlled to a maximum of 1.2 cows per stall. Strategic use of fans and soakers, or other cooling methods are essential components of lameness control in the summer. Finally, excellent hoof health requires a dedicated, well-trained hoof-trimmer rebalancing the claws of all the cows at least twice per year, and prompt effective treatment of the lame cow.

Key words: lameness, solutions

350 The national shortage of food animal veterinarians: What's being done to address the issue? D. G. Bristol*, *North Carolina State University, Raleigh.*

When the owner of a sick or injured animal cannot obtain access to prompt veterinary care for that animal, it creates a serious welfare issue. The cause of the shortages in food animal/production veterinarians is multifactorial, and while little can be done to change some of those causes, numerous actions have been taken to address the final result – the veterinary shortage. Survey data collected in 2006 and published by the AVMA indicated that only 10% of all veterinarians practice on food animals. This seminar will review both the causes and potential solutions to a shortage that impacts animal welfare and the safety of the US food supply. A survey by Lenarduzz et al. (2009) showed that contact with food animal practitioners during vet school was a factor in motivating a career choice in large animal practice. Experience with agriculture may encourage students to consider large animal practice. Some veterinary colleges have 4 or 5 places each year that are reserved for students interested in food animal agriculture. Some of these programs also include financial incentives to practice in rural areas. Other alternatives are developing centers for food animal excellence in several veterinary colleges. There is also a need to expose undergraduate students to food animals so they will develop an interest in them.

Key words: veterinarian, food animal, careers

351 Animal welfare issues: Organic and conventional. W. K. Fulwider*, *Cropp Cooperative, LaFarge, WI.*

The objective of this paper is to acknowledge differences between organic and conventional management regarding animal welfare. Lameness is the most serious welfare issue in dairy herds and leads to milk loss, more days to conception, and increased cull rates. Growth hormone (rBST) may negatively affect body condition, mastitis, and lameness. Parasites are one of the biggest challenges facing the organic industry. Organic management emphasizes prevention of lameness, parasites, displaced abomasums, acidosis, and problems associated with boredom such as tail-biting in swine by providing environments that reduce stress by allowing natural behaviors. Studies show that cattle with access to pasture have reduced lameness. Parasites can be

controlled with rotational and multi-species grazing. Chickens break up manure pats, Muscovy ducks keep fly numbers low, and Runner ducks help eliminate liver fluke problems. When in transition, new challenges make communication with experienced producers and specialists a must. Organic producers often use different breeds or genetic lines to prevent health problems. Hair sheep are resistant to parasites. Dairy cattle with New Zealand genetics may be better suited to grazing. Older genetic lines of Berkshire, Chester White, and Duroc hogs may be less aggressive and better suited to group systems and foraging. The US organic industry is often criticized for not allowing antibiotics. The organic standard states that an organic producer may not withhold medical treatment to preserve an animal's certified organic status. The treated animal must be permanently removed from organic production. Organic animals are housed more extensively to reduce stress and aggression so that procedures such as tail-docking hogs are unnecessary. Use of β-agonists such as ractopamine in swine and zilpaterol in beef may result in lower quality meat and increased welfare problems such as hoof cracking and animals that are difficult to handle. Organic farmers produce food humanely and without chemicals, hormones, or antibiotics. Good management, attention to detail, and continuous improvement are important components of every farm whether organic or conventional.

Key words: welfare, organic, livestock

352 Consequence of changing standards for somatic cell count on US Dairy Herd Improvement herds. H. D. Norman*, J. R. Wright, and R. H. Miller, *Animal Improvement Programs Laboratory, USDA-ARS, Beltsville, MD.*

Consequence of noncompliance with European Union (EU) and current US standards for somatic cell count (SCC) as well as SCC standards proposed by the National Milk Producers Federation was examined for US herds. Somatic cell scores (SCS) from 14,854 Dairy Herd Improvement (DHI) herds were analyzed. Herds had between 15 and 26 DHI tests from Jan. 2009 to Oct. 2010 and ≥ 10 cows. The SCC for individual cows came from their SCS by SCC = $2^{(SCS - 3)}$(100,000). As a proxy for bulk tank SCC, herd test-day SCC were derived by weighting each cow′s SCC by her test-day milk yield and were the basis for determining herds and milk that were SCC noncompliant. A herd was noncompliant for the EU SCC standard after 4 consecutive rolling 3-test geometric means were > 400,000 cells/mL. A herd was noncompliant for US SCC standards after 3 of 5 consecutive SCC tests were > 750,000 (current), > 600,000 (proposed), > 500,000 (proposed), or > 400,000 (proposed) cells/mL. Results were examined by month, herd size, and state. For current SCC standards, weighted means for US herd noncompliance from Nov. 2009 through Oct. 2010 was 0.9% for US and 7.8% for EU standards; noncompliance for proposed US SCC standards of 600,000, 500,000, and 400,000 cells/mL were 2.7, 6.2, and 14.1%, respectively. Only a US standard of 400,000 cells/mL was more restrictive than the EU standard. Only 0.2% and 3.1% of US milk failed current US and EU SCC standards, respectively. Compliance for US herds generally increased with herd size. For the current US SCC standard, 1.7% of herds were noncompliant when herd size was < 50 cows, but ≤ 0.1% of each of 4 herd groups with ≥ 200 cows were noncompliant. For the EU standard, noncompliance declined from 10.6% for herds with < 50 cows to 0.5% for herds with ≥ 1,000 cows. Herd noncompliance ranged from 2 to 15% for 6 states and Puerto Rico for the current US standard and from 20 to 35% for 9 states for the EU standard. If US producers must meet more stringent EU or proposed US standards for SCC, they will need to place more emphasis on sound milking management practices and do more culling to improve milk quality.

Key words: somatic cell, standards, milk quality

353 Current level of compliance with EU bulk tank SCC standards and proposed US standards based on data from four Federal Milk Marketing Orders. J. E. Lombard[1], H. D. Norman*[2], C. A. Kopral[1], J. M. Rodriguez[1], and J. R. Wright[2], *[1]USDA-APHIS-VS, Centers for Epidemiology and Animal Health, Fort Collins, CO, [2]USDA-ARS, Animal Improvement Programs Laboratory, Beltsville, MD.*

Milk quality in the United States is evaluated annually using bulk-tank somatic cell count (BTSCC) data provided by 4 of the nation's 10 Federal Milk Marketing Orders. The data represents more than 30,000 producers and 50% of milk produced in the US. The reported BTSCC is used for regulatory purposes to determine compliance with the current US limit of 750,000 cells/ml. If 3 of 5 consecutive monthly shipments exceed 750K then regulatory action is taken. The objective of this study was to evaluate compliance of producers with the newly proposed US BTSCC limits. BTSCC data from producers that shipped between 15 and 22 shipments between Jan. 2009 to Oct 2010 were included in the analysis. Four different SCC levels of compliance based on US standards were evaluated: 750K; 600K; 500K; 400K. In addition, the EU standard of 400K based on a 3 mo geometric mean was evaluated. For the 12 mo period ending Oct 2010, 1.0% of producers and 0.2% of milk exceeded the current US limit of 750K; 4.7% of producers and 1.4% of milk exceeded the proposed 600K limit. Although the proposed 400K limit would be the same in the US and the EU, differences in how the limits are calculated and used for regulatory purposes change the percent of producers in compliance in the 2 countries. Although 23.3% of producers exceeded the proposed US 400K limit, only 16.1% of producers would have exceeded the current EU standard. For herds shipping < 907 t of milk in the 12 mo period, 28.0% would have exceeded the proposed 400K US limit and 19.5% would have exceeded the current EU standard. Only 4.1% and 2.2% of herds shipping more than 9,072 t would have exceeded the proposed 400K US limit and current EU limit, respectively. If implemented, the proposed phased in reduction to a 400K BTSCC limit would result in a substantial increase in producers and milk, primarily those with < 100 cows, which would exceed the regulatory limit. Producer education and implementation of programs to lower BTSCC will be critical in minimizing the impact of the proposed reduction in BTSCC.

Key words: somatic cell, standards, milk quality

354 Latinos and animal agriculture. S. Archibeque-Engle* and I. N. Roman-Muniz, *Colorado State University, Fort Collins.*

The hypothesis of this project is that Latinos are critical to the sustainability of animal agriculture in the United States. The intellectual merit of this project is that it quantifies the need for educated animal scientists and identifies potential areas for growth. Since 1903, Colorado State University (CSU) has served as a leader in the Animal Sciences industry. In the early days of the department, undergraduate students had a significant tie to production agriculture, many of those students left family farms to obtain an education and they returned to family farms to put their educations to work once they finished college. Those who did not return to family farms went to work in production agriculture and served as the leaders who shaped the food supply that our country now enjoys. Most undergraduate students who come to CSU to study Animal Sciences in the 21st century no longer have a

tie to production agriculture or agriculture at all. In fact, over 80% of our undergraduates report that they have no agricultural experience (unpublished departmental data). In 2009 the state of Colorado was 20.3% Hispanic (Latino) (www.quickfacts.census.gov) and 90% of farm workers in the west and midwest are Hispanic (Von Essen et al., 1998; Kirkhorn et al., 2002; Mines et al., 1997). In Colorado counties where there is a large livestock industry like Weld and Prowers there is an even larger Hispanic population (27.0% and 32.9% Hispanic, respectively; www.quickfacts.census.gov) However, the Department of Animal Sciences undergraduate population is 5.5% Hispanic (Colorado State University Census Data, Fall 2010). The luxury of excluding any population from an agricultural education, especially given the importance of agriculture to the success of our country, does not exist. We need to educate those who have traditionally come to us (students from family operations), those who are currently coming to us (students from urban and suburban backgrounds), and those who have worked in agriculture in the US for a long time but have been absent from higher education classrooms: Latinos.

Key words: agricultural workers, higher education, animal sciences

355 Effect of live yeast supplementation on milk production and health status of lactating camels (*Camelus dromedarius*). P. Nagy*[1], E. Chevaux[3], M. Khettou[3], O. Marko[2], S. Thomas[2], U. Wernery[2], and J. Juhasz[2], *[1]Industries for Camel Milk and Products, Dubai, United Arabic Emirates, [2]Central Veterinary Research Institute, Dubai, United Arabic Emirates, [3]Lallemand SAS, Toulouse, France.*

Dromedaries have not been considered as valuable milk producing animals in the past and limited data are available on their dairy potential and possibilities for improvement. The use of live yeast as a nutritional tool to optimize digestibility of the diet has been extensively documented on ruminants. Though, camels are not true ruminants, their foregut is similar to the rumen, so dairy camels could also benefit from the supplementation of live yeast. The present study aimed at comparing 90 dairy camels (165 d in milk) evenly randomized into 2 dietary treatments (Control (C) vs. Levucell SC (LSC)) during 5 mo. Animals were milked twice daily, sampled for milk composition once a month and for blood parameters every 2 mo. Feed intake was monitored on a daily basis. Data were processed with the mixed model of SPSS 17.0. The average milk production of the camels fed the live yeast (*S. cerevisiae* I-1077) increased ($P < 0.01$) by 10% (7.26 ± 0.14 vs 7.99 ± 0.17 kg/d), without affecting milk fat % (2.46 ± 0.04 vs 2.49 ± 0.04), protein % (2.81 ± 0.02 vs 2.80 ± 0.02), total solids % (10.46 ± 0.06 vs 10.41 ± 0.06) and solids non fat % (8.10 ± 0.04 vs 8.02 ± 0.04) content for C vs LSC, respectively. However, lactose content was higher ($P < 0.01$) for C (4.33 ± 0.02 vs. 4.25 ± 0.02%). Protein yield was increased ($P < 0.05$) for LSC over C (213.6 ± 4.7 vs. 199.3 ± 4.7 g/day) whereas fat yield was numerically higher for LSC (187.6 ± 4.9 vs. 176.8 ± 4.9 g/day). No difference was found on SCC or TVC. Hematology values remained within the normal range. However, some of the blood nutritional markers indicated some difference in metabolism of C animals as illustrated by higher ($P < 0.01$) levels of creatine kinase (162.7 ± 5.8 vs. 124.3 ± 5.6 U/L) and lactate dehydrogenase (333.7 ± 5.3 vs. 311.9 ± 5.2 U/L). The liver activity was also stimulated for C (79.9 ± 1.3 vs. 71.7 ± 1.3 U/L AST), so did the kidney metabolism ($P < 0.05$) as shown by creatinine (193.9 ± 2.7 vs. 186.3 ± 2.6 µmol/L) and BUN (11.1 ± 0.2 vs. 10.5 ± 0.2 mmol/L) when compared with LSC. The supply of Levucell SC to lactating dromedary camels supported higher milk production and seemed to have played a role in optimizing protein metabolism.

Key words: dairy camel, live yeast

356 Why people become vegetarian and/or vegan: Results of a survey of US self-identified vegans. S. D. Lukefahr*[1], R. A. Cheeke[2], and P. R. Cheeke[3], *[1]Texas A&M University-Kingsville, 27510 NE Todd Dr., Corvallis, OR, [3]Oregon State University, Corvallis.*

A survey to identify why people choose to become vegan/vegetarian (V/V) was given to people from 14 US states attending V/V trade shows and festivals (e.g., VegFest). Background data included gender, age, education, farm background, animal experience, and dietary habits. Participants were asked the importance of factors in their decision to not consume animal-derived products. The factors were: 1. I am opposed to killing animals; 2. I am concerned with health issues; 3. I am concerned about residues of chemical feed additives and hormones; 4. I am opposed to intensive, confinement systems; 5. I am concerned with food safety issues; 6. I believe that animal production competes with humans for grains; 7. I am concerned about environmental issues; 8. It is "cool" and trendy to be a vegetarian; and 9. I became vegetarian because of peer pressure. The initial scale used in the 2009 survey ranged from extremely important, important, and not important, which was modified in 2010 to a more quantitative scale with 7 classes, ranging from extremely not important to extremely important. Data from 2009 surveys (n = 121) were analyzed by Chi-Square to test for relationships between survey scores for each question (Q) and background of the individual. Data from 2010 surveys (n = 37) were analyzed by ANOVA involving background factors as sources of variation. Results for 2009 and 2010 showed that most participants surveyed were females over 20 years of age with a college or university education, but had animal experience with only pets and no farm background. For 2009, an association was found ($P < 0.05$) between education level and Q5 that dealt with food safety issues. For 2010, dietary habit influenced ($P < 0.01$ to 0.10) responses to Q1, Q7, Q8, and Q9, whereas education and farm background influenced ($P < 0.05$) responses to Q4 and Q6, respectively. In conclusion, no single issue seems to be the dominant explanation for the selection of a non-animal product lifestyle.

Key words: vegetarianism, dietary choices, contemporary issues

357 Does pre-slaughter stress affect pork safety risk? M. H. Rostagno*, S. D. Eicher, and D. C. Lay, *USDA-ARS-LBRU, West Lafayette, IN.*

Salmonella is the top food safety priority for the pork industry. Although contamination of pork occurs along the slaughter and processing line, infected live pigs entering the abattoir constitute the original *Salmonella* contamination source. However, the extent of carcass contamination is not only determined by the number of pigs infected, but also by the levels of *Salmonella* entering the abattoir in the intestinal tract of slaughtered pigs. Therefore, a series of experiments was conducted to determine if common stressors occurring before slaughter affect the prevalence and levels of *Salmonella* in market pigs. Initially, a field study was conducted to determine the effect of transportation and lairage on the frequency of *Salmonella* shedding in market pigs. A follow up study was conducted under controlled conditions to determine the effect of feed withdrawal and transportation on the levels of *Salmonella* in the intestinal tract of infected market-weight pigs. Finally, a third study was conducted to determine the effect of transportation and mixing with unfamiliar pigs on the susceptibility of market-weight pigs to *Salmonella* infection. In the first study, *Salmonella* shedding increased ($P < 0.05$) from pre-transport (11.3%) to post-transport (20%), and from post-transport to post-lairage (42%). In the second study, feed withdrawal by itself or combined with transportation caused increased levels of *Salmonella* in the ileum ($P < 0.05$), whereas only the combination of feed withdrawal and transportation caused increased levels of *Salmonella* in the cecum ($P < 0.05$). In the third study, pigs subjected to transportation and/or mixing were colonized by higher ($P < 0.05$) levels of *Salmonella* in the ileum, whereas only pigs subjected to both stressors combined were colonized by higher ($P < 0.05$) *Salmonella* levels in the cecum. It is concluded that pre-slaughter stressors, such as transportation, feed withdrawal and mixing, affect pork safety risk by increasing frequency and levels of *Salmonella* in the intestinal tract of market-weight pigs.

Key words: *Salmonella*, stress, swine

358 Salt and nitrite at concentrations relevant to meat processing enhances Shiga toxin II production by *E. coli* O157:H7. S. M. Harris*, S. A. Olsen, J. Hu, M. Du, and M. J. Zhu, *Department of Animal Science, University of Wyoming, Laramie.*

Escherichia coli (O157:H7 is a major food safety threat. It has ability to produce several virulence factors. Shiga toxins (Stxs) are the key virulence factors of *E. coli* O157:H7 that are responsible for hemorrhagic colitis and serious renal failure. Despite the extensive study of *E. coli* O157:H7 survival during meat processing, the production of Stxs by *E. coli* O157:H7 during these processes has not been studied. This becomes a very important question since Stx2 is resistant to heat treatment. The objective of this study is to elucidate the effect of 2 essential additives in processed meats, salt and nitrite, on Stx2 production by *E. coli* O157:H7. *E. coli* O157: H7 (86–24) was treated with different concentrations of salt (1%, 2%, and 3%, W/V) or sodium nitrite (0, 100, 200, 300 ppm) solutions for 6 h. The Stx2 production and cfu were analyzed. After 6 h incubation, the number of *E. coli* O157:H7 in nitrite-100 ppm was not different from that of control (0 ppm). However, the number of *E. coli* O157:H7 in nitrite-200 ppm ($P < 0.1$) and nitrite-300 ppm ($P < 0.05$) were lower than control. Western blotting analysis indicated that adding 100 ppm and 200 ppm of nitrite in LB medium increased ($P < 0.1$) Stx2 production. Similarly, including 2% and 3% of salt decreased ($P < 0.05$) the final *E. coli* O157:H7 population, but supplementing 2% salt increased ($P < 0.05$) Stx2 production per cfu compared with that of control (1% salt), while including 3% salt decreased ($P < 0.05$) Stx2 production. Since 2% salt and 100–200 ppm nitrite are commonly used in processed meats, the current study indicated that salt and nitrite at these concentrations promote Stx2 production. Therefore, not only the survival of *E. coli* O157:H7 during meat processing is important, Stxs production by *E. coli* O157:H7 is another critical control point for producing safe meat products. (USDA AFRI 2009–65203–05716, 2010–65201–20599, Agricultural Experiment Station at University of Wyoming, NIH-INBRE P20RR016474).

Key words: *E. coli* O157:H7, Stx2, nitrite

359 Detection of major serotypes of Shiga-toxin producing *E. coli* in bovine feces by multiplex PCR. Z. Paddock*, X. Shi, T. G. Nagaraja, and J. Bai, *Kansas State University, Manhattan.*

Shiga-toxin producing *E. coli* (STEC) serotypes, particularly O157, are major food borne pathogens. Recently, non-O157 STEC serotypes have also become a major public health concern. Unlike O157, isolation and detection procedures for non-O157 have not been fully developed. Confirmation of non-O157 strains is generally based on agglutination with serotype-specific antisera, which is labor intensive and sometimes nonspecific. We have developed a multiplex PCR, based on O-specific antigen coding genes, rfbE of O157, and wzx and wfqB of non-0157, to distinguish the 7 major STEC serotypes, O26, O45, O103, O111, O121, O145, and O157. The specificity of the procedure was confirmed with pure cultures of STEC strains (n = 138). Our objectives were to evaluate whether the procedure could be used to detect STEC in feces and screen fecal samples before subjecting them to detection by cultural procedures. Fecal samples spiked with different concentrations of a mixture of 7 STEC strains were tested before and after 6 h enrichment in *E. coli* (EC) broth. Fecal samples (108 from feedlot and 108 from dairy cattle) were collected, enriched in EC broth, tested by the multiplex PCR. All samples (n = 216) were cultured for O157, while a subset of samples (n = 24) were cultured for the non-O157 STEC. All 7 serotypes were specifically amplified in spiked feces with detection limits of 6.7×10^5 cfu/g before enrichment and 8.0×10^1 after 6 h enrichment in EC broth. The multiplex PCR revealed a high prevalence of STEC, except O45 serotype, in cattle feces (Table). All samples that were culture positive for STEC were also positive by the multiplex PCR. The multiplex PCR may be used to identify feces positive for the 7 STEC before subjecting the samples for cultural methods, however, additional studies are needed to validate the procedure.

Table 1. Prevalence of Shiga-toxin producing *E. coli* (STEC) in cattle feces

STEC	mPCR positive (n=24)	Culture positive (n=24)	mPCR positive (n=192)	O157 culture positive (n=192)
O26	14	5	165	-
O45	2	0	106	-
O103	10	4	140	-
O111	0	0	34	-
O121	5	4	98	-
O145	0	0	8	-
O157	16	14	149	51

Key words: Shiga-toxin producing *E. coli*, multiplex PCR, cattle feces

360 Microbial contamination rates and antimicrobial resistance patterns in "no antibiotics added" labeled chicken products. J. Zhang*[1], A. Massow[1], M. M. Stanley[1], M. Papariella[1], X. Chen[3], B. Kraft[2], and P. D. Ebner[1], *[1]Purdue University Department of Animal Sciences, West Lafayette, IN, [2]Purdue University College of Veterinary Medicine, West Lafayette, IN, [3]University of Illinois at Urbana-Champaign Department of Animal Sciences, Urbana-Champaign.*

In the United States, poultry product labels can contain "no antibiotics added" if the animals were raised without the use of antimicrobials. In this study we compared microbial community structures of conventional chicken products (CONV; n = 201) with those of chicken products labeled as coming from birds raised without antimicrobials (NON; n = 201). Both CONV and NON products were equally likely to contain Enterococcus spp., (CONV: 17.4%; NON: 21.3%) or *Escherichia coli* (CONV: 25.9%; NON: 22.3%). CONV samples contained higher concentrations of coliforms (CONV: 3.0 $\log_{10}$cfu/mL; NON: 2.5 $\log_{10}$cfu/mL; $P < 0.05$). The number of samples positive for Salmonella was low in both groups, but statistically higher ($P < 0.05$) in NON (5.0%) vs. CONV (1.5%) samples. *E. coli* isolates from CONV samples were more frequently resistant to at least one antimicrobial (CONV: 61.3%; NON: 41.2%; $P < 0.05$). Four multidrug resistance patterns appeared twice or more in *E. coli* isolates obtained from both CONV and NON products. The most common patterns in both groups were tetracycline-sulfasoxazole followed by tetracycline-sulfasoxazole-trimethoprim/sulfamethoxazole and tetracycline-ampicillin. Enterococcus spp. isolates from both groups were equally likely to be resistant to at least one antimicrobial, but Enterococcus spp. isolates from CONV samples were more likely to be resistant to erythromycin, kanamycin or gentamicin ($P < 0.05$). Five multidrug resistance patterns were detected twice or more in Enterococcus spp. isolates from CONV products while 2 multidrug resistance patterns were detected in Enterococcus spp. isolates from NON products. In both groups the most common resistance pattern was erythromycin-tetracycline-tylosin tartrate. Taken together, these data indicate that CONV and NON products have similar contamination characteristics, however, bacteria isolated from CONV products may be more frequently resistant to some antimicrobials.

Key words: antimicrobial resistance, poultry, "no antibiotics added"

361 Antimicrobial activities and comparing bacterial membrane interactions of porcine lactoferricin derived peptides. F. Han*, Y. Liu, Y. Xie, Y. Gao, and Y. Wang, *Institute of Feed Science, Hangzhou, Zhejiang, China.*

Abstract: Antibiotic treatment of microbial infections is under scrutiny because of increasing conventional antibiotic resistance, and discovery of new classes of antibiotic agents is warranted. Antimicrobial peptides are part of innate defense system found almost in all organisms. Porcine lactoferricin (LFP-20) is an antimicrobial peptide identified in N terminus of porcine lactoferrin. To develop novel antimicrobial peptides with improved antimicrobial specificity as compared with LFP-20, we designed analogs LF-2, LF-4 and LF-6 with substituted alanine, serine, or tryptophan residues at the different positions of the molecule. Broth microdilution, hemoglobin release, WST-1 and $DiSC_35$ methods were used in this study. Statistical significance among independent groups was determined using one-way ANOVA. Analogs displayed a 2~16-fold higher antimicrobial activity than LFP-20 but did not induce increased hemolytic activity significantly ($P > 0.05$) to porcine erythrocyte below 32 μg/mL compared with LFP-20. Furthermore, the proliferations of porcine peripheral blood mononuclear cells were not influenced significantly ($P > 0.05$) by LF-2, LF-4 and LF-6 below 50 μg/mL. Except for 8 μg/mL and 16 μg/mL LF-4, the cytotoxicities of LF-2, LF-4 and LF-6 to PBMCs were not increased significantly ($P > 0.05$) below 32 μg/mL compared with LFP-20. To better understand the antibacterial mechanism of LFP-20 and its analogs, we studied their effect on the cytoplasmic membrane of *Escherichia coli*. LFP-20 was not effective in depolarizing the cytoplasmic membranes, whereas 3 analogs could gradually dissipated membrane potential of *Escherichia coli*, demonstrating a correlation between bactericidal activity and membrane depolarization. Compared with LFP-20, 3 analogs enhanced the *Escherichia coli* outer membrane permeability significantly ($P < 0.05$) at 8 ~32 μg/mL. LF-6 led to the most obvious inner membrane permeability of *Escherichia coli*. Collectively, these results suggest that the first target for 3 analogs on *Escherichia coli* may be the cytoplasmic membranes.

Key words: porcine lactoferricin, antimicrobial activity, antimicrobial mechanism

362 Nitrate and nitrite partition in cheese and whey during cheesemaking. F. F. Pinheiro, L. M. Fonseca*, M. O. Leite, M. M. O. P. Cerqueira, R. Rodrigues, C. F. A. M. Penna, and M. R. Souza, *Veterinary School/Universidade Federal de Minas Gerais, Belo Horizonte, MG, Brazil.*

Nitrate is used in the dairy industry as a preservative to prevent cheese blowing due to bacterial growth. However, due to health concerns, concentration limits for usage in countries where it is allowed are usually fixed at 50 mg/kg of nitrate in cheeses of medium and low moisture. The objective of this work was to evaluate the amount of nitrate in the curd and whey after addition to the milk used for Minas cheese production. Five batches of cheese were processed, and for each batch, potassium nitrate was added to the pasteurized milk (LTLT) at the following concentrations: 5g/100L, 15g/100L, and 40g/100L. One treatment was done without any nitrate addition. Nitrate was measured by spectrophotometric determination following modified Jones Method (AOAC 976.14), and raw milk composition was measured by infrared spectroscopy (Combisystem 2300, Bentley). Compositional analysis of cheese and whey were according to International Dairy Federation methods. Differences were evaluated by Duncan Test. Average composition of raw milk was 3.75g/100g, 3.30g/100g, 4.39g/100g, 12.47g/100g and 8,83g/100g for, respectively, fat, protein, lactose, total solids, and solids non fat. Cheese composition was 48.7g/100g of fat in dry matter, and, respectively, 17.2g/100g and 59.1g/100g for protein and moisture. Nitrate concentration in cheese was, respectively, 0 (non detectable), 12.1, 23.3, and 64.93 mg of nitrate/kg of cheese for treatments with addition of 0, 5, 15, and 40 g of nitrate/100L of milk. Fermentation did not affect partition of nitrate in curd and whey phases. Nitrate retained in cheese curd was about 3% of the initial amount, while 97% of the original nitrate was detected in the whey. Results confirm that nitrate addition at levels higher than 20g/100L of milk are risky, since levels close to 30g/100L will result in approximately 50mg of nitrate in the cheese. Further study is necessary to evaluate the impact of this preservative in the whey, since high amounts of nitrate/nitrite will remain in this phase, with serious concerns related to concentrated and dehydrated whey products. Acknowledgments: FAPEMIG, CNPq

Key words: nitrate, cheese, nitrite

363 Prevalence of *Coxiella burnetii* in bulk tank milk and associations with herd characteristics on US dairy operations. J. E. Lombard[1], S. N. Gibbons-Burgener[2], and C. P. Fossler*[1], *[1]USDA-APHIS-VS, Centers for Epidemiology and Animal Health, Fort Collins, CO, [2]University of Wisconsin, Madison, Madison.*

The objectives of this study were to estimate the prevalence of *C. burnetii* and evaluate herd-level factors associated with its presence. During the National Animal Health Monitoring System's Dairy 2007 study, bulk tank milk was collected and tested via PCR for *C. burnetii*, the causative agent of Q fever. Information regarding dairy cow health, reproduction, and productivity was also collected. Samples were collected from 528 operations during the months of March through August 2007. After adjusting for study design and incorporating weighting procedures, 76.9% of dairy operations had PCR evidence of *C. burnetii* in bulk tank milk. *C. burnetii* was detected in bulk tank milk on 69.8% of operations with less than 100 cows, 90.8% of operations with 100–499 cows, and 98.8% of operations with 500 or more cows. A higher percentage of bulk tank milk from operations in the West region (90.1%) were PCR positive for *C. burnetii* compared with those in the East region (75.7%). Weighted log-linear regression models for count data, which adjusted for herd size and region, were used to assess the effect of *C. burnetii* on multiple morbidity and mortality outcomes. Positive operations had a significantly higher percentage of calves born dead (6.0%) and a higher percentage of abortions (4.1%) than operations that tested negative (4.6 and 3.2%, respectively). In addition, positive operations removed a significantly higher percentage of cows due to reproductive problems. These findings provide further evidence that *C. burnetii* is more prevalent in the US dairy herd than previously thought. In addition, *C. burnetii* infection appears to be associated with abortions, calves born dead, and cows removed for reproductive problems. More research needs to be conducted to determine the source of *C. burnetii* on dairy operations, define the causal relationship between health outcomes, and to determine management practices that are likely to decrease transmission of the organism.

Key words: *Coxiella burnetii*, bulk tank milk, prevalence

364 Bulk milk somatic cell penalties in herds enrolled in dairy herd improvement programs. K. J. Hand*[1], A. Godkin[2], and D. F. Kelton[3], *[1]Strategic Solutions Group, Puslinch, ON, Canada, [2]Ontario Ministry of Agriculture, Food and Rural Affairs, Elora, ON, Canada, [3]University of Guelph, Guelph, ON, Canada.*

The objective was to assess the risk of bulk milk somatic cell count (BMSCC) penalties for herds enrolled in dairy herd improvement (DHI) programs compared with nonparticipatory herds. The data consisted of monthly average BMSCC for 2898 CanWest DHI herds and 1186 non-DHI herds in 2009, Ontario, Canada for a total of 48,250 records. The median average BMSCC (10^3 cells / ml) for CanWest DHI herds was found to be 228; whereas, the median in non-DHI herds was found to be 250. Two threshold BMSCC (10^3 cells / ml) penalty levels were considered, 399 and 499. For both penalty levels, the odds of a BMSCC exceeding either penalty threshold for DHI herds was modeled using a generalized mixed model with a binary link function. Random effects included herd; covariates included season of BMSCC (summer, May through September and winter, October through April), total milk shipped per month (l), fat paid per month (kg) and protein paid per month (kg). Furthermore, the odds of a DHI herd incurring a penalty under the Ontario Milk Act (where 3 out of 4 consecutive BMSCC exceeded penalty thresholds) was also examined and modeled with a similar generalized mixed model. The likelihood of a BMSCC exceeding a penalty threshold in a non-DHI herd compared with a DHI herd was found to be significantly greater than 1 at both penalty levels ($P < 0.004$). The likelihood of incurring a BMSCC penalty under the Ontario Milk Act was found to be not significant for a penalty threshold of 499 ($P = 0.18$), but significant for the penalty threshold of 399 ($P = 0.004$).

Key words: bulk tank, SCC, penalty

365 A novel analysis strategy of detection hydrolysate protein adulteration in milk. Z. Chen[1] and D. M. Barbano*[2], *[1]Analysis and Testing Center, Shandong University of Technology, Zibo, Shandong Province, PRC, [2]Department of Food Science, Cornell University, Ithaca, NY.*

Hydrolysate protein (HP) which has the analytical characteristics of protein molecules in the Kjeldahl total nitrogen test could pollute milk or be illegally added into milk to improve protein content would cause big food safety problem. The main component of HP is true protein, so it is difficult to distinguish HP true protein from milk. Hydroxyproline could be only used as identification tag for animal source protein (ISO 3496–1994). Therefore, how to detect exogenous true protein adulteration in milk is still a big challenge for milk quality control and food safety. Our objective was to develop an effective and quick analysis method to figure out HP adulteration in milk. Ultrafiltration (UF) and infrared (IR) analysis were considered to be appropriate techniques. Lactalbumin hydrolysate, casein hydrolysate (acid) and Vegetable Peptone No1 were used to simulate HP adulteration in milk. Every HP experiment (0, 1250, 2500, 3750 and 5000 mg/kg) was replicated 3 times. Stirred Cell 8400 with Micon Ultrafiltration Membrane and LactoScope FTIR were chosen as experiment instruments. 35 psi and 200 g was preferred to operation condition of UF. Excluding the cleaning procedure of UF, it takes 50 minutes for permeate collection and IR detection of one milk sample. All permeate protein is significantly correlated with the 3 HP added in milk ($P < 0.01$), the R square of 3 linear equation is 0.986, 0.897 and 0.953 respectively. The recovery percent of the 3 HP in permeate ranges from 81.32% to 107.25%. Compared with ISO 3496-1994, the proportion of true protein adulteration could be quantificationally and directly detected. The upper bound of 95% confidence interval for control milk permeate protein (n=9) is 0.0401%, it could be the lower limit reference critical value to distinguish whether HP adulteration in milk or not ($P < 0.05$). This paper developed a novel analysis strategy (UF, IR, critical value judgment), and it is verified to be an effective and quick analysis method to solve milk HP adulteration problem.

Key words: hydrolysate protein, milk adulteration, detection

366 Identification of a short isoform of the porcine prolactin receptor and its variants. J. F. Trott*, A. Schennink, and R. C. Hovey, *University of California, Davis.*

Prolactin (PRL) acts through the dimerizing PRL receptor (PRLR) to regulate more than 300 biological processes, particularly during reproduction and lactation, which are both critical for successful swine production. The actions of PRL are mediated by both long (LF) and short isoforms (SF) of the PRLR, where SF can interfere with the essential signaling function of the LF. We have cloned a SF of the porcine PRLR using 3′ RACE. This novel isoform of the pPRLR contains a short intracellular domain of 38 aa that is encoded by splicing from exon 9 to exon 11 on chromosome 16, where the LF splices from exon 9 to exon 10. Analysis of the expression of pPRLR-LF and short pPRLR-SF mRNA by qRT-PCR revealed differential expression of these isoforms with an average ~1000-fold higher level of expression of pPRLR-LF mRNA in 19 tissues. We have also identified polymorphisms within exon 11 that give rise to 4 different coding sequences for the pPRLR-SF. Full-length cDNA for all 4 alleles was generated by PCR and cloned behind the elongation factor 1-α promoter for functional studies, using transiently-transfected of Chinese Hamster Ovary cells. None of the pPRLR-SF alleles were able to activate 342 bp of rat β-casein promoter in response to insulin, dexamethasone and pPRL. All 4 pPRLR-SF alleles functioned as dominant-negatives against the differentiative function of the long pPRLR, where 2 of them completely inhibited long pPRLR activity when they were present at 4-fold excess ($P < 0.05$) whereas the other 2 required 6-fold higher levels to have the same effect ($P < 0.05$). The binding affinity of the 4 alleles of these pPRLR-SF for pPRL was unaffected by differences in the intracellular domain coding sequence ($P > 0.05$). In conclusion, we have identified a unique pPRLR-SF that suppresses the differentiative function of the pPRLR-LF, where the 4 novel pPRLR-SF sequences may differentially impact the phenotypic effects of PRL in swine.

Key words: prolactin, prolactin receptor, short form

367 Comparative transcriptome analysis of laser microdissected cells from bovine mammary gland. K. M. Daniels*[1], R. K. Choudhary[2], C. M. Evock-Clover[3], R. W. Li[3], W. Garrett[3], and A. V. Capuco[3,2], *[1]The Ohio State University, Wooster, [2]University of Maryland, College Park, [3]USDA-ARS, Beltsville, MD.*

Bovine mammary parenchyma (PAR) is a heterogeneous tissue. Laser microdissection (LMD) offers a refined strategy for excision, capture and interrogation of user-defined cell populations. Our objective was to use LMD to obtain homogenous cell populations from prepubertal PAR, followed by microarray analysis to characterize molecular signatures of various cells in PAR and to gain insight into interactions among cell types. Cryosections of PAR from 5 prepubertal Holstein heifers were prepared. Each slide was fixed in acetone:polyethylene glycol and stained with 0.1% nuclear fast red in 5% AlSO4, rinsed with PBS and dehydrated through 3 grades of ethanol. Cells from 4 locations within and near terminal ductal units (TDU) were captured. Basal layer and embedded layers of epithelium were obtained, as were intralobular and interlobular stroma. The 4 categories of cells from each heifer were lysed, cDNA synthesized, amplified and labeled for microarray analysis. The microarray (Roche Nimblegen, Inc.) represented over 45,000 bovine sequences and over 3800 genes were included in the analysis. Transcriptome analysis ($P \leq 0.05$; ≥ 2-fold change) of basal vs. embedded epithelial cells showed many genes involved in differentiation, with an enrichment of transcripts for nestin (stem cell marker), a noncoding maternally imprinted gene (H19), extracellular matrix proteins and metalloproteinases in the basal epithelium. Conversely, there was enrichment of a telomerase inhibitor (POT1) and phosphodiesterases in the embedded epithelial cells. Evaluation of gene expression in the basal epithelium vs. adjacent intralobular stroma showed greater expression of keratin 7, Msh homeobox (MSX2; likely morphogen) and protein tyrosine phosphatase 14. There was an enrichment of MEOX2, a mesenchyme inducer, and sphingosine-1-phosphate receptor 1. Results suggest presence of stem or progenitor cells in the basal epithelium and induction of myoepithelial differentiation via stromal factors. Comparisons of interlobular and intralobular stroma showed a prevalence of lipid associated genes (SCD, DGAT2) in the former. Utility of LMD in bovine mammary tissue was demonstrated.

Key words: laser microdissection, microarray

368 Acute DNA methylation changes are associated with involution and re-initiation of lactation in dairy cows. K. M. Swanson*[1], K. Stelwagen[2], R. A. Erdman[3], and K. Singh[1], *[1]AgResearch Ltd., Ruakura Research Centre, Hamilton, New Zealand, [2]Agri-Search, Hamilton, New Zealand, [3]University of Maryland, College Park.*

The onset of bovine mammary gland involution following the termination of milking results in a decline in milk protein gene expression, including the major milk protein αS1-casein. In a previous study DNA methylation, in the αS1-casein-encoding gene at a functional STAT5 binding site approximately −10kbp, was increased after 7d of involution. The aim of the present study was to determine whether DNA methylation plays an acute role in the downregulation of milk production during the reversible and irreversible phases of involution. Non-pregnant cows at mid-lactation were divided into 5 groups (n = 5/group). Mammary alveolar tissue was obtained at slaughter from lactating cows 6 h post-milking (control), cows with extended non-milking periods of either 7- or 28-d, and cows where milking was resumed for 7 d following these 2 dry periods. Re-initiation of milking following 7- or 28-d non-milking periods resulted in milk yield recoveries of 93 and 25% respectively. Quantitative MassARRAY methylation analysis revealed that methylation levels of 2 5methylCpG dinucleotides at the STAT5-binding site −10kb in the αS1-casein promoter were increased to 32% ($P < 0.1$) and 33% ($P < 0.05$) respectively following 7-d non-milking, then further to 38% ($P < 0.05$) and 50% ($P < 0.05$) respectively following 28-d non-milking, compared with lactating cows (22% and 13% methylation, respectively). Furthermore, the full recovery of lactation following re-initiation of milking after 7-d non-milking was associated with de-methylation of DNA, returning to levels similar to lactating control cows. However, the DNA methylation levels remained significantly higher ($P < 0.05$) than the lactating control cows following the re-initiation of milking after 28-d non-milking, in association with the low, partial recovery of milk yields. These results suggest DNA methylation at a functional STAT5-binding site of the αS1-casein-encoding gene may play a role in regulating reversible and irreversible involution.

Key words: DNA methylation, bovine αS1-casein, mammary involution

369 Ontogeny of nuclear and cytoplasmic myoepithelial markers during prepubertal bovine mammary development. S. Safayi*[1], N. Korn[1], A. Bertram[1], R. M. Akers[2], A. V. Capuco[3], S. L. Pratt[1], S. Calcatera[1], C. Klein[1], and S. Ellis[1], *[1]Clemson University, Clemson, SC, [2]Virginia Polytechnic Institute and State University, Blacksburg, [3]USDA-ARS, Beltsville Agricultural Research Center, Beltsville, MD.*

We previously reported that ovariectomy alters prepubertal mammary myoepithelial cell (MC) development, but the mechanisms involved are not well understood. We therefore surveyed expression of transformation-related protein 63 (P63) and the common acute lymphoblastic leukemia antigen (CD10) as differentiation markers to track the ontogeny of MC development. At 40d of age, Holstein heifers underwent either an ovariectomy (OVX; n = 16) or sham (INT; n = 21) operation. At d55, 70, 85, 100, 130 and 160 of age, groups of heifers were slaughtered to provide mammary parenchyma samples for multispectral imaging and subjective assessment of immunofluorescent staining for MC markers. Our qualitative evaluation showed P63-/CD10+, P63+/CD10-, double positive and double negative cells in both basal and suprabasal layers. The P63+ nuclei were observed in the basal layer at regularly spaced intervals. The interval between P63+ nuclei was reduced in older heifers regardless of treatment. Stromal CD10 expression also appeared to be more prominent in older heifers. In both OVX and INT heifers, P63 and CD10 expression was more heterogeneous at the distal ends of the ductular units compared with the subtending ducts. In INT heifers, there was a reduction in the interval between P63+ MC nuclei, compared with OVX heifers. Our observations suggest that expression of P63 in the basal layer of parenchyma from INT heifers was more consistent than in OVX animals. Our results provide support for the hypothesis that ovarian secretions affect the expression of both P63 and CD10. Additional quantitative analyses are now required to substantiate our assertions from the qualitative inspection.

Key words: myoepithelial cell, p63, CD10

370 Multispectral analysis of myoepithelial cell development in prepubertal bovine mammary gland. S. Safayi*[1], N. Korn[1], A. Bertram[1], R. M. Akers[2], A. V. Capuco[3], S. L. Pratt[1], and S. Ellis[1], *[1]Clemson University, Clemson, SC, [2]Virginia Polytechnic Institute and State University, Blacksburg, [3]USDA-ARS, Beltsville Agricultural Research Center, Beltsville, MD.*

We have previously reported that ovariectomy alters prepubertal development of mammary myoepithelial cells (MC), but the mechanisms involved are not well understood. We therefore analyzed the MC expression of differentiation markers α-smooth muscle actin (SMA) and the common acute lymphoblastic leukemia antigen (CD10). On d40, Holstein heifers underwent either an ovariectomy (OVX; n = 16) or sham (INT; n = 21) operation. At d55, 70, 85, 100, 130 and 160 of age, samples were collected and used for multispectral imaging to quantitatively assess immunofluorescent staining for target MC markers. Fluorescent intensity (FI) of the markers on each slide were normalized against a control sample and then evaluated statistically using PROC MIXED in SAS. Our results showed 250% more CD10+ cells contacting the luminal space in OVX compared with INT ($P = 0.04$). In the basal layer, CD10 FI was lower ($P = 0.04$) and SMA FI was higher ($P < 0.01$) in OVX than INT. The FI ratio of SMA to CD10, as a proxy indicator for MC differentiation, increased in OVX compared with INT after d55 ($P < 0.01$), and remained approximately 4 times higher from d100 onwards ($P < 0.01$). Intracellular distribution of markers within the basal layer showed basal localization of SMA, but apical CD10 staining. In both INT and OVX, there were also double negative cells expressing neither CD10 nor SMA that appeared to contact both the basal and luminal spaces. Our results show that ovariectomy affects MC expression of both SMA and CD10 as well the pattern of MC development. Given that MC are known to limit parenchymal growth in other species; our observations open new avenues for future studies on the regulation of prepubertal mammary development.

Key words: myoepithelial cell, CD10, smooth muscle actin

371 Lactogenic hormones and IGF-I do not regulate glucose transporter gene expression in the bovine mammary gland during the transition period. Y. Shao*[1], E. Wall[1], Y. Misra[1], X. Qian[1], R. Blauwiekel[1], T. McFadden[2], and F.-Q. Zhao[1], *[1]Laboratory of Lactation Physiology, Department of Animal Science, University of Vermont, Burlington, [2]Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Alberta, Canada.*

Glucose is essential for milk production as it is a major substrate and energy source for milk synthesis. Glucose uptake across the plasma membrane of mammary epithelial cells is mediated by transmembrane facilitative glucose transporters (GLUT). During the transition period, there is a marked increase in the expression of GLUT1, GLUT8, and GLUT12 in the bovine mammary gland. The objective of this study was to investigate whether the lactogenic hormones and/or IGF-I are the mediators of increased GLUT expression. In the first experiment, mammary tissue was obtained by biopsy from 2 primi- and 2 multiparous cows about 40 d before parturition. Mammary explants were cultured for 48, 72 and 96 h with the following hormone treatments: no hormone (control); 200 ng/ml IGF-I; 5 μg/ml insulin (INS); 5 μg/ml insulin + 1 μg/ml hydrocortisone + 5 μg/ml prolactin (IHPrl); and 5 μg/ml insulin + 1 μg/ml hydrocortisone + 5 μg/ml prolactin + 500 ng/ml estrogen (IHEPrl). The relative expression of β-casein, α-lactalbumin, GLUT1, GLUT8 and GLUT12 mRNA were measured by real time PCR. For β-casein and α-lactalbumin, IGF-I and INS had no effect, whereas IHPrl and IHEPrl increased mRNA several hundred fold ($P < 0.01$). Although insulin alone increased GLUT1 mRNA around 1.8 fold ($P < 0.05$), IGF-I, IHPrl and IHEPRL had no effect on GLUT1 or GLUT8 expression. There was no treatment effect on GLUT12 expression at 48 h, but IHPrl and IHEPrl decreased GLUT12 expression by 50% after 72 and 96 h ($P < 0.05$). In the second experiment, prolactin was administered twice a day to 5 cows during early lactation by intravenous injection at a dose of 1 μg/kg of BW. After 7 d of treatment, mammary tissue was obtained by biopsy from prolactin-treated cows and 5 control cows. Expression of GLUT1, 8 and 12 mRNA was measured by real time PCR, and there was no effect of prolactin on gene expression. Our data suggest that lactogenic hormones and IGF-I may not mediate the increase in GLUT expression in bovine mammary gland during the transition period.

Key words: glucose transporters, bovine mammary gland, lactogenic hormones

372 Lactogenic complex-induced mammary epithelial cell differentiation is associated with membrane compositional differences. N. Argov-Argaman*, K. Mida, and A. Shamay, *The Robert H. Smith Faculty of Agriculture, Food and Environment, The Hebrew University, Jerusalem, Israel.*

Mammary gland epithelial cell differentiation is induced by insulin (I), hydrocortison (F) and prolactin (Prl). Although the mammary epithelial cell proteome is well established, differentiation-associated changes in its lipidome composition are not well defined. A murine mammary

gland epithelial cell line (HC11) was used to study alterations in lipid composition of the cell and its membrane during differentiation. HC11 cells were exposed to one of the following hormonal treatments: IPrl, PrlF, and IF. Differentiation medium consisted of prolactin, insulin and hydrocortisone (n = 3 for lipid and 4 for gene expression analysis;2 biological replicated for each experiment). Lipid composition of fat and membrane cellular compartments were determined. Gene-expression levels of lipogenic and lipolytic enzymes, as well as of genes encoding enzymes that modulate fatty acid length and unsaturation level (i.e., elongases and desaturases, respectively) were measured. Overall, insulin was the main factor inducing alterations in membrane composition, which consisted of increased phosphatidylethanolamine (12+0.5 and 15+0.4 for PrlF compared with IFPrl, $P = 0.004$) and decreased sphingomyelin concentrations (2+0.3 and 37+0.4 for PrlF compared with IFPrl, $P = 0.0002$). Nonetheless, the differentiation medium, (IFPrl), had a stronger effect on phospholipid composition than all other treatments which included insulin. In addition, insulin increased the concentration of monounsaturated fatty acids (46+0.5 and 53+0.1 for PrlF compared with IFPrl, $P < 0.001$), but decreased that of polyunsaturated fatty acids in the membrane (17.5+0.3 and 11.1+0.1 for PrlF compared with IFPrl, $P < 0.001$). Gene expression of both desaturases and elongases (ELOVL 1, 3, 5, 6 and 7, Δ5, Δ6 and Δ9 desaturase) was elevated by differentiation medium only relative to all other treatments. The results suggest that membrane compositional differences in both polar lipids and fatty acids occur concomitantly with the differentiation of the mammary epithelial cells and suggest a role for membrane lipid composition in the acquisition of mammary cell characteristics.

Key words: milk, membrane, phospholipid

373 Intravenous supplementation of acetate, glucose or essential amino acids to an energy and protein deficient diet in lactating dairy goats: effects on milk production and mammary nutrient extraction. S. Safayi*[1,2] and M. O. Nielsen[1], *[1]University of Copenhagen, Frederiksberg, Great Copenhagen, Denmark, [2]Clemson University, Clemson, SC.*

The objectives were to study how mammary supply of essential amino acids (EAA) versus energy yielding substrates in the form of acetate (ACE) or glucose (GLU) would affect mammary nutrient uptake and milk (protein) synthesis in early (EL) and late lactating (LL) dairy goats. Four goats were fed a basal diet deficient in energy (90% of requirements) and protein (80% of requirements), and randomly allocated to 4 treatments in a balanced 4 × 4 Latin Square design. The treatments consisted of 4-d continuous intravenous infusions of isoosmotic isoenergetic solutions of EAA, ACE and GLU with saline (SAL) as control, having a 3-d rest period in between. Simultaneous arterio-venous blood samplings over each udder half/gland were performed every 4 h during the last 24 h of infusion. Milk production was recorded, and its fat and protein contents as well as some of the blood/plasma parameters/components were determined. In EL, milk yield or energy corrected milk yield (ECM) was stimulated by GLU ($P = 0.01$) and tended to be increased by EAA ($P = 0.06$) and ACE ($P = 0.06$). ACE and EAA (but not GLU) stimulated milk protein yield ($P = 0.06$ and 0.03, respectively for ACE and EAA), illustrating the importance of amino acid as well as ATP generation for support of protein synthesis in EL. Highest fat yield in EL was observed on ACE ($P < 0.05$). In LL, only EAA could raise milk protein yield ($P < 0.01$) and ECM ($P = 0.06$). In LL, GLU lowered milk fat percentage ($P = 0.01$). We conclude that an insufficient amino acid supply to the mammary gland of dairy goats can be compensated in EL but perhaps not in LL by increased mammary supply and uptake of an energy yielding substrate, provided this substrate specifically contributes to ATP generation in mammary epithelial cells. This suggests there might be scope for development of differential protein recommendations for ruminants in early and late lactation, and this issue should be pursued in future studies.

Key words: mammary metabolism, mammary nutrient uptake, arterio-venous concentration difference

374 Expression profiles of microRNAs from non- and lactating bovine mammary glands. Z. Li*[1,2], H. Y. Liu[1,2], and J. X. Liu[1,2], *[1]Institute of Dairy Science, College of Animal Sciences, Hangzhou, P.R. China, [2]MOE Key Laboratory of Molecular Animal Nutrition, Hangzhou, P.R. China.*

The microRNAs (miRNA) are small non-coding RNA molecules that are approximately 22 nucleotides (nt) in length. It has been reported that miRNAs are involved in the regulation of milk protein synthesis and development of mammary gland. However, little information is available on the function of miRNA in regulation of lactation. Therefore, clarifying of miRNA expression profiles in mammary gland are crucial to the understanding of the mechanism of lactation initiation. In this study, one healthy cow each from both non- and lactating stages was selected to collect mammary gland tissues. Two miRNA libraries were constructed and sequenced, respectively. The miRNAs (18–30nt) were sequenced by Solexa sequencing method. A total of 11,964,909 clean reads were obtained from lactating cows and 15,968,116 clean reads from nonlactating cattle. The sequencing data were analyzed using ACGT101-miR program. There were 962 pre-miRNAs encoding for 985 miRNAs, of which 946 were unique and 521 (52.9%) were expressed in both periods. Among the unique sequences, 284 were known as bovine miRNAs registered in the miRbase database; 96 miRNAs were conserved in other mammalian; and 566 miRNAs were bovine-novel candidates. Real-time quantitative PCR was used for validation of the sequencing results of 32 selected miRNAs which indicated great difference between 2 periods. It is observed that the results of over 50% of these miRNAs were consistent with Solexa sequencing data. There were 17 miRNAs expressed in higher level in lactating than in nonlactating bovine mammary glands. The high percentage of bovine-novel candidates indicated that many miRNAs in bovine mammary gland have not been identified. Further research is warranted to examine what kinds of miRNAs are involved in lactation and how they function in regulation of lactation.

Key words: bovine mammary gland, lactation, miRNAs

Meat Science and Muscle Biology Symposium: Meat in the Diet

375 Meat and human cancer. L. R. Ferguson*, *The University of Auckland, Auckland, New Zealand.*

There is a burgeoning literature associating a high intake of meat, especially red meat and processed meat, with an increased risk of various types of cancer in various human populations. However, red meat in particular is an important source of various nutrients with anticancer properties, including selenium, vitamins B6 and B12, and vitamin D. Additionally, the current evidence base suggesting cancer risk is mostly from association studies. Risk may not be a function of meat intake per se, but could reflect high fat intake, and/or carcinogens generated through various cooking and processing methods. Meat contains several potential anti-carcinogens, including omega-3 polyunsaturated fatty acids, and conjugated linoleic acid (CLA). Cancers associated with high meat consumption may be reduced by the addition of anti-carcinogens, during meat preparation or meat consumption, or through modification of food preparation methods. For example, a diet high in dietary fiber may enhance the excretion, and reduce the metabolism and DNA interaction, of some of the potential meat carcinogens. Adjusting the nature of the meat, the cooking methods, and the balance between meat and other dietary components may be critical to protecting human populations against any potential cancer risks.

Key words: meat, cancer, humans

376 Meat lipids in human health. S. McNeill*, *National Cattlemen's Beef Association, Centennial, CO.*

This objective of this presentation is to review the current evidence on saturated fatty acid content of meat and its implications on human health. Since the first edition of the Dietary Guidelines for Americans was issued in 1980, nutrition guidance for the American public has emphasized the need to reduce the total fat, saturated fat and cholesterol content in their diet, as a means of reducing risk of heart disease and other chronic diseases. When nutrient-focused guidance is translated to food-based recommendations, animal foods such as red meat, are often cited as food sources that need to be reduced to decrease these nutrients. Yet, over the last 30 years, the amount of total and saturated fat from red meat in the American diet has been declining. Today, greater than 90% of the total fat and saturated fat in the American diet comes from sources other than beef. Although underappreciated, red meat's lipid composition is predominately monounsaturated fatty acids and contains limited amounts of polyunsaturated fatty acids. Saturated fatty acids make up most of the remainder of total lipid profile. About one-third of beef's saturated fat content is the cholesterol-neutral saturated fatty acid, stearic acid. Consistent evidence from clinical trials indicates that the inclusion of lean beef in a well-balanced diet designed to manage cardiovascular risk is equally as effective as a diet of lean white meat for low-density lipoprotein cholesterol reduction. Additionally, recent research has challenged conventional thinking of the role of dietary saturated fat in chronic disease and accumulating supportive evidence demonstrates the macronutrient mix of the diet (amount and type of carbohydrate, protein and fat) can influence the effect of dietary saturated fat.

Key words: red meat, saturated fat, human health

377 Perspective on IOM report: Strategies to reduce sodium in the United States. C. A. Mireles DeWitt*, *OSU Seafood Research & Education Center.*

Last year a committee of 14 individuals across varied disciplines compiled a consensus report that recommends the measures would needed to be taken to successfully reducing sodium intake in the United States. The committee considered past efforts such as labeling, consumer education, and voluntary efforts by the industry. The committee also considered current efforts such as state and local labeling initiatives and sodium reduction efforts in other countries. Economic incentives such as agriculture subsidies, tax incentives, salt tax, cap and trade, and leveraging sodium reduction by use of government food purchase specifications were also considered. A review of the current literature on the role of sodium in terms of taste, flavor and functionality in foods was also performed to provide a framework for the possibility of technological advances that might aid sodium reduction. The food environment and sources of sodium (from both food processor and restaurants) were evaluated as well. All of the aforementioned considerations helped to shape the final recommendations. The recommendations were multifaceted with the "primary" objective focused on modifying the GRAS status of salt. The objective is to overview the IOM recommendations and provide insights into the types of strategies processors can use to reduce sodium.

378 Nitrite and nitrate in health and disease: A paradigm shift. N. S. Bryan*, *Institute of Molecular Medicine, UT Health Science Center, Houston, TX.*

Objective: To present the most recent published literature on the biological effects of nitrite and nitrate to establish the context for potential health benefits vs. potential risks or adverse effects. Nitrite and nitrate are indigenous to our diet and are formed naturally within our body from the oxidation of nitric oxide (NO). Emerging health benefits from dietary sources of nitrite and nitrate contradict decades of epidemiological research that have suggested an association of nitrite and nitrate in foods, primarily cured and processed meat, with certain cancers. The major source of exposure of nitrite and nitrate comes from the consumption of nitrate enriched vegetables. The preponderance of epidemiological studies shows a very weak association with consumption of meats and certain cancers, which contain very little nitrite and nitrate. Nitrite and nitrate in certain foods and diets can be metabolized to NO and promote cardiovascular benefits and cytoprotection. Summary: The cardiovascular benefits of nitrite and nitrate are beginning to be translated in humans by the increasing number of clinical trials using nitrite and nitrate. The collective body of evidence suggests that foods enriched in nitrite and nitrate provide significant health benefits with very little risk.

Key words: nitrite, processed meats, nutrition

Milk Protein and Enzymes Symposium: Milk Proteins and Peptides: Bioactivity and Digestion

379 Structural bases for the nutritional and biological properties of the caseins. H. M. Farrell Jr.*[1], E. L. Malin[1], E. M. Brown[2], and A. Mora-Gutierrez[3], *[1]USDA, ERRC, Dairy and Functional Foods RU, Wyndmoor, PA, [2]USDA, ERRC, Biobased and Other Animal Coproducts RU, Wyndmoor, PA, [3]Cooperative Agricultural Research Center, Prairie View A&M University, Prairie View, TX.*

Our understanding of the nutritional and biological properties of the caseins has paralleled the description of the chemistry of these proteins. For example, following the first amino acid analyses of the caseins, it became apparent that these proteins are an excellent source of the essential amino acids needed for human nutrition, and casein became the standard reference protein for nutritional studies. Upon elucidation of the primary sequences of the caseins, it was discovered that inherent in these sequences were several peptides, the so-called casomorphins, which if liberated during digestion would have physiological (endorphin-like) activity. The enumeration of other potentially biologically active peptides followed. In addition, anti-bacterial activities have been ascribed to several other casein peptides. Although many of these activities have been demonstrated in vitro, few have been demonstrated in vivo in clinical or feeding studies. Notable exceptions to this rule have been antihypertensive peptides, an anti-stress peptide from α_{S1}-casein, and the role of phospho-peptides in calcium uptake. The advent of 3D molecular modeling has now allowed us to portray these peptides at the molecular level and will allow the comparisons of the structures of the various biologically active peptides, leading to a better understanding of the molecular mode of action of the casein peptides.

Key words: casein structure, casein bioactive

380 Digestibility of whey protein aggregates and fibrils under simulated gastro-intestinal environments. H. Singh*, M. Peram, S. Loveday, B. Libby, and Y. Aiqain, *Riddet Institute, Massey University, Palmerston North, New Zealand.*

The digestion and metabolism of proteins continues to generate considerable scientific interest, driven mainly by the need to understand the release of bioactive peptides, and factors affecting protein allergenicity and satiety. It is well known that β-lactoglobulin (β-Lg), which represents about 60% of whey proteins in bovine milk, is resistant to hydrolysis by pepsin under gastric conditions because of its stable, globular tertiary structure at low pH (<pH 3). However, denatured β-Lg (caused by heating or high pressure) can be readily digested by pepsin under gastric conditions. Under denaturing conditions, β-Lg is able to form different kinds of aggregates, including spherical aggregates and elongated fibrils, depending on the protein concentration, pH, temperature and heating time. Although many studies on the mechanism of β-Lg aggregate formation and structures have been carried out, little work has been carried out on the digestion of different forms and structures of these aggregates under gastro-intestinal conditions. Therefore the objective of our study was to understand the relationship between heat-induced structural changes in β-Lg and in vitro gastric digestibility. Heating of β-Lg at 90°C and neutral pH resulted in the formation of non-native aggregates of different sizes (dimmers, trimers, oligomers), linked through disulfide and non-covalent bonds. The digestibility of non-native β-Lg aggregates varied significantly depending on the type of aggregates. Some dimers were resistant to digestion, while high molecular weight aggregates were digested fast. β-Lg fibrils formed by heating β-Lg solutions at 80°C and pH 2.0 for 20 h consisted of peptides, generated through acid/heat-induced hydrolysis. Using matrix-assisted laser desorption/ionization mass spectometry (MALDI-MS), we found that the peptides in the fibrils were more susceptible for pepsin attack than the other peptides, possible because of their hydrophobic nature.

Key words: whey proteins, digestibility, protein aggregation

381 Peptides derived from whey protein: Endothelium and vascular bioactive function. E. D. Bastian* and L. W. Ward, *Glanbia Nutritionals Inc., Twin Falls, ID.*

Novel, high-leucine peptides derived from whey protein were tested for vascular, endothelial response in 20 young individuals. A randomized, placebo-controlled, crossover design was used which consisted of 2 wk supplementation, 2 wk washout, and 2 wk crossover supplementation. Peptide and placebo dose was 5 g/day. Subjects participated in 2 vascular testing days, each preceded by 2 wk of supplementation. After consuming the dose, vascular function in the forearm was measured serially for 120 min. Macrovascular and microvascular function was assessed using brachial-artery, flow-mediated dilation (FMD) and venous-occlusion, strain-gauge plethysmography. Six blood draws were taken across the 120 min measurement period and analyzed for total nitrates/nitrites. Placebo had no impact on FMD at 30, 60 and 90 min post ingestion. When peptides were ingested, FMD increased at the 3 time points by 14.0, 26.9, and 15.4% compared with placebo and baseline measurements. Plasma total nitrates/nitrites significantly decreased for the 120 min post-ingestion period and were lower at 120 min in placebo (−25%) compared with peptide (−18%). These data indicate that supplementation with high-leucine, whey-derived peptides improves vascular function in young, healthy individuals.

Key words: bioactive, peptide, vascular

382 The structure of dairy products modifies the kinetics of protein hydrolysis and the release of bioactive peptides in the gut during digestion. D. Dupont*[1,2], K. Bouzerzour[1,2], F. Barbe[1,2], Y. Le Gouar[1,2], and O. Menard[1,2], *[1]National Institute for Agricultural research, Rennes, France, [2]Agrocampus Ouest, Rennes, France.*

Digestion provides nutrients and energy essential to the survival and growth of the organisms. But little is known about the influence of food structure on its digestibility and nutritional properties. The objectives of our group are therefore to understand how dairy products are disintegrated during digestion and how the structure of the matrix will modify the protein digestibility. To reach this goal, static and dynamic in vitro models simulating what happens in the GI tract have been developed and in vivo experiments have been performed using the pig as a model. Digested samples collected in the different parts of the gut were characterized by SDS-PAGE, ELISA and/or mass spectrometry in order to quantify and identify milk proteins and peptides throughout the GI tract. Two applications will be presented. In a first experiment, digestion of an infant formula by 28 days-old piglets showed that caseins were rapidly hydrolysed in the stomach whereas whey proteins were partially resistant. Large milk protein fragments were shown to resist digestion and were detected in the ileum. Peptides

known to carry biological (anti-hypertensive, immunomodulating) properties were identified in the small intestine of piglets. In a second experiment, six dairy matrices (liquid milks, acid and rennet gels with or without heat-treatment) of similar composition but with different microstructure were manufactured from the same raw skim milk in a pilot plant. Each sample was given to six multi-catheterized adult mini-pigs. Effluents were then taken at the very end of stomach during 7 h after the meal and milk proteins and peptides quantified. Compares to liquid milks, acid gels showed a delayed gastric emptying and a slower release of caseins and β-lactoglobulin in the duodenum. When gel was stirred, an intermediate behaviour was observed. Results also showed that heat treatment of milk induced a slower release of caseins in the small intestine. All these results emphasize the role played by the structure of the food matrix on the digestion of dietary proteins.

Key words: digestion, dairy products, milk proteins

383 Effects of dietary milk fat globule membrane in the gut and on systemic lipid metabolism. R. Ward*[1], R. Jimenez-Flores[2], A. Zhou[1], and K. Hintze[1], *[1]Utah State University, Logan, [2]California Polytechnic State University, San Luis Obispo.*

In milk, fat droplets are coated by an epithelial membrane that results from a novel secretion process within the mammary gland. The milk fat globule membrane (MFGM) is composed of primarily polar lipids and membrane proteins and is the most diverse fraction of milk. While MFGM is present in all dairy products to some extent, it is present in several co products of dairy processes such as churn buttermilk and whey, and may be recovered for use a bioactive ingredient. Despite the fact that MFGM is a unique ingredient in the food supply and it is rich in potentially bioactive constituents, few studies have been conducted to measure its effect on physiology and nutrition. In the last several years our labs have begun to investigate the potential of this material as a food ingredient through studies with cells in culture, with rodents, and currently with humans. Our results to date indicate that MFGM has myriad effects within the gut, and also appears to affect systemic lipid partitioning. For example, MFGM reduces the number of aberrant crypt foci in a rat model of colon cancer and that it prevents gut leakiness and systemic inflammation induced by lipopolysaccharide in mice. Furthermore, supplementation of rat diets high in sucrose with MFGM appears to reduce the development of fatty liver via effects on gene expression and lipid transport. Lastly, dietary MFGM has significant effects on the fecal microbiome profile and presence of fecal small molecules. In sum, these results indicate that inclusion of MFGM into food products may have demonstrable and valuable bioactive effects.

Key words: MFGM, gut, metabolism

384 Effects of creep feeding and supplemental glutamine or glutamine plus glutamate (AminoGut) on pre- and post-weaning growth performance and intestinal health of piglets. R. Cabrera*[1], J. Usry[2], E. Nogueira[3], M. Kutschenko[3], A. Moeser[1], and J. Odle[1], *[1]North Carolina State University, Raleigh, [2]Ajinomoto Heartland LLC, Chicago, IL, [3]Ajinomoto Brazil, Brazil.*

We determined the impact of creep feeding and adding either L-glutamine (GLN) or AminoGut (AG) to pre- and post-weaning diets on pig performance and intestinal health. Litters (n = 120) were randomly allotted based on litter size and sow parity to 4 treatments: 1) Non-creep fed (NC, n = 45); 2) creep fed control diet (CFCD, n = 45); 3) creep fed 1% GLN (CFGLN, n = 15); 4) creep fed 0.88% AG (CFAG, n = 15). No effects of creep feed on intake, weaning weight or mortality were detected ($P > 0.25$). After weaning, the NC and CFCD groups were divided into 3 groups (n = 15 each), receiving either a control nursery diet (NC-CD, CFCD-CD) or a diet supplemented with GLN (NC-GLN, CFCD-GLN) or AG (NC-AG, CFCD-AG). The litters creep fed diets containing GLN or AG also were supplemented with those AA in the nursery diets (CFGLN-GLN, CFAG-AG). GLN was added at 1% in all 3 phases and AG was added at 0.88% in phase 1 and 2 and at 0.66% in phase 3. Pigs receiving GLN in pre- and post-weaning diets (CFGLN-GLN) had the best G:F for the first 3-wk period ($P < 0.056$), exceeding controls (CFCD-CD) by 35%. The NC-AG group had ($P = 0.02$) the greatest feed intake in the last 3 wk of the study, exceeding controls (CFCD-CD) by 12%. Pigs creep fed a control diet with or without glutamine and fed with a post-weaning diet supplemented with glutamine (CFGLN-GLN, CFCD-GLN respectively) had the greatest ($P < 0.05$) villi height exceeding those which were creep fed with a control diet and later supplemented with AminoGut (CFCD-AG) by 18% and 20% respectively. Although this treatment (CFCD-AG) had the shortest villi among all treatments, they had the widest ($P = 0.1$) villi. We found that pigs creep fed with a diet supplemented with AminoGut and fed with a post-weaning diet supplemented with AminoGut (CFAG-AG) had the deepest ($P < 0.01$) crypts of all the treatments. In conclusion, supplementation of nursery diets with GLN in the first 3-wk improved feed conversion and with AG improved feed intake in the last 3-wk implicating possible improvement in intestinal health.

Key words: creep feed, glutamine, Amino-Gut

385 Metabolomic analysis of the response to weaning and dietary L-glutamine supplementation in piglets using gas chromatography/mass spectrometry. Y. Xiao*[1], T. Wu[1], B. Dai[2], S. Luo[1], J. Feng[2], and A. Chen[1], *[1]Zhejiang University, Hangzhou, Zhejiang, China, [2]Zhejiang Gomore Group, Hangzhou, Zhejiang, China.*

A novel metabolomic method based on gas chromatography/mass spectrometry (GC/MS) was applied to determine serum metabolites involved in responses to weaning and dietary glutamine supplementation in piglets. Thirty-six 21-d-old piglets were randomly assigned into 3 groups. One group continued to suckle from the sows, whereas the other 2 groups were weaned and their diets were supplemented with 1% L-glutamine (wt:wt) or isonitrogenous L-alanine, representing glutamine-supplemented group and weaned group. Serum samples were collected to characterize metabolites at 28-d-old. The GC/MS data was analyzed following the 2 sample *t*-test ($P < 0.05$)to explore the potential maker metabolites, and principal component analysis (PCA) was used to classify the different groups. Results showed that 17 metabolites were downregulated by both weaning and glutamine treatment compared with suckling piglets. These were mostly carbohydrates ($P < 0.05$) and lipids ($P < 0.05$), except for 2-hydroxybutanoic acid ($P = 0.031$), 4-hydroxypentenoic acid ($P = 0.048$), and phosphoric acid ($P = 0.0011$). Another 3 metabolites, creatinine ($P = 0.0208$), D-xylopyranose ($P = 0.0439$), and glyceryl monostearate ($P = 0.0414$), were reduced in weaned group . The level of 2-hydroxybutanoic acid ($P = 0.0077$), creatinine ($P = 0.0003$), D-xylopyranose ($P = 0.0006$), palmitelaidic acid ($P = 0.0016$) and α -L-galactofuranose ($P = 0.0495$) were greater in the glutamine-supplemented piglets than in the weaned ones. Based on the data, correlation network for weaned and suckling piglets revealed that weaning disturbed the lipid, carbohydrate and amino acid metabolism, whereas the metabolic state was partially improved by glutamine supplementation. Principal component analysis demonstrated that suckling piglets were metabolically distinct from their weaned and glutamine-supplemented counterparts, and yielded a separate clustering of profiles between glutamine group and weaned group. These novel findings provide fresh insight into the complex metabolic mechanisms of weaning and show the influence of dietary glutamine supplementation in piglets.

Key words: glutamine, metabolomics, weaning

386 Feed efficiency of 7- to 16-kg pigs is maximized when additional lysine is supplied by L-Lys instead of intact protein, but is not affected when diets are supplemented with differing sources of non-essential amino acid nitrogen. C. K. Jones*[1], J. A. Acosta[2], M. D. Tokach[3], J. L. Usry[4], C. R. Neill[5], and J. F. Patience[1], *[1]Iowa State University, Ames, [2]Universidad Nacional de Colombia, Bogotá, Columbia, [3]Kansas State University, Manhattan, [4]Ajinomoto Heartland LLC, Chicago, IL, [5]Pig Improvement Company, Hendersonville, TN.*

Little is known about how the pig′s response to Lys changes due to differences in protein source. A total of 540 (Exp. 1, 6.7 kg, 6 pigs/pen) or 450 (Exp. 2, 6.6 kg, 5 pigs/pen) PIC pigs were used in 2 14-d experiments to evaluate if the source of non-essential AA nitrogen (NEAA; Exp. 1) or source of additional Lys (Exp. 2) affects the Lys requirement of pigs. In both experiments, there were 9 replicates/treatment. The NEAA were supplied by L-Glu and L-Gly or L-Gly, L-Ala, L-Pro, and L-His, while additional Lys was supplied by L-Lys HCl or SBM. Pigs were fed 1 of 10 dietary treatments that included 1 of 5 levels of standardized ileal digestible Lys (1.2, 1.3, 1.4, 1.5, and 1.6%). There were no ($P > 0.24$) protein source × Lys level interactions. In Exp. 1, ADG increased linearly ($P < 0.0001$) and quadratically ($P = 0.02$) with increasing Lys level, while G:F increased in a linear ($P < 0.0001$) manner. Linear 1-slope broken-line analyses of all treatments revealed optimum ($P = 0.0004$) ADG was obtained at 1.36% Lys. The source of NEAA did not affect ADG ($P = 0.82$) or G:F ($P = 0.90$). In Exp. 2, both ADG and G:F increased linearly ($P < 0.0001$) with increasing Lys level. Broken-line analyses showed optimum ($P = 0.0001$) ADG was obtained at 1.47% Lys. While the source of Lys did not affect ($P = 0.48$) ADG, supplying Lys from L-Lys rather than SBM resulted in improved ($P = 0.01$) G:F, particularly at the level closest to the breakpoint (pairwise comparison of additional Lys sources at 1.5% Lys: $P = 0.01$). In summary, feed efficiency of nursery pigs is affected by Lys source, but not by source of non-essential AA nitrogen.

Table 1.

Source of non-essential AA	Exp. 1 Lys level	ADG, g/d	G:F	Source of additional Lys	Exp. 2 Lys level	ADG, g/d	G:F
L-Glu and L-Gly	1.2	330	0.73	L-Lys	1.2	312	0.74
	1.3	362	0.76		1.3	338	0.80
	1.4	401	0.80		1.4	368	0.81
	1.5	375	0.80		1.5	381	0.85
	1.6	395	0.85		1.6	367	0.85
L-Gly, L-Ala, L-Pro, and L-His	1.2	320	0.71	SBM	1.2	316	0.72
	1.3	374	0.77		1.3	334	0.78
	1.4	387	0.81		1.4	347	0.78
	1.5	385	0.80		1.5	365	0.79
	1.6	409	0.86		1.6	379	0.86
SEM		17.1	0.018	SEM		16.9	0.015
P =	Lys level	<0.0001	<0.0001	*P* =	Lys level	<0.0001	<0.0001
P =	NEAA source	0.82	0.90	*P* =	Additional Lys source	0.48	0.01

Key words: lysine, nutrient requirement, pig

387 Effect of increasing levels of lysine in the diet on growth performance and carcass and meat quality of growing-finishing pigs. L. Cámara[1], M. P. Serrano[1], J. I. Morales[1], E. Alcázar[2], J. L. Sánchez[2], and G. G. Mateos*[1], *[1]Departamento de Producción Animal, UPM, Ciudad Universitaria, s/n. [28040], Madrid, [2]S.A.T. Vallehermoso, Ctra. La Solana a Infantes, km [9]. [13248], Alhambra, Ciudad Real.*

A trial was conducted to study the effect of level of Lys in the diet on productive performance and carcass and meat quality of pigs from 26 to 124 kg BW. A total of 480 crossbreds pigs (Large White × Landrace females crossed with Duroc male and PIC 410 sires) were used. Half of the animals were gilts and half males castrated at 4 d. The feeding program consisted of 5 periods with 5 dietary Lys levels each. Diets within each period were formulated to have the same NE (2,425 kcal/kg) but differed in digestible Lys content (1) Control (C); 2) C - 6%; 3) C - 12%; 4) C + 6%; and 5) C + 12%). The digestible Lys content of the control diets was 1.02, 0.86, 0.75, 0.70, and 0.58% for each of the 5 periods. In all cases, the other indispensable AA were formulated on an ideal protein basis. Each treatment was replicated 8 times. The experimental unit was the pen for all traits (12 pigs each for productive traits and 4 carcasses chosen at random for carcass and meat quality traits). From 26 to 44 kg BW, pigs fed diets with +12% and +6% Lys had better G:F than those fed the −6% and −12% Lys diets ($P = 0.024$) with pigs fed the control diet being intermediate. From 63 to 80 kg BW pigs fed diets with +12% and +6% Lys had better G:F than fed the control or the −6 and −12% Lys diets ($P = 0.042$). Cumulatively, pigs fed +12% and +6% Lys diets and control diet had better G:F ($P = 0.007$) than pigs fed −6% and −12% Lys diets. An increase in Lys content of the diet increased linearly carcass lean ($P = 0.011$) and quadratically the percentage of protein of the meat ($P = 0.020$), but no differences were detected for carcass fat or percentage of primal cuts. Under the conditions of the experiment, the use of 1.08%, 0.91%, 0.80%, 0.70%, and 0.58% digestible Lys for each of the periods considered in diets containing 2,425 kcal NE/kg, is recommended.

Key words: carcass and meat quality, dietary lysine, pig growth

388 Apparent prececal digestibility of amino acids and performance of broiler chickens fed soybean meal-based diets. A. F. Agboola*[1] and E. A. Iyayi[1], *[1]Department of Animal Science, University of Ibadan, Ibadan, Oyo, Nigeria, [2]University of Ibadan, Ibadan, Oyo, Nigeria.*

The apparent prececal amino acid digestibility of soybean meal (SBM) at varying levels of inclusion (0, 10, 20, and 30%) was determined for broiler chicks in a 7-d experiment. The feed ingredient SBM used served as the sole source of amino acids, as other feed ingredients were fixed. The birds received a commercial broiler starter diet during the first 14 d posthatch. On d 14, birds were sorted by body weight and randomly distributed into 4 dietary treatments in a completely randomized design. Each diet was comprised of 4 replicates of 5 birds per replicate from d 14 to 21 posthatch. On d 21 posthatch, birds were asphyxiated with CO2 and digesta samples from the terminal ileum were collected. Titanium dioxide was included as the indigestible dietary marker. In general, the concentration of essential amino acids (AAs) was highest in the 30% SBM diet as compared with other diets with the least in the control diet. The digestibility of all the essential AAs shows significant ($P < 0.05$) increases with inclusion of SBM in the diets. Arginine digestibility in birds fed 20% SBM was highest (94.92%) as compared with other essential amino acids, whereas threonine had the lowest digestibility value across the treatments. Lysine and methionine digestibilites in birds improved significantly ($P < 0.05$) at 20% SBM inclusion level. Increasing amounts of soybean meal had no significant effect on the weights of the birds but birds on the SBM diets had significantly ($P < 0.05$) higher weights and weight gain than those on the control diet. Feed intake was significantly increased ($P < 0.05$) in birds with increasing SBM levels while the feed conversion ratio was significantly ($P < 0.05$) improved. In conclusion, the data from the present study show that there are considerable differences in varying levels of SBM in the digestibility of their amino acids and growth performance for broiler starters. Therefore, it is imperative to consider lower levels of SBM inclusion, as levels above 20% resulted in decreased digestibility of amino acids.

Key words: prececal digestibility/amino acids, performance/soybean meal, broiler chickens

389 Amino acid digestibility and energy content in Dried Fermentation Biomass, Peptone 50, and P.E.P. Two Plus fed to weanling pigs. R. C. Sulabo*[1], J. K. Mathai[1], J. L. Usry[2], B. W. Ratliff[3], D. M. McKilligan[3], and H. H. Stein[1], *[1]University of Illinois, Urbana, [2]Ajinomoto Heartland LLC, Chicago, IL, [3]TechMix LLC, Stewart, MN.*

Two experiments were conducted to determine the standardized (SID) ileal digestibility of AA (Exp. 1) and the DE and ME content (Exp. 2) in Dried Fermentation Biomass (DFB), Peptone 50 (PEP50), and P.E.P. Two Plus (PEP2+) fed to weanling pigs and to compare these values to those in fish meal. DFB (Ajinomoto Heartland LLC) is a co-product from AA production and PEP50 and PEP2+ (TechMix LLC) are produced from hydrolyzed pig intestines. In Exp. 1, 12 barrows (BW: 11.5 ± 1.1 kg) were allotted to a replicated 6 × 6 Latin square design with 6 diets and 6 periods. One diet was based on SBM as the sole source of AA and 4 additional diets were formulated based on a combination of SBM and DFB, PEP50, PEP2+, or fish meal. A N-free diet was used to calculate endogenous losses of AA. The SID of Lys in DFB were greater (93.8 vs. 87.2%; $P < 0.01$) than in fish meal, but were similar for all other indispensable AA. The SID of Lys was less ($P < 0.01$) in PEP2+ (84.1%) than in DFB, but was similar to those in PEP50 (87.5%) and fish meal. Except for the SID of Thr, PEP50

had similar SID for all indispensable AA compared with fish meal. The SID of all indispensable AA except for Trp was less ($P < 0.05$) in PEP2+ than in any of the other ingredients. In Exp. 2, 40 barrows (BW: 12.8 ± 1.4 kg) were used with 5 diets and 8 replicate pigs per diet. A basal diet consisting of 96.4% corn and 4 diets with corn and DFB, PEP50, PEP2+, or fish meal were formulated. The DE (5,781 kcal/kg DM) and ME (5,560 kcal/kg DM) in DFB were similar to those in PEP2+ (5,300 and 4,959 kcal/kg DM), but were greater ($P < 0.01$) than in PEP50 (5,003 and 4,744 kcal/kg DM) and fish meal (4,586 and 4,180 kcal/kg DM). The DE and ME in PEP2+ were also greater ($P < 0.01$) than in fish meal, but were similar to those in PEP50. The ME in PEP50 was not different from the ME in fish meal. In summary, DFB, PEP50, and PEP2+ had similar AA digestibility, but greater energy value than fish meal.

Key words: alternative feedstuffs, amino acids, pigs

390 Digestibility of amino acids in corn, corn co-products, and bakery meal fed to growing pigs. F. N. Almeida*, G. I. Petersen, and H. H. Stein, *University of Illinois, Urbana.*

The objectives of this experiment were to measure the apparent ileal digestibility (AID) and the standardized ileal digestibility (SID) of CP and AA in bakery meal, corn gluten meal, corn gluten feed, corn germ meal, and hominy feed and to compare these values to the AID and SID of CP and AA in corn and distillers dried grains with solubles (DDGS). Eight growing barrows (initial BW: 82.5 ± 5.5 kg) were randomly allotted to an 8 × 8 Latin square design with 8 diets and 8 periods. Diets contained corn, DDGS, bakery meal, corn gluten meal, corn gluten feed, corn germ meal, or hominy feed as the sole source of protein and AA. An N-free diet was used to measure basal endogenous losses of AA and protein. Pigs were fed the experimental diets during 8 7 d periods with ileal digesta being collected on d 6 and 7 of each period. Results indicated that the SID of Lys in corn gluten meal (78.7%) was greater ($P < 0.01$) than in DDGS, bakery meal, corn germ meal, and hominy feed (46.0, 48.4, 68.4, and 58.8%, respectively). The SID of all indispensable AA except Arg, Leu, and Met in bakery meal were not different from DDGS. For corn gluten feed, the SID of all indispensable AA were not different from corn, except Arg, His, Leu, and Met, which had SID values that were less ($P < 0.01$) than in corn, but for most indispensable AA, the SID in corn gluten feed was not different from the SID in DDGS. The SID of all indispensable AA in corn germ meal except Arg, His, Leu, and Met were not different from corn. Likewise, the SID of all indispensable AA in corn germ meal except Arg and Leu were not different from DDGS. For most of the indispensable AA in hominy feed, the SID was not different from corn. All indispensable AA in hominy feed had SID values that were not different from the SID of AA in DDGS, except for Arg and Lys, which had greater ($P < 0.01$) SID than in DDGS. In conclusion, bakery meal is a poor source of digestible AA when compared with other corn co-products. Corn gluten meal has SID values for most AA that are greater than in DDGS, bakery meal and other corn co-products.

Key words: AA digestibility, corn co-prodcuts, pigs

391 Effect of L-Trp supplementation on growth performance pigs transitioning from nursery to finisher pens in a commercial farm. Y. B. Shen*[1], G. Voilqué[1], D. Kendall[2], D. Sykes[2], and S. W. Kim[1], *[1]North Carolina State University, Raleigh, [2]Murphy-Brown LLC, Rose Hill, NC.*

Transition period from nursery to finisher pens can be a stressful time for pigs physically and socially. Tryptophan serves as the precursor for the synthesis of serotonin which is a cerebral neurotransmitter with a key role in stress adaption. The aim of this study was to evaluate the effect of L-Trp supplementation on growth performance of nursery pigs transitioning from nursery to finisher pens. Six-hundred 74 pigs in 40 pens were used in a randomized complete block design study. Pigs were allotted to 2 treatments representing supplementation of 0% and 0.8% L-Trp. Both diets were isonitrogenous using L-Ala as a non-specific N source. Two neighboring pens shared a common feeder, and thus 2 neighboring pens were the experimental unit (n = 10 per treatment). Experimental period was composed of 5 d in nursery and 7 d in finisher. After 12 d feeding of experimental diets, pigs were provided a common diet for additional 7 d. Pigs in 2 neighboring pens were mixed on d 5 (when pigs were moved from nursery to finisher) and again on d 8. Body weight and feed intake were measured on d 5, 8, 12, and 19. During the first 5 d in nursery pens, growth performance was not affected by L-Trp supplementation. During d 5 to 8 in finisher pens, supplementation of 0.8% L-Trp improved ADG (549 vs. 669 g; $P = 0.017$) and G:F (0.558 vs. 0.690; $P = 0.001$) whereas ADFI was not affected by L-Trp supplementation. During d 8 to 12, supplementation of 0.8% L-Trp did not affect ADG, ADFI, and G:F. During the entire 12-d L-Trp supplementation period, pigs fed diet with 0.8% L-Trp tended to grow faster (511 vs. 556 g; $P = 0.092$) and more efficiently (G:F; 0.559 vs. 0.611; $P = 0.043$) compared with pig fed diet with 0% L-Trp. During the entire 19-d, pigs fed diet with 0.8% L-Trp had greater ADG (654 vs. 696 g; $P = 0.016$) and G:F (0.603 vs. 0.646; $P = 0.001$) compared with pig fed diet with 0% L-Trp but without affecting ADFI. Collectively, dietary L-Trp supplementation improved growth performance of pigs transitioning from nursery to finisher pens with new physical and social environment.

Key words: pig, transition period, tryptophan

392 Effect of L-Trp supplementation on growth and stress responses of nursery pigs fed diets varying large neutral amino acid concentrations. Y. B. Shen*, G. Voilqué, and S. W. Kim, *North Carolina State University, Raleigh.*

Tryptophan competes with large neutral amino acids (LNAA) for LNAA transporter to cross the blood-brain barrier. Availability of Trp in the brain is a limiting factor of serotonin synthesis. Thus, the ratio between Trp and LNAA in diets would affect serotonin synthesis in the brain, which plays a critical role in mediating stress. This study evaluated the effect of L-Trp supplementation on nursery pigs fed diets varying LNAA concentrations. Forty-eight barrows at 6 wk of age were housed individually and randomly allotted to 4 dietary treatments based on a 2x2 factorial arrangement (n = 12). First factor was L-Trp supplementation (0 or 0.6%) and the second factor was LNAA concentrations (4.5 or 3.8%). Pigs were fed the diets for 7 d. Body weight was measured on d 4 and 7. Saliva and blood were collected on d 4 and 7. During the first 4 d, pigs fed diets with 0.6% L-Trp increased ADG (341 vs. 264, g; $P = 0.022$) and G:F (0.453 vs. 0.321; $P = 0.001$) compared with pigs fed diets with 0% L-Trp and the effects of L-Trp on ADG and G:F were enhanced by 74% ($P = 0.079$) and 59% ($P = 0.040$), respectively, when dietary LNAA concentration was reduced from 4.5 to 3.8%. During the entire 7 d, L-Trp supplementation improved ($P = 0.004$) G:F of pigs (0.423 vs. 0.345) and lowering LNAA further enhanced ($P = 0.025$) the effects of L-Trp by 79%. Supplementation of 0.6% L-Trp reduced malonedialdehyde in plasma (19.16 vs. 25.14, μM; $P = 0.027$) and hypothalamus (24.92 vs. 34.47, μmol; $P = 0.024$) indicating reduced lipid peroxidation. Sali-

vary cortisol concentration was not affected by L-Trp supplementation but reduced (1.90 vs. 2.46, ng/mL; $P = 0.017$) when dietary LNAA concentration was reduced from 4.5 to 3.8%. Plasma urea nitrogen was reduced (5.18 vs. 4.29, μg/mL; $P = 0.018$) by L-Trp supplementation. Collectively, supplementation of 0.6% L-Trp improved G:F, and reduced systemic and hypothalamic lipid peroxidation. These effects were further enhanced by reducing dietary LNAA concentration.

Key words: pigs, stress, tryptophan

393 Feeding modality affects muscle protein deposition by influencing protein synthesis but not degradation in muscle of neonatal pigs. S. W. El-Kadi*[1], A. Suryawan[1], M. C. Gazzaneo[1], R. A. Orellana[1], N. Srivastava[1], H. V. Nguyen[1], R. Murgas-Torrazza[1], G. E. Lobley[2], and T. A. Davis[1], *[1]USDA/ARS Children's Nutrition Research Center, Dept. Pediatrics, Baylor College of Medicine, Houston, TX, [2]Division of Obesity and Metabolic Health, Rowett Institute of Nutrition and Health, University of Aberdeen, Aberdeen, UK.*

Neonatal pigs can serve as dual-use models for nutrition research in animal agriculture and biomedical fields. To determine how feeding modality by either intermittent bolus or continuous schedule affects protein anabolism and catabolism, neonatal pigs (n = 6/group, 9-d-old) were overnight fasted (FAS) or fed continuously (CON) or intermittently (INT; 7 × 4 h meals) for 28h. During the last 8 h, pigs were infused with [$^2H_5$]phenylalanine and [$^2H_2$]tyrosine and amino acid (AA) net balances were measured across the hindquarters for the last 4h. Glucose, insulin, branched-chain AA (BCAA), phenylalanine (Phe) and tyrosine (Tyr) arterial levels, and whole body Phe and Tyr rates of appearance were greater ($P < 0.05$) in INT after the meal but not in the CON or FAS groups. Whole body Phe hydroxylation was greatest for INT ($P < 0.05$). Across the hindquarters, BCAA, Phe, and Tyr were net removed (different from zero, $P < 0.05$) for INT and CON but not for FAS pigs. Hindquarters net protein deposition was stimulated following the meal for INT as compared with CON and FAS groups ($P < 0.001$). This was because protein synthesis increased following feeding for INT ($P < 0.001$) but remained unchanged for CON and FAS pigs, while no temporal changes in protein degradation occurred in any of the diet treatments. These results suggest that muscle protein accretion is enhanced with intermittent to a greater extent than continuous feeding, mainly by increasing protein synthesis. (Supported by NIHAR444474 and USDA/ARS 6250–51000–055)

Key words: amino acid, protein turnover, pig

394 Arginine deficiency is responsible for high rates of mortality in low-birth-weight piglets. G. Wu*, X. L. Li, R. Rezaei, and D. A. Knabe, *Texas A&M University, College Station.*

Pigs exhibit the most severe naturally occurring intrauterine growth retardation (IUGR) among livestock species. Under current feeding conditions, approximately 25% of live-born piglets have a birth weight of less than 1.1 kg, and they represent 76% of preweaning deaths. In the present study, we conducted 2 series of experiments to test the hypothesis that arginine deficiency may contribute to high rates of mortality in IUGR piglets. In Experiment 1, normal-birth-weight (NBW) and IUGR piglets, which were 1.43 ± 0.03 and 0.90 ± 0.04 kg ($P < 0.01$) at birth, respectively, were used for blood sampling at birth and thereafter. In Experiment 2, beginning at birth, IUGR piglets received oral administration of either L-arginine-HCl (0.1 g/kg BW) or an isonitrogenous amount of L-alanine twice daily. In each experiment, there were 40 piglets per group at birth. Data, expressed as means ± SEM, were analyzed by ANOVA and X2 analysis. Results of Experiment 1 indicated that concentrations of arginine in plasma of NBW and IUGR piglets at birth were 145 ± 4 and 81 ± 2 μM ($P < 0.01$), respectively. Concentrations of ammonia in plasma of NBW and IUGR piglets at birth were 72 ± 3 and 128 ± 5 μM ($P < 0.01$), respectively. During the first 3 wk of life, 7.8% and 46% of NBW and IUGR piglets died ($P < 0.01$), respectively. Analysis of blood samples obtained from IUGR piglets immediately after death revealed low concentrations of arginine (48 ± 4 vs. 130 ± 6 μM; $P < 0.01$) but high concentrations of ammonia (279 ± 13 vs. 145 ± 10 μM; $P < 0.01$), when compared with surviving IUGR piglets. Findings from Experiment 2 showed that arginine administration increased ($P < 0.01$) concentrations of arginine in plasma by 58%, while reducing ($P < 0.01$) concentrations of ammonia in plasma by 47% and preweaning mortality by 83%. Interestingly, arginine administration only modestly enhanced ($P < 0.01$) the daily weight gain of IUGR piglets by 21%. Thus, arginine deficiency is primarily responsible for high rates of mortality in IUGR piglets, but their maximal growth is limited by yet an unidentified factor. (Supported by AFRI-USDA grants.)

Key words: arginine, IUGR, mortality

Physiology and Endocrinology: Growth and Metabolism

395 ASAS Early Career Award Presentation: Placental programming: How the maternal environment can impact placental growth and function. K. A. Vonnahme*, C. O. Lemley, L. E. Camacho, L. A. Lekatz, D. A. Redmer, L. P. Reynolds, and J. S. Canton, *Center for Nutrition and Pregnancy, Department of Animal Sciences, NDSU, Fargo.*

As placental growth and vascularity precedes exponential fetal growth, not only is proper establishment of the placenta important, but a continual plasticity of placental function throughout gestation. Inadequate maternal environment has been documented to alter fetal organogenesis and growth, thus leading to improper postnatal growth and performance in many livestock species. The timing and duration of maternal nutritional restriction appears to influence the capillary vascularity, angiogenic profile, and vascular function of the placenta in cattle and sheep. Moreover, upon realimentation, it appears as if the placenta may try to "overcompensate" allowing for enhanced blood flow and nutrient delivery. In environments where fetal growth and/or fetal organogenesis are compromised, potential therapeutics may augment placental nutrient transport capacity and improve offspring performance. Supplementation of specific nutrients, including selenium and protein, as well as hormone supplements, such as indolamines during times of nutrient restriction may assist placental function. Current use of Doppler ultrasonography has allowed for repeated measurements of uterine and umbilical blood flow including assessment of uteroplacental hemodynamics in cattle and sheep. Moreover, these variables can be monitored in conjugation with placental capacity and fetal growth at specific time points of gestation. Elucidating the consequences of inadequate maternal intake on the continual plasticity of placental function will allow us to determine the proper timing and duration for intervention.

396 Blood metabolites and hormones as potential markers of body reserves dynamic and energetic balance in ruminants. E. González-García*[1], N. Debus[1], P. Hassoun[1], S. Camous[2], M.-R. Aurel[3], F. Bocquier[1], and F. Barillet[4], *[1]INRA UMR[868], Systèmes d'Èlevage Méditerranées et Tropicaux (SELMET), Montpellier, France, [2]INRA UMR[1198], Biologie du Développement et Reproduction (BDR), Domaine de Vilvert, Jouy-en-Josas Cedex, France, [3]INRA UE[0321], Domaine Expérimental de La Fage, Roquefort-Sur-Soulzon, France, [4]INRA UR[0631], Station d'Amélioration Génétique des Animaux (SAGA), Chemin de Borde Rouge, Auzeville, BP [52627], Castanet-Tolosan Cedex, France.*

Under strict controlled conditions, and throughout a whole lactation period, we evaluated the consistence of some plasma metabolites and hormones as potential markers of body reserves status (mobilization or accretion) in ruminants. Forty-eight confined primiparous (PRIM; n = 48) and multiparous (MULT; n = 48) dairy Lacaune ewes were monitored from late pregnancy to late lactation in a 2 × 2 × 2 factorial design. Parity (PRIM or MULT), litter size (singletons –SING– or twins –TWIN) and energetic balance (milked once –ONE– or twice –TWO) were the fixed effects. NEFA, glucose (GLUC) and triglycerides (TRIG) plasma metabolites, and leptin (LEPT), insulin (INSU) and tri-iodothyroidine (T3) hormones were monitored. Animals received a 70:30 hay:concentrate TMR diet. Blood samples (10 mL) were individually collected (≈biweekly) early morning by jugular venipuncture in EDTA or heparin tubes. Plasma was harvested from blood samples that were centrifuged immediately after collection. After centrifugation, samples were transferred to 5-mL tubes and frozen at –20°C until analyses. Energy restriction (i.e., TWO higher energy expenditure than ONE) resulted in higher concentrations of NEFA (PRIM, $P < 0.001$; MULT, $P < 0.05$); in contrast, concentrations of INSU (PRIM, $P < 0.05$; MULT, $P < 0.001$) decreased until 1 mo after ONE; in MULT ewes, LEPT consistently decreased in TWO when compared with ONE (11.15 ± 0.571 vs. 14.31 ± 0.676, $P < 0.05$). However, LEPT was affected ($P < 0.05$) by litter size × number of milking interaction in PRIM, SING × ONE and SING × TWO ewes showing the highest (12.33 ± 1.04) and lowest (7.36 ± 0.989 ng.mL^{-1}) values, respectively. Ewes with TWIN had higher NEFA and lower INSU or LEPT than SING from before lambing until weaning. T3 results showed contradictory variability. Either for parity or number of milking, no differences at all were found for TRIG. For GLUC, differences (ONE > TWO) appeared just 1 wk after passing to ONE. Even when differences in BW or BCS were not found, NEFA, LEPT and INSU showed the higher sensitivity as potential markers of body reserves mobilization under the conditions of this experiment.

Key words: metabolites, hormones, markers of body reserve status

397 Metabolic gene expression in bovine ruminal tissue in response to age and pre and postweaning plane of nutrition. A. Naeem*, J. Stamey, J. K. Drackley, and J. J. Loor, *University of Illinois, Urbana.*

We evaluated expression of 22 genes encoding enzymes involved in ketogenesis, cholesterogenesis, TCA cycle flux, long-chain fatty acid (LCFA) oxidation, and transcriptional regulation in ruminal tissue of male Holstein calves fed a conventional milk replacer (20% CP, 20% fat; 1.25% of birth BW as solids) and starter (19.6% CP, DM basis; control) or enhanced milk replacer (28.5% CP, 15% fat; 2% of BW; ENH) and enhanced starter (25.5% CP, DM basis). All calves were weaned on d 42. Groups of calves in control and ENH were harvested after 43 d (wk 5) and 71 d (wk 10) of feeding. There was marked upregulation of HMGCS2, the rate-limiting enzyme of hepatic mitochondrial ketogenesis in non-ruminants, between wk 5 and 10 regardless of diet. This response paralleled an increase in plasma BHBA concentration (0.09 vs. 0.24 mmol/L) between wk 5 and 10. Expression of other ketogenic (BDH1, HMGCL), cholesterogenic (HMGCS1), and TCA cycle-related enzymes (LDHA, GOT2, PCCA) also increased by wk 10 regardless of diet. A higher expression of CPT1A and ACADVL at wk 5 in calves fed ENH vs. control suggested greater LCFA oxidation potentially driven by the greater intake of LCFA from milk replacer. This suggestion is supported by the greater concentration of plasma NEFA (128 vs. 95 μEq/L) at wk 5 due to ENH vs. control. Expression of peroxisome proliferator-activated receptor-δ increased ~8-fold between wk 5 and 10 regardless of diet, suggesting a role for this nuclear receptor in postweaning ruminal tissue development. In conclusion, several metabolic enzymes were upregulated at wk 10 regardless of diet suggesting a coordinated response to support ruminal tissue development. The mRNA of HMGCS2 accounted for ca. 50% of total genes measured (e.g., HMGCS1 was 0.2%), suggesting this enzyme is key for regulating ketogenesis in ruminal epithelium as in liver. Enhanced nutrition during the first 5 wk of life had minor effects on the selected genes.

Key words: ketogenesis, nuclear receptor, dairy calf

398 Functional genomics of liver in crossbred beef cows in two forage allowances during gestation and lactation period. J. Laporta*[1], G. Greif[2], P. Zorrilla[2], H. Naya[2], G. J. M. Rosa[3], and M. Carriquiry[1], *[1]Facultad de Agronomía, Universidad de la República, Montevideo, Uruguay, [2]Instituto Pasteur, Montevideo, Uruguay, [3]University of Wisconsin, Madison.*

Beef cows in rangeland conditions are subjected to climate variations that affect pasture quality and availability along the year as cow physiological stage changes from pregnancy (autumn-winter) to calving (spring) and lactation (spring-summer). A large-scale microarray experiment was conducted using 8 Angus-Hereford crossbred cows in high and low forage allowances (10 vs. 6 kg of DM/100 kg of LW/d) to study the molecular basis of such physiological processes. Liver biopsies were collected at −170, −15, +15 and +60 d relative to parturition and total RNA was extracted. RNA integrity and quality were evaluated using the Agilent 2100 Bioanalyzer (RIN 6.4 ± 0.4). A single-channel microarray analysis was performed using Agilent 4x44K Bovine (v2) Gene Expression array. After data cleaning and normalization, a 2-way ANOVA test was performed using Agilent GeneSpring (v11.5) Software. Significance levels were adjusted for multiple comparisons using a false discovery rate of 0.2. Out of 2,484 differentially expressed genes, 2,353 changed across time (169 ≥ 2.5 fold change), and 146 with forage allowance, but there was no significant interaction between the 2 factors. Differentially expressed genes were hierarchically clustered to study expression profiles and a Gene Set Enrichment Analysis was performed. More than 45 significant ($P \leq 0.01$) gene sets across time (only for −170 vs. −15 d) with positive (metabolism of RNA, mRNA splicing, proteasome, protein export, TGF signaling pathway) and negative (fatty acid, pyruvate, steroid, glucose, glycolysis and gluconeogenesis, lipid and lipoprotein metabolism; cholesterol biosynthesis; PPAR signaling pathway, among others) enrichment scores (ES) were identified. No genes sets were enriched for peripartum and lactation period. Only 3 genes sets were positively enriched ($P \leq 0.01$) when high vs. low forage were compared: glycolysis, gluconeogenesis, and glucose metabolism. These results contribute to identify pathways that are up or downregulated as physiological stage of cows change as well as due to the different levels of nutrition in grazing conditions.

Key words: microarrays, liver, grazing

399 Alterations in the somatotropic axis during a dual stress and *M. haemolytica* challenge in beef steers. S. M. Falkenberg*[1], J. A. Carroll[2], M. A. Ballou[5], J. L. Sartin[3], J. O. Buntyn[1], T. Elsasser[4], S. Kahl[4], and T. B. Schmidt[1], *[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 Lab, USDA-ARS, Beltsville, MD, [5]Texas Tech University, Lubbock.*

The objective of this trial was to characterize the potential impact of individual and multiple stressors before, simultaneously, and post *M. haemolytica* (MH) challenge on the somatotropic axis. Forty-eight beef steers (207.7 ± 22.1 kg BW) vaccinated against MH were randomly assigned to 1 of 8 treatments (trt). Treatments consisted of steers that received MH (given at 0 h for all 8 trts) and corticotrophin releasing hormone + arginine vasopressin in tandem as the stressor (Stress) administered before, simultaneously, or after the challenge. The 8 trt were: 1) MH only; 2) Stress at −7 h + MH; 3) Stress at 0 h + MH; 4) MH followed by Stress at 7 h; 5) Stress at −7 h and 0 h + MH; 6) Stress at −7 h and 7 h + MH; 7) Stress at 0 h and 7 h + MH; and 8) Stress at −7 h, 0 h and 7 h + MH. Steers were fitted with jugular catheters and rectal temperature (RT) probes on d −3, moved to stanchions, given a day to acclimate (d −2), baseline samples obtained on d −1, and the challenge was given on d 0. There were trt x time interactions or trt effects ($P < 0.05$) observed for cortisol (CORT), growth hormone (GH), insulin-like growth factor-I (IGF-I), and RT. Differences were observed ($P > 0.05$) in overall GH and IGF-I as well as concentrations before the MH challenge for trts that received multiple Stress challenges or Stress during and after the MH challenge. No differences were observed ($P > 0.05$) for change in GH and IGF-I concentrations after the MH challenge. Furthermore, no differences were observed ($P > 0.05$) in GH and IGF-I for trts that did not receive any Stress or Stress trt before the MH challenge. The results indicate the MH challenge altered GH and IGF-I in vaccinated calves regardless of the timing associated with the applied stress. However, the data also suggest that stressors can impact the overall regulation of GH and IGF-I when stressors occur during and after infection with MH even in animals protected by vaccination against MH.

Key words: cattle, immune, stress

400 Effects of plane of nutrition and 2,4-thiazolidinedione on insulin responses and adipose tissue gene expression in dairy cattle during late gestation. K. M. Schoenberg* and T. R. Overton, *Cornell University, Ithaca, NY.*

The objective was to determine effects of an insulin–sensitizing agent (thiazolidinedione, TZD) and dietary energy level on glucose and fatty acid metabolism during late gestation. Multiparous Holstein cows (n = 32) 50 d before expected calving date were assigned to 1 of 2 dietary energy levels for 3 wks (High, 1.52 Mcal/kg NEL; or Low, 1.34, Mcal/kg NEL) and received daily 4.0 mg TZD/kg BW (TZD) or Saline i.v. for the final 2 wk. Cows administered TZD had higher plasma glucose (62.5 vs. 59.6 mg/dL; $P = 0.03$) than Saline cows and cows fed the High diet had higher plasma insulin (35.1 vs. 25.3 μIU/mL; $P = 0.03$) compared with those fed the Low diet. All cows were subjected to an i.v. glucose tolerance test (GTT; 0.25 g dextrose/kg BW) and an insulin challenge (IC; 1.0 μg/kg BW) 110 min later. High cows tended to have a lower area under the curve (AUC) for plasma glucose during GTT (1895 vs. 2410 mg/dLx90 min; $P = 0.13$) than Low cows; however, Low cows had more negative NEFA AUC (–4838 vs –2137 μEq/Lx90 min; $P = 0.04$) and greater NEFA clearance rates (1.35 vs. 0.63%/min; $P = 0.01$) during GTT, suggesting differential responses of glucose and fatty acid metabolism in response to diet. During IC, TZD cows had more negative glucose AUC (–45.0 vs. –12.1 mg/dLx15 min; $P = 0.08$) than Saline, suggesting that TZD–treated cows had greater responses to insulin. Interactions of diet and TZD were only significant ($P = 0.04$) for NEFA responses to IC such that Low cows receiving TZD had a negative AUC (–80 μEq/L x 15 min), cows fed the High diet and treated with either saline or TZD had slightly positive AUC (65 and 67 μEq/L x 15 min, respectively), and cows fed the Low diet receiving Saline had the most positive AUC (517 μEq/Lx15 min). Cows fed the High diet had greater lipoprotein lipase mRNA expression (2.2 vs. 1.6; $P = 0.10$) and peroxisome proliferator–activated receptor–γ expression (2.4 vs. 1.3; $P = 0.02$) in adipose tissue collected by biopsy at the end of the study. These results indicate that energy level and insulin–sensitizing agents affect glucose and lipid metabolism during the dry period.

Key words: insulin, thiazolidinedione

401 Effects of overstocking on glucocorticoid production and analytes associated with energy metabolism. J. M. Huzzey*[1], D. V. Nydam[1], R. J. Grant[2], and T. R. Overton[1], *[1]Cornell University, Ithaca, NY, [2]W. H. Miner Institute, Chazy, NY.*

The objective of this study was to determine if overstocking alters energy metabolism and glucocorticoid production. Four groups of 10 dry Holstein cows (~60 d prepartum) were exposed to 2 treatments: Control (1 lying stall/cow and 0.67m linear feed bunk (FB) space/cow) and Overstocked (0.5 stalls/cow and 0.34m FB/cow) in a replicated 2 × 2 crossover design with 14–d treatments. Plasma NEFA, glucose and insulin were measured from blood sampled every 2 d of each treatment and during an intravenous glucose tolerance test (GTT: 0.25g dextrose/kg BW) performed on d 13. Feces, collected every 2 d, were analyzed for fecal cortisol metabolites (FCORT). Plasma cortisol response to an intravenous ACTH challenge (0.125 IU ACTH/kg BW) was measured on d 14. Data from individual cows were averaged to create a group mean and all statistical analyses used group as the experimental unit. Average DMI per cow was greater during the overstocked treatment relative to the control period (15.9 vs. 14.9 kg/d, $P < 0.001$). NEFA and glucose concentrations were higher during the overstocked treatment (0.11 vs. 0.09 mEq/L and 65 vs. 64 mg/dl respectively, $P < 0.05$); however, when stratified by parity these responses were limited to heifers ($P < 0.01$). Overstocking had no effect on insulin concentration during the treatment period ($P > 0.20$) while FCORT tended to be higher (19 vs. 16 ng/g fecal DM, $P \leq 0.14$) during overstocking. During the GTT, cows took longer to return to basal glucose concentration (55.1 vs. 51.5 min, $P = 0.05$), tended to have greater area under the curve estimates for glucose (2837 vs. 2630 mg/dl × 120 min, $P = 0.06$), had lower peak insulin concentrations (201 vs. 260 μIU/L, $P = 0.02$), and tended to have a reduced rate of NEFA decline from circulation (1.4 vs. 1.9 μEq/L per min, $P = 0.1$) following the overstocked treatment. Cortisol production after administration of ACTH was not affected by stocking density treatment ($P > 0.48$). Overstocking alters energy metabolism. These effects seem to be mediated through changes in insulin production rather than insulin resistance; the role of glucocorticoids in influencing these effects is still unclear.

Key words: overstocking, energy metabolism, cortisol

402 Effect of milking frequency and feeding level in early lactation on metabolites in grazing dairy cows. J. K. Kay*, C. V. C. Phyn, A. G. Rius, S. R. Morgan, T. M. Grala, and J. R. Roche, *DairyNZ, Hamilton, New Zealand.*

Study objectives were to investigate the effect of milking frequency (MF) at 2 feeding levels (FL) in early lactation on plasma metabolite content. Multiparous Holstein-Friesian cows (n = 120), grazing a generous pasture allowance (residuals of 1,600 kg DM/ha) and milked twice daily (2X) from calving until 34 ± 6 DIM were allocated to one of 4 treatments in a 2 × 2 factorial arrangement. Treatments were 2 MF (2X or once daily; 1X) and 2 FL (UnRes: 15 kg DM/cow/d or Res: 9kg DM /cow/d) for 3 wk. After treatment, all animals were offered a generous pasture allowance and milked 2X for 20 wk. Individual blood samples collected weekly from 2 wk pre- until 20 wk post-treatment were analyzed for NEFA, BHBA, glucose, aspartate aminotransferase (AST) and glutamate dehydrogenase (GDH). Differences were significant when $P < 0.05$. During the treatment period plasma glucose decreased with pasture restriction and increased with reduced MF. A MF x FL interaction indicated that increases in glucose during 1X milking were greater in Res compared with UnRes cows. One to 8 wk post-treatment, glucose remained less in Res cows and greater in cows milked 1X; however, by 9–20 wk post-treatment there was no effect of MF or FL. Plasma NEFA and BHBA increased with pasture restriction and decreased with reduced MF. When cows were milked 1X, the decrease in NEFA with reduced MF was greater in UnRes than Res cows, while the decrease in BHBA was greater in Res than UnRes cows. Post-treatment (1–8 wk) there was no effect of MF on NEFA or BHBA, however NEFA was greater in UnRes compared with Res cows. By 9–20 wk post-treatment neither NEFA nor BHBA were affected by FL. Liver function enzymes (AST and GDH) increased during pasture restriction but were not affected by MF. These metabolite data are consistent with the previously reported decrease in milk production and improved LWT with reduced MF. In summary, results indicate reducing MF improves energy balance in both restricted and unrestricted grazing cows and may have implications for management strategies when pasture availability is limited.

Key words: milking frequency, nutrition, grazing

403 Insulin-glucose clamps and intramammary LPS challenge: cross reactions between metabolism and mammary immune response. M. C. M. B. Vernay, L. Kreipe, H. A. van Dorland, R. M. Bruckmaier, and O. Wellnitz*, *Veterinary Physiology, Vetsuisse Faculty, University of Bern, Bern, Switzerland.*

Insulin, a central regulator of carbohydrate and fat metabolism, influences the immune system. The aim of this study was to evaluate the effects of a 3-d hypoglycemia and hyperinsulinemia/euglycemia on the bovine mammary immune system. Seventeen midlactating, non pregnant, anestric dairy cows received an insulin infusion (HypoG; n=5; constant plasma hypoglycemia of 2.32 ± 0.3mmol/l), an euglycemic hyperinsulinemic clamp (EuG; n=6; insulin infusion rate: 0.62mU/kg/min), or saline solution (control; n=6) for 56 h. 48 h after the start of infusion two udder quarters were challenged with lipopolysaccharide (LPS). Only significant results ($P \leq 0.05$) are shown. Intramammary LPS challenge induced an insulin resistance indicated by an increase of plasma insulin (between 32 and 252μU/L) in all groups, while glucose remained stable in controls, glucose infusion rates in EuG had to be markedly reduced (from 2.9 to 0.9 mmol/kg/min), and insulin infusion rates in HypoG had to be increased (from 0.2 to 0.9 mU/kg/min) to maintain constant glucose levels. AUC of plasma insulin was 333 in control, 875 in EuG, and 529 in HypoG. Hourly measurements of SCC showed increases to $>10^6$ cells/mL in LPS treated quarters without differences between groups. mRNA abundance of immune parameters in mammary tissue biopsies before and 8 h after LPS administration was quantified by qRT-PCR: LPS induced an increased expression (between 2.1 and 8.4 crossing points) of tumor necrosis factor-α, interleukin (IL)-8, −1β, and −10, and serum amyloid A (SAA). IL-1β, IL-10, and SAA were higher expressed (difference between 2.2 and 3.6 crossing points) in LPS treated quarters of EuG than of HypoG. In conclusion, intramammary LPS challenge induces insulin resistance characterized by increased insulin release independently of insulin and glucose plasma concentrations before challenge. Increased plasma insulin occurs concomitantly with changes of the mammary immune response to LPS based on mRNA expression of measured immune factors. The results indicate cross-reactions between insulin resistance and cytokine release in the bovine mammary gland.

Key words: insulin, mammary immunity, intramammary LPS challenge

404 Insulin sensitivity in tropically adapted cattle selected for residual feed intake. G. L. Shafer*[1,2], A. W. Lewis[1], L. C. Caldwell[2], A. N. Hafla[2], G. E. Carstens[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) identifies animals requiring less feed to achieve the same performance. This study evaluated the effect of a glucose (G) challenge on efficient (L) and inefficient (H) tropically adapted yearling bulls and heifers. Bonsmara heifers (n = 24) and Santa Gertrudis bulls (n = 16) were tested at different times and data analyzed separately. Animals were infused with a 50% dextrose solution at 0.5 mL/kg BW by catheter. Blood was collected at −5, 0, (heifer: 5), 10, 15, 20, (bull: 30), 40, 60, 80, 100, 120, 140, 160, and 180 min relative to challenge. Insulin (I) was determined by RIA and G by colorimetry. Repeated measures ANOVA were conducted using the MIXED model of SAS for analysis of RFI, time, and their interactions on I, G and insulinogenic index (IND). Time to peak I and half-life of G were analyzed using GLM. In bulls, time affected ($P < 0.001$) I and G. RFI did not affect ($P > 0.05$) I peak or peak time in bulls. L and H bull I peaks were (mIU/mL) 50.6 ± 13.3 and 67.7 ± 13.3, respectively and I peak times (min) were 46.2 ± 23.1 and 81.2 ± 23.1, respectively. RFI did not affect ($P > 0.05$) G half life in bulls. IND was affected by RFI ($P < 0.05$), but not time. L and H bull IND ($\Delta I/\Delta G$) were 0.17 ± 0.02 and 0.26 ± 0.02, respectively. Among heifers time affected ($P < 0.0001$) I and G. There was no RFI x time interaction ($P > 0.05$) for I or G. RFI did not affect ($P > 0.05$) I peak or peak time. L and H heifers had I peaks (mIU/mL) of 108.0 ± 12.0 and 75.5 ± 12.6, respectively and I peak times (min) were 16.6 ± 1.0 and 18.6 ± 1.0, respectively. RFI did not affect ($P > 0.05$) G half life in heifers. L and H heifer G half lives were (mg/dL) 80.0 ± 3.1 and 77.0 ± 3.2, respectively and G Half life times (min) were 33.2 ± 2.5 and 36.9 ± 2.6, respectively. IND was affected by RFI ($P < 0.05$), but not time. L and H heifer IND ($\Delta I/\Delta G$) were 0.44 ± 0.02 and 0.29 ± 0.03, respectively. L heifers had a higher I response than H heifers. The opposite response was seen in bulls. There may be differences in energy metabolism between genders and breeds. Further research will be required to explain the opposite results of Bonsmara heifers and Santa Gertrudis bulls.

Key words: insulin, glucose, residual feed intake

Production, Management and the Environment & Forages and Pastures Joint Symposium: Environmental Impact of Beef and Dairy Systems

405 An overview of the environmental impact of beef and dairy systems. J. L. Capper*, *Washington State University, Pullman.*

The livestock industry faces the challenge of providing sufficient safe, affordable, nutritious animal protein to feed the population while maintaining environmental stewardship. Ruminant production systems have been criticized for their contribution to global greenhouse gases, yet US beef and dairy systems have considerably reduced resource use and carbon emissions over time. Advances in nutrition, genetics and management allowed dairy cow productivity to increase 4-fold between 1944 and 2007, with 21% of the animals, 23% of the feed, 35% of the water and 10% of the land required to produce one kg of milk in 2007 compared with 1944. Similar advances in the US beef industry facilitated a 31% increase in beef yield per animal and 124-d reduction in the time period from birth to slaughter between 1977 and 2007. Feedstuff use was thus reduced by 19%, water use by 14%, land use by 34% and the carbon footprint was 18% lower per kg of beef in 2007. Environmental gains result from a combination of improved productivity and reduced resource requirements within the non-productive sector of the supporting population. Individual cow and herd data records suggest that the dairy industry may continue to considerably improve milk yield before a plateau is reached. Further gains may be made by reducing population body mass – producing cheddar cheese from Jersey cows (454 kg mature weight) with increased milk component concentrations (4.8% fat and 3.7% protein) compared with their Holstein cohorts (680 kg mature weight; 3.8% fat and 3.1% protein) reduced the carbon footprint per kg of cheese by 20% despite the greater Holstein milk yield (29.1 kg/d vs. 20.9 kg/d). Within the beef industry, desirable slaughter weight appears to have plateaued at an average of 590 kg, yet resource use and waste output may be mitigated by improving growth rate. Indeed, growth-enhancing technology use within conventional beef production reduced land use by 45% and carbon emissions by 42% per kg of beef compared with grass-finished systems. To improve future environmental sustainability it is crucial to maintain access to management practices and technologies that improve productivity.

Key words: greenhouse gases, environmental impact, productivity

406 Whole farm assessment—Using precision agriculture to assess, measure, and mitigate environmental impacts of on-farm practices. Y. Wang*, *Dairy Research Institute, Rosemont, IL.*

The objective of this presentation is provide an example of a modeling tool that helps individual dairy producers assess and mitigate on-farm GHG emissions. The greenhouse gas (GHG) life cycle assessment (LCA) for fluid milk, commissioned by the Innovation Center for US Dairy and conducted by the Applied Sustainability Center at the University of Arkansas, evaluated GHG emissions for milk production in the United States. On-farm activities accounted for more than 70% of emissions. A compendium study is also underway to assess other impacts such as eutrophication, land use, biodiversity, and toxicity. Together, these LCAs will provide the basis for the development of easy-to-use measurement tools for producers. One such tool is Dairy FarmSmart, a modeling tool that allows farmers to assess, measure, and mitigate on-farm environmental impacts based upon farm-specific climate, air quality, soil, land, and watershed information. Two existing modeling tools, DeNitrification-DeComposition (DNDC) and Water Use and Quality Assessment, are integrated and enhanced. DNDC is used for predicting crop growth, soil temperature and moisture regimens, soil carbon dynamics, nitrogen leaching, and emissions of trace gases. The Water Use and Quality Assessment is based on the fluid milk LCA. It includes implementation of the P-eutrophication model at a local scale and a multi-scale link to the larger scale with the 0.5 by 0.5 degree watershed (approximately 50 km by 50 km.); hydrological balance of the local streams and river from plot scale up to the 0.5 degree regional scale; evaluation of local impacts of water use at farm level; and integration of the farm's direct local impact within the overall life cycle impact assessment. The desired outcome is to give producers the ability to identify on-farm management practices that will minimize GHG emissions and maximize conservation efforts.

Key words: greenhouse gas emissions (GHG), life cycle assessment (LCA), environmental impact

407 Measurement strategies for reducing enteric methane from beef and dairy production. K. A. Beauchemin* and S. M. McGinn, *Agriculture and Agri-Food Canada, Lethbridge, AB, Canada.*

There is considerable uncertainty in the estimates of enteric methane (CH_4) production from ruminants attributed to variability at the farm level due to diet and management. Quantification of enteric CH_4 emissions is essential for understanding underlying processes controlling methanogenesis, assessing mitigation practices and producing national greenhouse gas inventories. Various techniques are available for measuring enteric CH_4 production, and several factors need to be considered when selecting the most appropriate technique. Most important is an understanding of the required level of accuracy and precision. When evaluating mitigation strategies, it is essential to use a measurement technique and experimental design that will enable detection of differences between treatments, which are often small (<15%). Whole animal chambers have a high degree of accuracy and precision, and are therefore ideal for treatment comparisons. However, dry matter intake and diet composition of animals in chambers can differ from their herd mates. The sulfur hexafluoride (SF_6) tracer technique allows measurement of enteric CH_4 emissions of ruminants in their natural environment. A permeation tube filled with SF_6 is inserted into the rumen of the animal and a collection apparatus is mounted on or near the animal. The tracer technique has greater between-animal and within-animal variability than chambers, and consequently a large number of animals (~4-times more than chambers) and multiple measurement days are needed. Micro-meteorological techniques are useful for measuring emissions from groups of animals (pens, small paddocks, entire feedlots, barns) and are ideal for inventory purposes. Recent advances have shown that they can also be used to evaluate treatment differences, although replication of groups can be difficult. Several newer methods such as laser guns, feeders equipped with sensors, and assessment of milk fatty acid profiles may offer potential for monitoring emissions on commercial farms. Each technique for measuring enteric CH_4 has its advantages and limitations, and the ideal method of choice depends on the objective of the study.

Key words: methane, greenhouse gases, measurement

408 Dairy cropping systems and air quality. F. M. Mitloehner*, *University of California, Davis.*

Recent studies have identified animal feeds as a significant volatile organic compound (VOC) source contributing to regional ozone challenges. Specifically, the ozone formation potentials of livestock feed emissions were measured on representative field samples using a transportable smog chamber. Seven feeds were considered: cereal silage (wheat grain and oat grain), alfalfa silage, corn silage, high moisture ground corn (HMGC), almond shells, almond hulls, and total mixed ration. The VOC flux measured from silage and total mixed ration was two orders of magnitude higher than comparable fluxes from animal waste. Chamber measurements confirm that animal feed VOC emissions are significantly higher than animal waste emissions and several of the animal feed derived VOCs have potentially high ozone formation potentials. While recognizing the importance of this environmental challenge, it is important to note that loss of these volatile gases has also financial implications to the dairy producer. Dry matter losses can range from 10 to 25% and while the majority of gas losses is CO_2, VOC constitute a significant portion of overall feed losses that might be preventable though optimized silage management.

Key words: silage, ozone, volatile organic compounds

409 Cow of the future—A research roadmap for mitigating enteric methane emissions from dairy cattle. W. R. Wailes*[1], J. R. Knapp[2], and M. D. Welch[3], *[1]Colorado State University, Fort Collins, [2]Fox Hollow Consulting LLC, Columbus, OH, [3]Dairy Research Institute, Rosemont, IL.*

The Innovation Center for US Dairy has committed to reducing greenhouse gas emissions from dairy production by 25% (from 2008 levels) by 2020. Enteric methane emissions are the largest contributor to greenhouse gas emissions in the dairy chain, comprising approximately 35% of the total greenhouse gas emissions associated with US dairy production. The objective of this presentation is to present a roadmap for future research that reduces enteric methane per unit of milk produced by cows during the process of feed digestion. This roadmap, called the Cow of the Future Research Agenda, identifies and evaluates research opportunities that will lead to future mitigation technologies and applications. An expert panel of university and industry-based scientists identified 8 categories of future research needs: rumen microbial genomics and ecology; rumen function and modifiers; enhancing feed quality and feed ingredient usage to improve digestibility and feed efficiency; genetic approaches to increase individual cow productivity; management approaches to increase individual cow productivity; management of herd structure to reduce number of cow-days of non-productive animals (replacement heifers and dry cows); development and refinement of methane measurement techniques; and modeling efforts to quantitatively integrate the knowledge gained in the above areas. Implementation of existing technologies and management practices in the dairy industry along with continued genetic progress in milk yields is expected to result in 10 to 12% reductions of methane emissions per unit of milk over the next decade. To achieve the additional 13 to 15% reduction to reach the overall goal of a 25% reduction requires investment in research to identify and develop new strategies. The desired outcome of the Cow of the Future Research Agenda is to encourage research and development in the designated categories by fostering collaborative grant submissions and providing opportunities for collegial interaction by hosting symposia such as Production, Management and the Environment & Forages and Pastures Joint Symposium and other conferences.

Key words: dairy, enteric methane, greenhouse gas emissions (GHG)

410 Diet formulation as an effective tool for mitigating the environmental impact of dairy and beef cattle operations. A. N. Hristov*, *Pennsylvania State University, University Park.*

Dairy and beef cattle operations are responsible for a significant portion of the N, P, ammonia, and green-house gas (GHG) agricultural emissions in the US In watersheds with intensive animal production (the Chesapeake Bay, for example), agriculture can account for as much as 30 to 50% of the total N and P loads. Gaseous emissions from animal facilities or field application of manure can also be a significant contributor to the environmental footprint of the livestock industries. It has been repeatedly demonstrated that nutrient emissions from animal operations are directly related to composition of the diet fed and whole-farm nutrient inputs. In all cases, the possibility of reducing the environmental impact of dairy and beef cattle operations through nutrition is intrinsically related to improving feed efficiency. For example, an average dairy cow will utilize approximately 25 to 28% (SD = 41 and 36, respectively) of the feed N for milk protein secretion. Beef cattle typically retain 10 to 20% of the intake N as weight gain. Highly efficient dairy systems, however, may capture up to 38 or even 40% of the feed N into milk protein. To a large part, this increased efficiency is a result of diet formulation and reduced feed N input. More efficient utilization of feed N for production purposes corresponds to lower manure N losses and gaseous emissions. Feeding to or below NRC requirements (both dairy and beef) has been shown to have a marked impact on P losses with no measurable effect on animal productivity, reproduction, or health. Reducing inputs of some nutrients (particularly N), however, can negatively impact animal productivity (or milk composition in dairy cows). Formulating for metabolizable protein and perhaps supplementation with synthetic amino acids, for example, may be a feasible approach for maintaining production with low-N input rations. In some cases, targeting efficiency, not necessarily maximum production, may be a viable nutrient management strategy.

Key words: environmental impact, diet formulation, livestock

411 Managing the environmental impact of pasture production systems. K. A. Johnson* and C. D. Gambino, *Washington State University, Pullman.*

All animals impact their environment. The form and magnitude of that impact depends on the animal system. There is increasing interest in producing animal products using pasture systems and these systems must be designed and managed to be productive and minimize environmental impact. Grazing cattle affect the environment through plant selection, trampling of plants, deposition of fecal and urinary nutrients, leaching of nitrogen (N), and emission of greenhouse gases (GHG) from enteric fermentation or soil biogeochemical processes. Grazing cattle spatially redistribute plant-N which causes N-cycling changes in plants and soil which alters the carbon:N ratio of plants. Trampling can increase litter turnover, and nutrient cycling can accelerate in patches where manure and urine are deposited. The primary GHG associated with pasture systems are methane (CH_4) and nitrous oxide (N_2O) although some ammonia (NH_3) losses do also occur. Manipulation of pasture composition through fertilization, management-intensive grazing systems, and strategic supplementation can affect the GHGs emitted by livestock and soils. Factors affecting N_2O emissions from grazing lands include the ecosystem (pasture or rangeland), animal management (timing and duration of grazing and stocking rate),

riparian area management, and fertilization (timing and application method). Grazing animals affect soils in both direct and indirect ways. Manure deposition on the soil directly affects soil microbial activity, N mineralization rate, and ultimately plant productivity. Indirectly, grazing can lead to death of leaves, decomposition of litter, enhanced soil microbial activity, N mineralization and altered plant productivity. Management intensive grazing strategies that maintain plants in the vegetative stage (reduced fiber) can alter ruminal fermentation to decrease CH_4 emissions. Fertilization strategies that provide plants with N when they are actively growing reduce leaching of NO_3-, NH_3 volatilization and N_2O emissions. Prior to implementation, pasture production systems should be designed, assessed and managed as a dynamic system to minimize environmental impact.

Key words: pasture, greenhouse gases, management

412 Ruminal degradable sulfur from organic and inorganic sources in beef cattle finishing diets. J. O. Sarturi*, G. E. Erickson, T. J. Klopfenstein, and C. D. Buckner, *University of Nebraska, Lincoln.*

The relationships between ruminal hydrogen sulfide concentration ([H_2S]) and ruminal degradable S intake (RDSI), total sulfur intake (TSI) or pH variables were evaluated in beef cattle finishing diets. Ruminally cannulated steers (n = 5; BW = 486 ± 39 kg) were assigned randomly in a 5 × 5 Latin square design and fed once daily during five 21-d periods. Steers were fed a corn control diet (CON), inorganic S source (ammonium sulfate; INORG), organic S source (corn gluten meal; ORG) fed at 9.8 or 23.3%, or wet distillers grains with solubles (WDGS) fed at 50%. Dietary S was 0.20, 0.37, 0.31, 0.46 and 0.50% for CON, INORG, low and high ORG, and WDGS, respectively. A laboratory procedure was developed to estimate RDS coefficients for individual ingredients, and used as base for the RDSI calculations. Samples (1.5 g of DM) were incubated (26 h) in triplicate with 75 mL of ruminal fluid (heifers [n = 2; BW = 320 kg] fed 60% corn base diets) and 75 mL of McDougall's Buffer. After incubation, bottles were cooled in ice, centrifuged (18,623 g; 20 min; 4°C), decanted, and the precipitate was dried at 100°C and analyzed for S. Standards containing 25:75, 50:50 and 75:25% of starch: solkafloc were used to estimate incorporated S due to bacterial growth, and subtracted from the other samples based on digestibility coefficients. Statistical analyses were conducted using the GLIMMIX procedure of SAS, with day as a repeated measure for RDSI, pH and [H_2S]. The TSI were 21.9, 37.0, 34.0, 50.5 and 54.9 g/d (SEM = 1.89) and RDSI were 16.5, 32.1, 19.9, 24.4 and 36.2 g/d (SEM = 1.06) for CON, INORG, low and high ORG, and WDGS diets, respectively ($P < 0.01$). The RDSI was able to explain 64.9% of the [H_2S] variation through a linear (y = −34.74 + 2.36 * RDSI) relationship ($P < 0.01$), whereas TSI explained only 24.4%. When area below pH 5.6 was added to the RDSI model it accounted for 3.5 more percentage units of the [H_2S] variation. Availability of S for ruminal fermentation provides an important tool for ruminal [H_2S] prediction; more than total S intake or ruminal pH.

Key words: hydrogen sulfide, intake, ruminal degradable sulfur

413 Effects of trace mineral injections on measures of growth and trace mineral status of pre-weaned beef calves. J. D. Arthington*[1] and L. J. Havenga[2], *[1]University of Florida, Range Cattle Research and Education Center, Ona, [2]Multimin USA Inc., Fort Collins, CO.*

The objective of this experiment was to determine the effects of injectable trace minerals (ITM) on measures of trace mineral status and performance in pre-weaned beef calves. Brahman x Angus beef calves were assigned to treatment in alternating birth order (n = 75 calves/treatment). Treatments consisted of 1 mL s.c. of ITM (MultiMin 90; MultiMin USA, Inc., Fort Collins, CO) or 1 mL of sterile saline. The ITM product contained 60, 10, and 15 mg/mL of Zn, Mn, and Cu, as disodium EDTA chelates, and 5 mg/mL of Se, as Na selenite. Treatments were re-administered to all calves 2 additional times before weaning (approximately 100 and 200 d of age) for a total of 3 treatment administrations. Calves were weaned at approximately 250 d of age. Throughout the study, cow and calf pairs grazed summer bahiagrass pastures with free choice access to a salt-based mineral premix containing 14% Ca, 9% P, 24% NaCl, 0.20% K, 0.30% Mg, 0.20% S, 0.005% Co, 0.15% Cu, 0.02% I, 0.05% Mn, 0.004% Se, 0.3% Zn, 0.08% F, and 82 IU/g of vitamin A. Individual calf body weight was recorded at birth (d 0) and on d 100, 150, 200, and 250 (weaning). Trace mineral status of calves was assessed in liver biopsy samples (n = 12 heifers/treatment) collected on d 150, 200, and weaning (d 250). Liver samples were analyzed for concentrations of Co, Cu, Fe, Mn, Mo, Se, and Zn. Individual calf was the experimental unit. Administration of ITM had no impact on calf BW gain (average = 0.79 kg/d; SEM = 0.015). Although bull calves were heavier ($P < 0.001$) at birth compared with heifers (35.4 vs. 30.8 kg; SEM = 0.73), there were no gender x treatment interactions. Trace mineral status of calves was nutritionally adequate for both treatments on all sampling dates; however, administration of ITM resulted in greater ($P \leq 0.02$) overall average concentrations of liver Cu and Se and a lesser ($P = 0.05$) liver Fe concentration compared with saline-injected calves. In summary, injectable trace minerals administered to mineral-adequate, pre-weaned beef calves, provided greater liver Cu and Se concentrations, but did not impact ADG, compared with saline-injected control calves.

Key words: beef, calves, trace minerals

414 Effect of chromium supplementation on finishing Nellore bulls performance, carcass characteristics, and liver abscesses. R. S. Marques[1], A. M. Pedroso*[2], C. T. S. Dias[1], L. R. M. Pinto[1], and F. A. P. Santos[1], *[1]University of Sao Paulo, College of Agricultural Sciences, Piracicaba/SP, Brazil, [2]Embrapa Cattle Southeast, Sao Carlos/SP, Brazil.*

This trial was designed to determine the effects of increasing organic chromium levels on performance of finishing Nellore bulls fed rations containing (DM%) 16.7% sugar cane bagasse, 69.97% fine ground corn, 9.73% soybean meal, 1.01% urea, 2.58% mineral and vitamin mix, and 30mg/kg of monensin. Four treatments were compared: 0; 0.2; 0.4 or 0.6 mg/kg DM of organic chromium. Two hundred and 30 7 Nellore bulls (337 kg initial BW) allotted in 40 pens (10 pens/treatment) were used in a complete randomized blocks design. Parameters evaluated were dry matter intake (DMI), average daily gain (ADG), feed efficiency (ADG/DMI), hot carcass weight (CW), fat thickness (FT), rib eye area (REA) and liver abscesses. Data were analyzed using PROC GLM of SAS. Dry matter intake, average daily gain, feed efficiency, hot carcass weight, fat thickness and rib eye area were not affected by treatments. Incidence of liver abscesses was negligible.

Table 1. Dry matter intake (DMI), average daily gain (ADG), feed efficiency (ADG/DMI), hot carcass weight (CW), fat thickness (FT) and rib eye area (REA)

	Cr, mg/kg DM					
	Control	0.2	0.4	0.6	*P*-value	SEM
ADG (kg/d)	1.54	1.48	1.50	1.50	0.8889	0.042
DMI (kg/d)	9.41	9.74	9.58	9.69	0.5893	0.179
ADG/DMI	0.165	0.156	0.157	0.158	0.4699	0.014
CW (kg)	277.58	260.49	278.96	279.97	0.1581	6.81
REA (cm^2)	71.27	71.34	70.85	70.38	0.7176	0.761
FT (mm)	5.05	5.24	5.19	5.20	0.9235	0.177

Key words: additives, chromium, feedlot

415 Meta-analysis of the effect of dietary sulfur on feedlot health. C. A. Nichols*[1], V. R. Bremer[1], A. K. Watson[1], C. D. Buckner[1],

J. L. Harding[1], D. R. Smith[2], G. E. Erickson[1], and T. J. Klopfenstein[1], *[1]Department of Animal Science, University of Nebraska-Lincoln, Lincoln, [2]School of Veterinary Medicine and Biomedical Sciences, University of Nebraska-Lincoln.*

A meta-analysis of University of Nebraska-Lincoln (UNL) finishing trials was conducted to evaluate the effect of dietary sulfur and other dietary components on feedlot health. Health outcomes included polioencephalomalacia (PEM), bovine respiratory disease, infectious pododermatitis (foot rot), and, ruminal tympany (bloat). Likewise, ruminal degradable sulfur (RDS) concentration is proposed as an alternative to S concentration, with degradability assigned to feed ingredients similar to protein degradability. The effect of RDS on PEM was also evaluated. The analysis used Poisson regression to evaluate health records and diet information from 17,080 cattle from 69 feeding trials conducted within an 8 year time period in the UNL research feedlot and included only finishing periods. There was no significant relationship ($P > 0.05$) between dietary sulfur level and footrot (n = 484 cases), and, bloat (n = 21 cases). An interaction between dietary sulfur and forage NDF ($P < 0.01$) affected the incidence of PEM cases. For a given level of forage NDF, the incidence of PEM increased as dietary sulfur concentration increased in the diet; however, for a given dietary sulfur concentration, the relative risk for PEM decreased as forage NDF increased. Also, in this multivariable model cattle diagnosed with respiratory disease were more likely to be diagnosed with PEM ($P = 0.02$). A significant relationship was detected between RDS and PEM ($P < 0.01$). As RDS as a % of DM increased in the diet, the incidence of PEM increased. Unlike total dietary sulfur, there was no significant interaction between RDS and forage NDF ($P = 0.12$). In this multivariable model, increasing forage NDF decreased the risk for PEM. Conversely, respiratory disease diagnosis increased the risk but the cause and effect are unclear. Increasing total dietary sulfur, or increasing RDS increased the incidence of PEM in feedlot cattle. Model fit and lack of forage NDF interaction support that using RDS is likely a better predictor of PEM.

Key words: distillers grains plus solubles, polioencephalomalacia, sulfur

416 Effect of delaying the feeding of high sulfur diets to feedlot cattle until after adaptation to a finishing diet. M. E. Drewnoski* and S. L. Hansen, *Iowa State University, Ames.*

Elevated concentrations of dietary sulfate have been shown to decrease intake and reduce gain of cattle and can lead to a neurological disorder called polioencephalomalacia (PEM). Sulfate is reduced by ruminal bacteria to toxic hydrogen sulfide (H_2S). Both the incidence of PEM and ruminal concentrations of H_2S in feedlot cattle appear to be greatest during the first 30 d on a full finishing diet. We hypothesized that delaying exposure to high sulfate diets until cattle are fully adapted to a high concentrate diet would reduce the peak ruminal H_2S concentration and thus reduce potential for toxicosis. Sixty Angus crossbred steers (386 kg SE ± 13) were blocked by weight and randomly assigned to 1 of 12 pens and one of 3 dietary treatments, including 1) a control diet (0.3% sulfur) fed throughout the trial (C), 2) a high S diet (0.6% sulfur) fed throughout the trial (HS), or 3) the control diet fed during the transition period and for the first 28 d of the finishing period then switched to HS diet for the reminder of the trial (DS). Rumen H_2S concentrations and pH of 2 steers per pen were measured 6 h after feeding on d 1, 7, 14, 28, 35, 42, 56 and 70 of finishing. Ruminal pH did not differ due to treatment ($P = 0.79$) but was greater ($P < 0.05$) on d 56 (5.85) compared with previous days (5.57). Peak H_2S concentration of DS (3425 ppm) occurred on d 56 (28 d on HS diet) but was lower ($P < 0.05$) than peak H_2S for HS (5288 ppm) which occurred on d 7. Peak H_2S of the C (2583 ppm) occurred on d 7 and did not differ ($P = 0.23$) from the peak of DS but was less ($P < 0.05$) than HS. Sulfur intake (39.3 g/hd) of C at peak H_2S was less ($P < 0.01$) but DM intake (13.0 kg/hd) of C was greater ($P < 0.01$) than DS (66.8 g/hd; 12.7 kg/hd) and HS (65.7 g/hd; 10.8 kg/hd) at peak H_2S. Sulfur and DM intake of DS did not differ ($P > 0.60$) from HS at peak H_2S. These data suggest that potential for toxicosis was reduced by delaying feeding of high S diets until after steers had received a high concentrate finishing diet for 28 d.

Key words: cattle, hydrogen sulfide, sulfur

417 Effects of zinc and copper source and concentration on feedlot performance and carcass characteristics in yearling steers. M. G. Dib*[1], J. J. Wagner[1], K. Perryman[2], J. W. Spears[3], and T. E. Engle[2], *[1]Colorado State University, Fort Collins, [2]Micronutrients, Indianapolis, IN, [3]North Carolina State University, Raleigh.*

Crossbred steers (n = 288; initial BW = 320 kg ± 10.2) were used in a randomized complete block design to evaluate the effect of source and concentration of Zn and Cu on live performance and carcass characteristics. Steers were blocked by weight and randomly assigned to one of the 4 treatments (8 pens per treatment). Treatments included: 1) 90 ppm of Zn from ZnSO4 and 15 ppm of Cu from CuSO4 (Control, 100% sulfate); 2) 67.5 ppm of Zn from ZnSO4 plus 22.5 ppm of organic Zn and 11.25 ppm of Cu from CuSO4 plus 3.75 ppm of Cu from organic Cu (Organic, 75% sulfate, 25% organic); 3) 90 ppm of Zn from tetra-basic ZnCl and 15 ppm of Cu from tri-basic CuCl (100% Hydroxy); and 4) 54 ppm of Zn from tetra-basic ZnCl and 9 ppm of Cu from tri-basic CuCl (reduced Hydroxy, 60%). All steers were fed a typical high concentrate steam flaked corn based finishing diet twice daily. Steers were individually weighed on d −1, 0, 35, 70, 104, 173 and 174. On d 175, steers were transported to a commercial abattoir for slaughter. Initial and final BW, average daily gain, dry matter intake, and gain-to-feed were similar ($P > 0.10$) across treatments and averaged 318.9 kg, 586.5 kg, 1.54 kg/hd/d, 8.80 kg/hd/d, and 0.1753, respectively. Furthermore, hot carcass weight, subcutaneous adipose depth, Longissimus muscle area, calculated YG, marbling score and dressing percentage were similar ($P > 0.10$) across treatments. There was a trend ($P < 0.12$) for treatment to affect the likelihood that an individual carcass within each pen would grade USDA average Choice or higher (7.1, 9.7, 19.7, and 16.4% for the Control, Organic, Hydroxy 100, and Hydroxy 60 treatments, respectively). Results suggest that supplementing Zn and Cu from tetra-basic ZnCl and tri-basic CuCl at 60% of the level provided from sulfate or a sulfate-organic mixture will result in similar performance and carcass characteristics. Further research is necessary to determine the response of different amounts of tetra-basic ZnCl and tri-basic CuCl in finishing diets on cattle performance and carcass merit.

Key words: trace mineral source, tetra-basic zinc, tri-basic copper

418 Effects of supplemental copper and Linpro on performance and carcass characteristic of beef heifers. C. A. Alvarado*, C. C. Aperce, K. A. Miller, C. L. van Bibber, S. Uwituze, and J. S. Drouillard, *Kansas State University, Manhattan.*

Crossbred yearling heifers (n = 261; 351 ± 23 kg initial BW) were used in a randomized complete block experiment with a 2 × 2 factorial treatment arrangement to evaluate effects dietary copper (10 or 100 mg/kg

added copper) and Linpro (0 or 10% of diet DM) on feedlot performance and carcass traits. Linpro is an extruded blend of flaxseed and field peas containing added vitamins and minerals (22% CP; 23% fat). Heifers were blocked by initial BW into heavy and light groups and assigned randomly to experimental pens containing 10 or 11 heifers each. Pens (n = 24) were assigned randomly to each of the 4 treatments. Cattle were fed once daily and had ad libitum access to feed and water. Basal diets included (DM basis) 35% wet corn gluten feed, 35% dry-rolled corn, 15% pelleted soybean hulls, 10% corn silage, vitamins, and minerals, and provided 14% crude protein, 300 mg/d monensin, 90 mg/d tylosin, 2200 IU/kg vitamin A, 0.7% Ca, and 0.7% K. For Linpro treatments, the extrudate was added at 10% of the diet DM, replacing soybean hulls. Heifers were implanted (Revalor-200), dewormed (Safe-Guard), and vaccinated against common viral and clostridial diseases (Vista 3, Vision 7). Starting 23 d before harvest, zilpaterol was added to the diet for 20 d. Heavy and light blocks were harvested on d 117 and 132, respectively. There were no interactions between levels of copper and Linpro ($P > 0.10$), and copper level had no impact on performance or carcass traits ($P > 0.10$). Cattle fed Linpro treatments consumed less DM than their counterparts fed diets without (13.6 vs 14.1 kg/d; $P < 0.05$) and had greater gain efficiency (0.137 vs 0.129; $P < 0.01$), but there were no effects on ADG ($P > 0.05$). Carcass traits (HCW, LM area, KPH, 12th-rib fat thickness, marbling, and USDA quality and yield grades) were unaffected by diet ($P > 0.10$). Cattle fed Linpro had fewer severe (A+) liver abscesses ($P < 0.05$), but total incidence of liver abscesses was not different ($P > 0.10$). Results indicate that elevated copper levels do not impact performance or carcass traits of finishing cattle. Linpro can be used effectively as an energy source in finishing cattle diets.

Key words: copper, flaxseed, Linpro

419 Chromium supplementation alters the performance and health of feedlot cattle during the receiving period. B. C. Bernhard*[1], R. J. Rathmann[1], D. N. Finck[1], W. Rounds[2], and B. J. Johnson[1], *[1]Texas Tech University, Lubbock, [2]Kemin Industries Inc., Des Moines, IA.*

Crossbreed steers (n = 180; 230 ± 6 kg) were fed during a 56-d receiving period to determine if supplementing chromium (Cr; KemTRACE Chromium Propionate 0.04%, Kemin Industries) would improve feedlot performance and health of newly received cattle. A completely randomized block design (36 pens; 9 pens/treatment; 4 pens/block; 5 steers/pen) was used. Chromium premixes were supplemented to add 0 (Con), 0.1, 0.2, or 0.3 mg/kg of Cr to the total diet on a DM basis. Cattle were weighed every 14 d. Shrunk body weights, ADG, DMI, G:F, and number of times treated for morbidity (treated if rectal temperature ≥39.7°C) were recorded. Feedlot performance and morbidity data were analyzed as orthogonal contrasts in the MIXED and GLIMMIX procedure of SAS, respectively, with pen serving as the experimental unit. No differences were detected between treatments for BW, ADG, DMI, and G:F through the first 14 d ($P \geq 0.14$). From d 0 to d 28, DMI tended to linearly increase ($P = 0.07$) and ADG increased linearly ($P = 0.04$) as Cr levels increased. During the same period, BW and G:F showed a significant quadratic effect ($P \leq 0.05$) with 0.1 mg/kg being the least desirable and 0.3 mg/kg being the most accelerated. From d 0 to d 56, BW ($P = 0.08$) and DMI ($P = 0.12$) displayed a tendency to increase linearly, and consequently ADG and G:F increased linearly ($P \leq 0.05$) as Cr concentrations increased. Morbidity results showed a tendency ($P = 0.07$) for a linear decrease in the number of head treated at least once for respiratory symptoms as the Cr concentration was increased. The addition of 0.3 mg/kg of Cr resulted in the greatest performance advantages and reductions in the incidences of morbidity; and when specifically compared with the Con displayed an 8 kg improvement in BW ($P = 0.12$), 4.2% increase in G:F ($P = 0.10$), 10.8% enhancement on ADG ($P = 0.04$), and over 18% fewer cattle were treated at least once ($P = 0.05$). Results of this study indicate that supplementation of Cr to the basal diet can have beneficial effects on the performance and health of newly received steers during the first 56 d on feed.

Key words: chromium propionate, receiving cattle, feedlot performance

420 Chromium supplementation alters the glucose and lipid metabolism of feedlot cattle during the receiving period. B. C. Bernhard*[1], N. C. Burdick[2], R. J. Rathmann[1], D. N. Finck[1], J. A. Carroll[2], A. N. Loyd[2], and B. J. Johnson[1], *[1]Texas Tech University, Lubbock, [2]Livestock Issues Research Unit, USDA-ARS, Lubbock, TX.*

Crossbreed steers (n = 20; 235 ± 4 kg) were fed 53 d during a receiving period to determine if supplementing chromium (Cr; KemTRACE ChromiumPropionate 0.04%, Kemin Industries) would alter the glucose or lipid metabolism of newly received cattle. Chromium premixes were supplemented to add 0 (Con) or 0.2 mg/kg of Cr to the total diet on a DM basis. Cattle were fitted with jugular catheters on d 52. A glucose tolerance test (GTT) and an insulin sensitivity test (IST) were conducted on d 53 by infusing the steers with 1 mL of a 50% glucose solution/kg of BW (Dextrose 50%, Durvet, Inc.) at 0900 h and 0.1 IU of bovine insulin/kg of BW at 1400 h, respectively. Blood samples were collected at −60, −45, −30, −15, 0, 7.5, 15, 30, 45, 60, 90, 120, and 150 min relative to each infusion. Serum was isolated to determine glucose, insulin, and nonesterified fatty acid (NEFA) concentrations. Data were analyzed using the Mixed procedure of SAS specific for repeated measures with each steer serving as the experimental unit and fixed effects of treatment, time, and their interaction. Throughout the GTT no differences were detected in glucose concentrations or pre-infusion insulin concentrations ($P > 0.50$), but insulin concentrations post-infusion tended to be greater for the Cr steers ($P = 0.06$). In addition, NEFA concentrations during the GTT were lower ($P \leq 0.01$) for Cr steers both pre- and post-infusion. During the IST there was no treatment effect on glucose concentrations pre-infusion ($P = 0.38$), while post-infusion glucose concentrations were greater ($P < 0.01$) in the Cr steers. During the same test, there was no treatment effect detected for insulin concentrations ($P > 0.33$), but at 7.5 min there was a trend for the insulin concentrations of the Con steers to reach a higher peak ($P = 0.12$). Concentrations of NEFA were lower ($P < 0.01$) both pre- and post-infusion during the IST for Cr steers. Results of this study indicate that supplementation of Cr to the basal diet can alter insulin sensitivity and lipid metabolism of newly received steers during the first 53 d on feed.

Key words: chromium propionate, receiving cattle, glucose and lipid metabolism

Ruminant Nutrition: Dairy: Forages and Fiber

421 Milk production responses to soybean meal and canola meal in dairy cows fed grass silage based diets—A meta-analysis. P. Huhtanen*[1], M. Hetta[1], and C. Swensson[2], *[1]Swedish University of Agricultural Sciences, Umeå, Sweden, [2]Swedish Dairy Association, Lund, Sweden.*

Most feed protein evaluation predict a higher metabolizable protein (MP) for soybean meal (SBM) compared with canola meal (CM), but the data from production trials comparing SBM and CM have generally failed to prove this. A data set from production trials in which SBM, CM, heat-treated-CM (TCM) and a mixture of SBM and fishmeal (SFM) was collected from milk production trials. Prerequisites of the data to be included were that detailed information of diet composition, intake and milk production were reported and that the protein feeds were fed at least at 2 levels. Grass silage or mixtures of grass and whole-crop silages were used as forages and cereal grains (barley, oats and corn) were the major concentrate ingredients. The data set included in total 292 treatment means (122 comparisons) that were distributed as follows: SBM 46 (22), CM 120 (55) TCM 82 (29) and FSM 44. A mixed model regression analysis with random study effect was used to compare intake and production responses between the protein sources. Dietary CP concentration or intake of CP and ME were used as independent variables. All protein sources increased DMI, but the responses of 0.29 and 0.34 kg/1%-unit increase in dietary CP concentration was greater ($P < 0.01$) compared with SBM (0.11) with SFM displaying an intermediate response (0.20). Feeding CM or TCM produced greater ($P < 0.01$) milk yield responses than SBM (3.4 ± 0.19 and 3.7 ± 0.25 vs. 2.1 ± 0.25) per kg increase in CP intake. However, because of different DMI effects ECM responses to incremental ME intake were similar (0.16 to 0.18 kg ECM/MJ ME). Marginal milk protein yield responses (g/kg increase in CP intake) were greater ($P < 0.01$) with CM (136 ± 5.4) and TCM (133 ± 8.5) compared with SBM (988.0), but not when compared with SFM (125 ± 9.4). The difference between CM and SBM was even greater when expressed per kg MP predicted according to NRC (2001) system (381 ± 18 vs. 197 ± 17 g/kg MP). It is concluded that CM can be substituted for SBM on isonitrogenous basis without compromising milk production, and that MP systems tend to underestimate productive value of CM compared with SBM.

Key words: canola meal, milk production, soybean meal

422 Intake and milk production of dairy cows fed diets including low lignin/high fiber digestibility corn silage. N. B. Litherland*[1], H. G. Jung[1,2], and J. G. Linn[1], *[1]University of Minnesota, St Paul, [2]USDA-ARS, St Paul, MN.*

The objective of this study was to evaluate the effect of increasing digestible NDF content of lactating dairy cow diets on DMI and milk yield by feeding increasing proportions of low lignin (BMR) corn silage (CS). Control (B73) and BMR (B73bm3) inbred corn lines were ensiled in a poly-bag in September 2009. Silage pH was 3.8 for both silages and lactic-to-acetic acid ratio was 3.7:1 for control and 3.2:1 for BMR silages. Control and BMR CS, respectively, contained (DM-basis) 9.7 and 8.3% CP, 46.6 and 45.8% NDF, 2.9 and 2.6% lignin, and 15.8 and 17.7% starch. In vitro 48 h NDF digestibility was greater for BMR (72.1%) than control (57.0%) CS. Fifty Holstein and cross-bred dairy cattle producing 43.5 kg milk/d and 80 d in milk were assigned to 5 treatments. Diets included 0%BMR-100% Control (0BMR), 25%BMR-75% Control (25BMR), 50%BMR-50%Control (50BMR), 75% BMR-25%Control (75BMR), or 100%BMR-0%Control (100BMR) CS. All diets contained equal amounts of CS (43% of diet DM) and were balanced for 25 kg DMI and 43 kg of milk. Because the control CS contained less grain, more dry ground corn was added to the amount of control CS in the diets to keep starch equal. Diets contained 51.1% DM, 23.3% forage NDF, 17.2% CP, 19.0% ADF, 31.1% NDF and 24.5% starch. Cows were fed the diets for 56 d from February through April 2010. Data were analyzed using Proc Mixed in SAS as a completely randomized design with repeated measures and the least significant difference test was used for mean separations when main effects were significant ($P < 0.05$). DMI averaged 24.5 kg/d (SEM = 1.9) and was similar among diets (100BMR DMI was only 1.9 kg/d greater then 0BMR). Milk yield and 3.5%FCM yield averaged 48.6 kg/d (SEM = 2.1) and 37.1 kg/d (SEM = 1.8), and were similar among diets (100BMR averaged 1.7 kg/d greater milk yield than 0BMR). Dairy efficiency was not different and averaged 1.6 (SEM = 0.1). Milk fat and protein were similar among diets and averaged 3.2% (SEM = 0.1) and 3.1% (SEM = 0.1), respectively. Although BMR CS typically improves cow performance, in this trial greater in vitro digestibility of CS NDF did not enhance DMI or milk production.

Key words: corn silage, fiber, digestibility

423 Effects of supplementing starch or sugar pre-and postpartum to dairy cows fed TMR with wheat straw or grass hay prepartum: Performance, metabolism and health. N. B. Litherland*[1], L. Davis[2], S. Emanuele[2], and H. Blalock[2], *[1]University of Minnesota, St Paul, [2]Quality Liquid Feeds Inc., Dodgeville, WI.*

The objectives of this study were to determine if varying prepartum forage source and periparturient supplemental energy source affects periparturient performance and health. Sixty multiparous Holstein and crossbred cows were used in a completely randomized design with 4 treatments:1) Wheat straw (WS) prepartum (12.5% CP, 42.2% NDF, and 1.4 Mcal/kg NEL) + corn pre and postpartum (WSC), 2) WS prepartum (12.7% CP, 41.8% NDF, and 1.4 Mcal/kg NEL) + molasses-based Liquid Feed (LF) pre and postpartum (WSL), 3) Grass hay (GH) prepartum (13.8% CP, 37.8%NDF, and 1.5 Mcal/kg NEL)+corn pre and postpartum (GHC), 4) GH prepartum (13.9% CP, 37.4%NDF, and 1.5 Mcal/kg NEL) + LF pre and postpartum (GHL). Prepartum dietary treatments were initiated at dry off and postpartum diets were fed from parturition through 56 d in milk. After calving, cows were fed one of 2 diets formulated to support 45 kg/d of 3.5% FCM. The LF diets provided 2.7% of diet DM prepartum as supplemental sugar, and 1.5% postpartum. Data were analyzed using PROC MIXED in SAS as a randomized design with 4 treatments. WSC and GHC tended ($P = 0.08$) to consume more starch and WSL and GHL cows consumed more ($P < 0.05$) sugar. For WSC, WSL, GHC, and GHL treatments, prepartum DMI averaged 13.3, 12.8, 15.0 and 13.6 kg/d (SEM = 0.9; $P = 0.45$), postpartum DMI averaged 20.1, 17.8, 21.0 and 18.8 kg/d (SEM = 1.0; $P = 0.15$), yield of 3.5% FCM averaged 45.8, 45.2, 43.1 and 44.2 kg/d (SEM = 1.7; $P = 0.71$), and dairy efficiency (kg 3.5% FCM/kg DMI) averaged 2.4, 2.6, 2.2, and 2.4 (SEM = 0.1; $P = 0.27$), respectively. Yield and percentage of fat and protein were similar. There were no differences in prepartum or postpartum condition score or body weight loss. Prepartum energy balance tended ($P = 0.06$) to be higher for WSC and GHC compared with WSL and GHL. Prepartum serum NEFA were higher for WSL and GHL (SEM = 18.9; $P < 0.05$) and averaged 85.5, 177.1, 92.2, and133.1μ/mL for WSC, WSL, GHC,

and GHL. In conclusion, cows fed diets varying in energy and forage source performed similarly during the periparturient period.

Key words: energy source, forage, transition cow

424 Alternative models of kinetics impact indigestible neutral detergent fiber and estimates of ruminal digestibility. D. R. Mertens*, *Mertens Innovation & Research LLC, Belleville, WI.*

This project evaluated the interactions among models of digestion kinetics and methods of estimating indigestible NDF (iNDF) on steady-state predictions of ruminal digestibility. In vitro fermentations > 96 h suggest that some forages may have 2 pools of potentially digestible NDF. A sequential multi-pool equation was used to simulate digestion curves from known inputs (indigestible fraction = 0.2 or 0.4 of NDF; slowly digestion fraction = 0.3, 0.2, or 0.1 of NDF; lag rate = 0.25/h; fast and slow digestion rates = 0.06, 0.12, or 0.18 and.012, 0.008 or 0.004/h) that mimic typical digestion kinetics of alfalfa (A) and grass (G) forages. Kinetic parameters were estimated from simulated data using SAS NLIN for a 2-pool model (discrete lag, single digestible and iNDF pools) using results for 3, 6, 9, 12, 18, 24, 36, 48, 60 and 72 h; and for a 3-pool model (discrete lag, rapidly and slowly digesting and iNDF pools) using results for 6, 12, 24, 48, 72, 96, 120, 144, 192 and 240 h. Fitting a 2-pool model to simulated 3-pool digestion curves resulted in compromised estimates of rates of digestion and iNDF. The 2-pool model generated iNDF that were 1.3 (A) and 1.6 (G) larger than the known iNDF; whereas, rates of digestion were 0.63 (A) and 0.67 (G) of the known fast digestion rate. The 2-pool kinetic parameters resulted in ruminal digestibilities that were 0.95 of the known calculated values for A and G. For a 2-pool model, iNDF is estimated most closely by 72 h measurements. Even with no random variation and long fermentation times, fitting the 3-pool model generated iNDF pools that were 0.88 (A) and 0.85 (G), and fast and slow digestion rates that were 0.7 to 0.8 of the known values. The 3-pool model resulted in ruminal digestibilities that were 0.98 of the true values for A and G. At 240 h, the residue was 1.1 to 1.2 larger than the known iNDF. It was concluded that adding a second slowly digesting pool to describe NDF digestion results in improvements in the estimation of ruminal fiber digestion that are small in relation to the variation among in vitro measurements and kinetic parameters using nonlinear estimation.

Key words: digestion kinetics, rate, indigestible fiber

425 Comparison of alternative methods, sample grinds, and fermentation times for determining indigestible neutral detergent fiber. J. Boyd*[1] and D. R. Mertens[2], *[1]US Dairy Forage Research Center, Madison, WI, [2]Mertens Innovation & Research LLC, Belleville, WI.*

The objectives of this study were to evaluate the effects of sample grind, fermentation method, and time on the determination of indigestible neutral detergent fiber (iNDF). Samples of alfalfa hay and silage; corn stalks and silage; and ryegrass and mixed grass hays were ground through 2-mm and 1-mm screens in a cutter mill and 1-mm screen in a cyclone mill. Both 1-mm ground samples were fermented in flasks (in vitro, IV) or in F57 filter bags in a rotating jar system for 0, 48, 72, 96, or 144 h. In situ (IS) samples were fermented for 0, 48, 72, 96, 144, 240, and 288 h in animals fed either TMR, alfalfa silage, or grass hay, and these same donors were used to make a composite inoculum for the in vitro and rotating jar fermentations. For in situ, 2-mm samples were fermented in Ankom in situ bags and 1-mm cyclone samples were fermented in F57 filter bags. Fermentation residues were extracted in neutral detergent using crucibles with silica sand for IV or using the A200 fiber analyzer for all bags. Only samples fermented for > 96 h were evaluated as estimates of iNDF. Data were analyzed using Proc MIXED of SAS with run within method and repetition within run as random variables. Across all samples, 288 h IS obtained the smallest iNDF for the 1- and 2-mm grinds, and they were not different ($P < 0.05$) from 1- and 2-mm grinds of 240 h IS or from both 1-mm grinds for 144 h IV. Bags appeared to impede measurement of iNDF. At 144 h, the IV results of both grinds were lower ($P < 0.05$) than both grinds in F57 bags in the rotating jar system and the 1-mm cyclone grind in F57 bags fermented IS. The 2-mm grind fermented in IS bags at 144 h IS were not different from IV results at 144 h. In general, IS fermentation took nearly twice as long to obtain iNDF similar to IV results. Differences in iNDF among treatments were greater for more slowly fermenting substrates (corn stalks and mixed grass hay). In summary, measurement of iNDF is affected by time and fermentation system, but less so by grinding through 1- or 2-mm screens.

Key words: Indigestible fiber, digestion kinetics, in vitro, in situ

426 Effects of daily ingredient dry matter adjustment of total mixed ration using Intelligent Ration Monitoring (IRM) NIR forage analyzer on commercial dairy farm performance. D. N. L. da Silva*[1], A. Barbi[2], A. Ghiraldi[2], D. Allen[3], and N. B. Litherland[1], *[1]University of Minnesota, St Paul, [2]Dinamica Generale, Poggio Rusco, Italy, [3]Gar-Lin Dairy, Eyota, MN.*

The objectives of this study were to determine the effects of daily adjustment of ingredient dry matter (DM) using a near-infrared reflectance (NIR) IRM (Intelligent Ration Monitoring) system on diet composition, dry matter intake (DMI), and milk and component yield. We hypothesized that daily mechanical adjustment of DM would reduce TMR DM variability and improve dairy efficiency (DE) compared with conventional ingredient DM adjustment (weekly hand sampling). Five hundred dairy cows in 2 pens (n = 250) on a commercial dairy were used in a crossover design with 9 week periods. Pens were balanced by milk yield (52.9 and 51.8 kg/cow/d) and days in milk (110.5 and 111.8). Two dietary treatments: (Control) weekly correction of ingredient DM of corn silage, alfalfa silage and high moisture corn by drying for 12 h 100C oven; (IRM) the IRM system scanned individual ingredients and adjusted DM at each feeding. Diets had the same composition and only varied by method of DM adjustment. Cows were fed twice and milked 3 times daily. Data were analyzed using Proc Mixed in SAS with repeated measures when appropriate and PDIFF used for mean separation when main effects were significant ($P < 0.05$). Control and IRM TMR DM averaged 45.9 and 46.0% (SEM = 0.83;P = 0.93). TMR starch, CP, ADF and NDF were similar. Nutrient composition of TMR refusals was not different. DMI per cow averaged 26.5 and 26.9 kg/d (SEM = 1.3; $P = 0.7$). DM refusal %/cow/d averaged 5.0 and 4.7 (SEM = 1.5; $P = 0.6$). Milk and 3.5% FCM yield averaged 52.9 and 52.8 (SEM = 1.3; $P = 0.9$) and 56.5 and 54.6 (SEM = 2.3; $P = 0.1$) for control and IRM. Percent milk protein was higher (2.9 vs. 3.0 SEM = 0.2) (Trt × week; $P < 0.05$) for IRM but protein yield was similar between treatments. Milk fat % and yield averaged 3.8 and 3.7 (SEM = 0.2; $P = 0.7$) and 2.0 and 1.9 kg/d (SEM = 0.1; $P = 0.3$) for control and IRM. DE averaged 2.2 and 2.0 (SEM = 0.1; $P = 0.1$) for control and IRM. IRM cows performed as well as those fed using traditional DM adjustment.

Key words: NIR, precision feeding, dry matter

427 Effects of prepartum supplementation of starch or sugar to dairy cows fed TMR with thirty percent wheat straw or grass hay on colostrum yield and composition. N. B. Litherland*[1], L. Davis[2], S. Emanuele[2], and H. Blalock[2], *[1]University of Minnesota, St Paul, [2]Quality Liquid Feeds Inc., Dodgeville, WI.*

Sixty multiparous Holstein and crossbred cows, balanced by 305ME and parity, were used in a completely randomized design (CRD) with 4 prepartum treatments: 1) Wheat straw (WS) + corn (WSC) (12.5% CP, 42.2% NDF, 20.1% starch, 3.6% sugar and 1.4 Mcal/kg NEL), 2) WS + molasses-based Liquid Feed (LF) (WSL) (12.7% CP, 41.8%NDF, 18.7% starch, 6.3% sugar and 1.4 Mcal/kg NEL), 3) Grass hay (GH) + corn (GHC) (13.8% CP, 37.8%NDF, 20.1% starch, 5.1% sugar and 1.5 Mcal/kg NEL), 4) GH + LF (GHL) (13.9% CP, 37.4%NDF, 18.7% starch, 7.9% sugar and 1.5 Mcal/kg NEL). The LF diets provided 2.7% of diet dry matter as supplemental sugar. Prepartum diets were formulated to meet NRC, 2001 recommendations at 28 kg DMI/d. Treatments were fed from dry-off until calving; 41 d SEM = 2.0. Data were analyzed using Proc Mixed in SAS as a CRD and PDIFF used for mean separation when main effects were significant ($P < 0.05$). WSC and GHC tended ($P = 0.08$) to consume more starch and WSL and GHL cows consumed more ($P < 0.05$) sugar prepartum. DMI averaged 13.3, 12.8, 15.0 and 13.6 kg/d SEM = 0.9; $P = 0.45$). Calf birth weight averaged 46.1, 48.3, 49.1, 48.0 kg ($P = 0.91$; SEM = 3.0). First-milking colostrum yield averaged 9.2, 9.6, 9.0, and 10.9 kg for WSC, WSL, GHC, and GHL ($P = 0.67$; SEM = 1.6). Among treatments, 13.3% of cows produced <5.0 kg of colostrum. Pearson correlation for colostrum yield, prepartum intake of DM, OM, CP, NDF, ADF, starch, and DMI one week prepartum were not significant. Colostrum yield tended to be positively correlated with prepartum sugar intake ($P = 0.07$). Colostrum DM % tended to be higher for WSL compared with WSC ($P = 0.07$; SEM = 1.2) and averaged 26.6, 31.1, 30.8, and 28.3 for WSC, WSL, GHC, and GHL. Colostrum minerals were analyzed using inductively coupled plasmid analysis. Colostrum mineral yield was similar and averaged (SEM) 25.4g (3.7) Ca, 21.6 g (3.1) P, 3.8 g (0.6) Mg, 15.7 g (2.3) K, 15.0 g (2.0) S, and 6.7 g (1.0) Na. Prepartum sugar intake, colostrum yield and composition should be further explored.

Key words: transition cow, colostrum, sugar

428 Effects of corn gluten feed and effective NDF on ruminal pH and productivity of lactating dairy cattle. M. L. Sullivan*[1], K. N. Grigsby[2], and B. J. Bradford[1], *[1]Department of Animal Science and Industry, Kansas State University, Manhattan, [2]Cargill Incorporated, Blair, NE.*

Corn gluten feed (CGF), a by-product of the wet milling industry, is commonly substituted in lactating dairy rations for corn, corn silage, and alfalfa hay. Previous research at Kansas State University showed that increasing CGF in the diet decreased ruminal pH. The objective of this study was to maintain at least 10% of particles ≥18 mm in length across diets. We hypothesized that as CGF increased in the diet, DMI and milk yield would increase while ruminal pH would be maintained. Seven ruminally cannulated, lactating Holstein cows (4 multiparous, 3 primiparous) were used in an incomplete 4 × 4 Latin square design. Treatments included 0, 11, 23 or 34% CGF while utilizing alfalfa to maintain particle size. Four 21 d periods were used with 17 d of adaptation and 4 d of sample collection. Free floating ruminal pH probes were utilized during sampling periods and recorded pH every 5 min. Particle size of TMR and orts were analyzed using a Penn State Particle Separator. Across treatments CP and NDF were held constant. Results were analyzed with mixed models to test the fixed effect of treatment. All diets contained >10% of particles ≥18 mm; however, as CGF increased, the percent of particles ≥18 mm significantly ($P = 0.01$) decreased. Interestingly, with increasing CGF, cows sorted for the particles ≥18 mm ($P = 0.03$) while sorting against particles on the bottom screen ($P = 0.002$) and pan ($P = 0.01$). With increasing CGF, ruminal pH was not affected, yet DMI ($P = 0.02$) and milk yield ($P = 0.02$) significantly increased in a quadratic fashion with peak response for the 23% diet. Milk protein, lactose and fat percentages were not affected; however, milk protein ($P = 0.004$) and lactose ($P = 0.02$) yields showed a significant increase as a result of the increased milk production. Additionally, efficiency was not affected by the treatments as there were no differences in ECM/DMI. Thus it was demonstrated that if minimal particle size is maintained as CGF increases in the diet, DMI and milk yield increase while maintaining ruminal pH.

Key words: corn gluten feed, ruminal pH, particle size

429 Feeding forage cubes to identify divergence for residual feed intake in dairy cows. G. C. Waghorn*[1], K. A. Macdonald[1], S. R. Davis[2], and R. J. Spelman[3], *[1]DairyNZ, Hamilton, New Zealand, [2]Via-Lactia Biosciences, Auckland, New Zealand, [3]Livestock Improvement Corporation, Hamilton, New Zealand.*

Selection for divergence between individuals for efficiency of feed utilization (residual feed intake, RFI) has widespread application in the beef industry and is usually undertaken when animals are fed diets based on silages with grain. The objective of this research was to develop a feeding system (using Gallagher, Hamilton, New Zealand, electronics) and measure RFI for growth in Holstein/Friesian heifers (aged 5–9 mo), and evaluate divergent individuals for RFI for lactation. A forage diet (alfalfa cubes) was fed because the New Zealand dairy industry (4.4 milking cows in lactation) relies heavily on forage feeding. Genetic markers will be identified for the trait. The evaluation was undertaken over 3 years with 1052 animals fed in a facility for 6 weeks, and weighed 3 x weekly. The mean age at entry was 170 d, BW 171 kg, and mean daily dry matter (DM) intakes averaged 7.9 kg. BW gain (all animals) averaged 0.88 kg/day. RFI was determined as the residuals from the regression of mean intake on mean $BW^{0.75}$ and daily BW gain of individuals. Actual and fitted intakes were strongly related (R2 = 0.82). In terms of gross efficiency (feed intake/BW gain), RFI + year explained 43% of the variation, BW gain + year, 66% and RFI + BW gain + year 79% of variation (all $P < 0.001$). Daily BW gains (kg) of the most and least efficient 10% averaged 0.88 sd 0.15 and 0.88 sd 0.12 ($P = 0.568$) respectively, and the divergence between mean intakes was 1.72 kg DM/d. Comparable values for the most and least efficient 5% were 0.86 sd 0.15 and 0.90 sd 0.12 kg/d respectively ($P = 0.067$), and the divergence in mean intakes was 2.24 kg DM/d. Justification for using RFI for gain in peri-pubertal heifers to identify divergence for lactation was based on the biochemical bases of efficiency for production (milk or meat) and maintenance, and the high proportion of dietary energy used for maintenance in growing cattle and over a cows lifetime. The selection is currently being evaluated in lactating cows.

Key words: residual feed intake, forages, divergence

430 A mathematical model to predict the size and rate of digestion of a fast and slow pool of NDF and the indigestible NDF. E. Raffrenato*, C. F. Nicholson, and M. E. Van Amburgh, *Cornell University, Ithaca, NY.*

Many models that predict rate and extent of digestion of neutral detergent fiber (NDF) in the rumen assume first-order processes, in which the rates of digestion and passage are proportional to the mass of NDF in the rumen. Our objective was to improve the prediction of digestible NDF and to quantify, using a minimum of fermentation points, 2 pools of potentially digestible NDF, pdNDF1 and pdNDF2, and their respective rates. Based on fermentations from 0 to 240 h among 34 forages (grasses, conventional and bmr corn silages, alfalfas) 3 pools were described by NDFt = pdNDF1 * $e^{-k1(t-L)}$ + pdNDF2 * $e^{-k2(t-L)}$ + iNDF, where NDFt is the residue at time t; L is the lag; k1 is the rate of digestion of pdNDF1; k2 is the rate of digestion of pdNDF2; and iNDF the indigestible NDF on NDF basis. A non-linear estimation allowed the computation of the pool sizes and respective rates. Using 3 points on the degradation curve, with 240 h as the proxy for iNDF, we optimized the same model in Vensim® (Ventana Systems Inc., Belmont, MA, 2005) to obtain rates and pools. In addition, the same optimization was also performed with 2 points and a forage group-specific range for iNDF. Parameters (with and without iNDF) obtained per forage were compared with kinetics data from the non-linear estimation, using R^2 and RMS at convergence for ranking purposes, for the whole equation, and RMSE and MSPE. The highest R^2 (0.98) and lowest RMS (0.0010) were obtained when using 48, 120 and 240 h of NDF residual or when using 30 and 120 h and a range for the forage group-specific iNDF (R^2 = 0.92; RMS = 0.0021). Correlations were in both cases consistently high for all parameters (r = 0.76 to 0.99). Results demonstrate that a better description of the heterogeneity of NDF disappearance is possible with a minimum of fermentation time points. Due to the variable nature of the pool sizes and rates, forage specific equations should be developed for better estimations of the forage specific characteristics and iNDF estimation.

Key words: modeling, NDF digestibility, rate of digestion

431 Rates of particle size reduction and passage are faster for legume compared to C3 grass resulting in lower rumen fill and less effective fiber. K. L. Kammes* and M. S. Allen, *Michigan State University, East Lansing.*

Rates of particle size reduction in, and passage from, the rumen were evaluated for diets containing legume (alfalfa, A) or C3 grass (orchardgrass, O) silages as the sole forage using 14 ruminally and duodenally cannulated cows. The experiment was a crossover design with 2 18-d treatment periods. Silages were chopped to 1 cm theoretical length of cut and contained 42.3 and 58.2% neutral detergent fiber (NDF) for A and O, respectively. Both diets contained 25% forage NDF and 30% total NDF. Feed, orts, rumen, and duodenal samples were wet sieved to fractionate particles above (large, L) and below (small, S) 2.36 mm. Indigestible NDF (iNDF), determined by 240 h in vitro fermentation, was used as a flow marker. Milk yield (36 kg/d), milk components, and dry matter intake (24 kg/d) were similar for A and O ($P > 0.10$). Particle size distributions of NDF consumed (75% L and 25% S) were similar for both treatments, but iNDF (% of total NDF) consumed was much greater for A compared with O (54.2 vs. 27.4%, $P < 0.0001$). Rumen pools of L NDF, total NDF, and dry matter (3.2 vs. 4.4 kg, 6.2 vs. 6.8 kg, and 10.6 vs. 12.6 kg, respectively; $P < 0.05$) and total rumen contents wet weight and volume (83 vs. 93 kg and 98 vs. 109 L, respectively; $P < 0.01$) were smaller for A compared with O. Ruminating time per kg forage NDF consumed was 7% greater for O than A ($P < 0.05$). Rate of reduction of iNDF from L to S was greater for A than O (5.7 vs. 3.1%/h, $P < 0.0001$) as was rate of passage of iNDF and potentially digestible NDF in S (6.3 vs. 4.9%/h, $P < 0.05$). The proportion of NDF in the rumen below the threshold for passage (S) was 62.9 and 55.3% for A and O, respectively. However, the rate of passage of iNDF in S was positively correlated with the rate of reduction of iNDF from L to S for A ($P < 0.05$) but not for O ($P = 0.56$). Faster rate of passage of S for A suggests less selective retention because of a smaller rumen pool of L NDF for A compared O. Although particle size reduction is a prerequisite to passage, it is less of a constraint to passage for C3 grass compared with legume.

Key words: particle size, passage kinetics, rumen fill

432 Individual variability of NDF intake and feed conversion efficiency in pasture-based systems. S. C. Garcia*[1], F. Bargo[2], and R. K. Jhajj[1], [1]*The University of Sydney, Camden, NSW, Australia,* [2]*Elanco Animal Health Southern Cone (Argentina & Chile), Buenos Aires, Argentina.*

Mean daily intake and milk yield data of lactating Holstein-Friesian dairy cows from 7 studies (mostly grazing) conducted in USA, Australia and New Zealand were combined to quantify the variability in neutral detergent fiber intake (NDFI) and its relationship with feed conversion efficiency in pasture-based systems. Intake of grazing cows was estimated by external markers. Within study, data from individual cows were classified according to milk yield level (low, medium or high) to avoid confounding effects with study of origin. Data were analyzed using a mixed-effects model and by regression analysis. On average, mean body weight (BW) was similar ($P \geq 0.05$) across the 3 groups. Milk yield varied from 17 to 30 L/cow $^{-1}$) but mean dry matter intake (DMI) increased ($P \leq 0.001$) by only 13% (as % of BW) between low and high milk yield groups, respectively. Mean daily NDFI (1.28% body weight) was similar ($P \geq 0.05$) across the 3 groups and close to the widely accepted upper maximum (≈1.2% BW) for lactating cows. However, the variation in NDFI among individual cows was much larger than expected. Consistently across all studies NDFI (%BW) by individual cows increased linearly as total actual daily NDFI (kg/cow) increased, when a flatten of the relationship would be expected to occur at ≈1.2% BW if a true physical limitation to intake were present. The NDFI by individual cows ranged from 0.5 to 2.9% of BW, with the upper 20% of the cows in the data set eating in excess of 1.6% BW. The observed variability was similar in pattern across all studies, suggesting it was more related to intrinsic animal than feed factors. Feed conversion efficiency increased as milk yield increased, but was unrelated ($P \geq 0.05$) to individual variation in DMI per cow. Feed conversion efficiency decreased as NDFI (% BW) increased, particularly for cows in the high and medium yield categories. Results indicate that using a fixed value of maximum potential NDFI for individual cows would be misleading, particularly for grazing animals, highlighting the need of more individualized approaches to feeding management of cows in pasture–based systems.

Key words: NDF intake, dairy cows, feed conversion efficiency

433 Cereal nutrition of periparturient ewes: Corn versus wheat-barley. A. Nikkhah*, M. Karam Babaei, and H. Mirzaei, *University of Zanjan, Zanjan, Iran.*

The objective was to establish effects of peripartal dietary grain choice, grain level, and interactions on ewe metabolism. Twenty Afshari × Merino ewes (80.3 ± 2.0 kg BW) were used in a completely randomized design study from 24 d prepartum through 21 d postpartum. Ewes were kept indoor in individual boxes (1.5 × 2.5 m) and received once daily at 0900 h an either 1) higher or 2) lower concentrate total mixed ration (TMR), based on either 1) solely corn grain (CO) or 2) 50:50 blend of wheat and barley grains (WB). Ewes were stepped into the postpartum diet via feeding 2 prepartum diets. DM based dietary forage for all groups had 3:1 ratio of chopped alfalfa hay:corn silage, mixed with concentrates. For the higher grain level, forage to concentrate ratio was respectively 65:35 and 60:40 for the 2 prepartum diets, and 50:50 for the postpartum diet. The respective ratios for the lower grain level were 75:25, 70:30 and 65:35. Prepartal DMI increased by feeding CO vs. WB. Feeding CO, and not WB, at higher vs. lower level improved postpartum DMI (2.3 vs. 2.0 kg/d, $P < 0.05$). Lambing DMI tended to increase with the higher vs. lower WB (1.59 vs. 1.37 kg/d, $P < 0.10$). DM intake was greater postpartum vs. lambing (2.1 vs. 1.5 kg/d, $P < 0.05$). Feeding CO vs. WB, and feeding both CO and WB at lower vs. higher level increased fecal pH. Postpartal rumen pH decreased by feeding the higher vs. lower WB (5.7 vs. 6.2, $P < 0.05$). Rumen propionate decreased (20.4 vs. 18.9 mmol/L), and acetate (67 vs. 70 mmol/L) and acetate to propionate ratio (3.3 vs. 3.7) decreased by feeding higher vs. lower levels of both CO and WB. Colostrum properties, peripartal urine pH, lamb weight, and placenta weight and expulsion time were unaffected. Milk yield (1.64 vs. 1.27 kg/d) and fat yield (99 vs. 81 g/d) were increased by higher levels of CO and WB. Plasma glucose was higher for higher vs. lower WB (57.6 vs. 52.2 mg/dL). Feeding CO vs. WB tended to reduce peripartal plasma NEFA (0.25 vs. 0.28 mmol/L) and increased insulin to NEFA ratio (2.47 vs. 1.77). Novel findings provide evidence on independent and interactive effects of dietary cereal choice and level on periparturient sheep metabolism and performance.

Key words: cereal, periparturient, sheep

434 Effect of replacement of barley grain with oak acorn (*Quercus persica*) on Markhoz kids' performance. E. Foroutan*, O. Azizi, G. H. A. Sadeghi, F. Fatehi, and S. H. Karimi, *Department of Animal Science, Faculty of Agriculture, College of Agricultural and Nature Science, University of Kurdistan, Sanandaj, Kurdistan, Iran.*

The past researches have showed that Oak acorn can be replaced by barley grain in ruminant ′s diet. The results of some studies indicate that acorns contain an anti-nutritional factor (tannin) that has some effects on ruminants such as a reduction in nutrients digestibility. High level of tannin can reduce voluntary feed intake, whereas low to moderate level may improve the digestive utilization of feed mainly due to a reduction in protein degradation in rumen and an increase in amino acid flow to the small intestine. There is evidence that goats may be less susceptible to toxic effects of tannin, and microbial tanninase enzymes are thought to be responsible. Therefore, the aim of this study was to investigate the effect of replacing oak acorn with barley grain on dry matter intake (DMI), water intake (WI), live weight (LW), average daily gain (ADG) and feed conversion ratio (FCR). Twenty-four Markhoz kids (mean BW 16.93Â ± 1.25 kg and 4–5 mo of age) were used in a randomized complete design with 4 treatments (diets) including: a) control (barley), b) 8% oak acorn, C) 17% oak acorn, and d) 25% oak acorn of dry matter diet. The forage to concentrate ratio was a 60:40 in diets. The experimental period lasted for 105 d. the Last square means of dry matter intake (g/d) and water intake (l/d) were 880, 903, 942, 961 and 2.578, 2.653, 2.753, 2.798, respectively for treatments 1 to 4 and there was not any significant effect of treatments on these parameters ($P > 0.05$). LW, ADG, and FCR were 30.683, 31.117, 31.567, 31.950 and 130, 136, 140, 141 and 6.87, 6.67, 6.78, 6.86, respectively for treatments 1 to 4 and there were not any significant effects between treatments for LW (kg), ADG (g/d) and FCR ($P > 0.05$). Based on our results it can be concluded that acorns can substitution with barely at 25% without any problem on kid′s performance.

Key words: Markhoz kids, oak acorn, performance

435 Performance of pre-weaned WAD lambs fed Mexican sunflower leaf meal (MSLM) based diets. A. H. Ekeocha*, A. O. Akinsoyinu, and O. Makinde, *University of Ibadan, Ibadan, Oyo, Nigeria.*

Studies were conducted using 16 West African Dwarf (WAD) lambs selected from 16 ewes brought to heat (estrus) by synchronization and served by 2 rams. The experimental animals were placed at 6 weeks of age and were fed with grass (*Panicum maximum*) plus concentrate diet mixture of sunflower leaves (MSL) and wheat bran (WB) such that 0%, 15%, 30% and 45% of wheat bran was replaced by weight with MSL gravimetrically. Diet A served as control while animals on diets B, C and D received Mexican sunflower leaf (MSL) at 15, 30 and 45% respectively. The experiment lasted for 7 weeks. Feed and water were provided ad libitum and routine vaccination and medication administered. Parameters measured were weight gain, dry matter intake, weaning weight and feed conversion ratio (FCR). The dry matter intake (DMI)g/day was highest for lambs on diet C (30%MSL)(156.94) followed by B (15%MSL)(156.53) > A (0%MSL)(154.29) > D(45%MSL) (152.04) g/day respectively. This increase was numerically higher than observed values for animals on treatments A (0%MSL) and B(15%MSL) but statistically significant ($P < 0.05$) when compared with animals on treatments D(45%MSL). This trend was observed for weight gain and weaning weight. Values obtained for FCR (2.30, 2.33, 2.30 and 2.38) for lambs on treatments A,B,C and D respectively were not significantly affected by treatment ($P > 0.05$). The low FCR (2.30–2.38) obtained in this study is an indication of high digestibility and utilization of the experimental rations by pre-weaned lambs and this could be attributed to low fiber content (15.70–17.50%), low ADL (7.92–9.85) of the rations, high daily weight gain (63.85 - 68.16 g/day) and lamb weaning weight (7.40 – 8.00 kg). Results from this study showed that 30% MSLM based diet were acceptable to the pre-weaned lambs as it supported dry matter intake, optimum weight gain, weaning weight and feed conversion ratio before diminishing return sets in.

Key words: performance, pre-weaned, West African dwarf lambs

436 Effects of including okara into the diet of weanling crossbred Boer goats and its impact on growth and performance. L. L. Ramsey*, F. R. B. Ribeiro, J. J. Heitholt, J. A. Carter, W. S. Stewart, and D. D. Weir, *Texas A&M University-Commerce, Commerce.*

Reducing the total cost of feedstuffs is a primary concern for livestock producers. Okara shows promise as a byproduct feedstuff because it

provides an excellent source of protein and can be substituted in an animal's diet to minimize feed costs. The objective of this study was to determine if including okara, to the diet of weanling crossbred Boer goats would impact their growth and performance. Okara is a cost-free insoluble pulp extract remaining after producing soymilk that has 35.5% CP, 13.6% ADF, 19.8% NDF, 1.15 Mcal/lb NE_m and 0.81 Mcal/lb NE_g. A preliminary study in 2009 with 10 yearlincrossbred Boer does, half of which received a 10% okara diet, indicated no effects on growth and performance. In this 2010 study, 25 weanlings (14 wethers and 11 does) were blocked by gender and randomly assigned based on BW to one of 2 treatments, an okara group (OG, n = 13) and a control group (CG, n = 12). Measurements were taken every 14 d and consisted of hip height (HH) girth circumference (GC), BW and daily feed intake. Variables that were calculated were ADG, HH gain (HHG), GC gain (GCG) and daily DMI (DDMI). All weanlings grazed on a 2-acre paddock that consisted of coastal bermudagrass, coastal bermudagrass hay and water ad libitum. The CG were fed daily a diet that was composed of commercially available pelleted feed, 16% CP, at a rate of 1.5% of their BW for 98 d. The OG diet was composed of 80% commercial feed and 20% oven-dried okara, at a rate of 1.5% of their BW for 98 d. There were no gender effects or interactions with treatment were found for any of the variables measured; thus, only means for treatment are presented. Results showed that there were no significant differences ($P > 0.05$) in HHG (0.046 vs. 0.050 cm), GCG (0.040 vs. 0.035 cm), ADG (0.046 vs. 0.044 kg) and DDMI (193 vs. 182 g/day) between the CG and OG, respectively. These 2010 results, combined with those of 2009 preliminary study, indicate that replacement of a commercial feed with up to 20% okara in the diet of crossbred weanling Boer goats will not compromise their growth and performance.

Key words: goat, okara, performance

437 Energy and protein requirements of Canindé, Moxotó and Boer crossbred goats in semi-arid region of Brazil. M. L. Chizzotti*[1,2], K. C. Busato[2,1], T. S. Silva[2], R. T. S. Rodrigues[2], C. W. S. Wanderley[2], I. F. Silva[2], and G. G. L. Araújo[3], *[1]Universidade Federal de Lavras, Lavras, MG, Brazil, [2]Universidade Federal do Vale do São Francisco, Petrolina, PE, Brazil, [3]Embrapa CPATSA, Petrolina, PE, Brazil.*

This study was designed to determine protein and energy requirements for growth and maintenance of the Brazilian indigenous breeds Canindé and Moxotó and F1 Boer crossbreds with nondescript goats raised on semi-arid region of Brazil. A comparative slaughter trial was conducted with 60 goats (20 of each breed group), averaging 15 kg of initial body weight (BW). The baseline group consisted of 5 animals of each breed group. The remaining goats were allocated on 3 treatments: ad libitum intake and fed 50 or 75% of the ad libitum intake, and were fed 90 d. Diet consisted of 40% of *Pennisetum purpureum* and 60% of concentrate. A digestion trial was conducted in parallel to determine the metabolizable energy intake (MEI). Animals were kept in individual stalls, partially shaded, in the middle of a native Caatinga area, to replicate the semi-arid environment. The maintenance requirement for net energy (NEm) was calculated by the equation $HP = a \times e^{(b \times MEI)}$, where HP is the heat production. The net energy requirement for growth (NEg) was determined by the equation $a \times EBG^b \times EBW^{0.75}$, where EBW is the empty BW, a and b are the antilog of the intercept and the slope of the linear regression of the log of RE (kcal/kg $EBW^{0.75}$) on the log of the empty body gain (EBG), while the growth requirement for net protein (NPg) was calculated by the equation $NPg = w \times z \times EBW^{z-1}$, where w and z are the coefficients of the regression of the logarithm of the body protein on the logarithm of EBW. The NPm was assumed to be 6.25 times the intercept of the linear regression of the retained N on N intake. There were no differences ($P > 0.05$) in NEm and NPm among breeds, and the overall values found were 74.1 $kcal.kg^{-0.75}$ of $EBW.d^{-1}$ for NEm and 1.9 g $CP.kg^{-0.75}$ of $EBW.d^{-1}$ for NPm. There were also no differences ($P > 0.05$) in NEg and NPg among breeds, which can be estimated as NEg (Mcal d^{-1}) = $0.1560 \times EBW^{0.75} \times EBG^{0.716}$ and NPg (d^{-1}) = $0.217 \times EBW^{-0.0574} \times$ EBG. The requirements of Brazilian indigenous and crossbred goats raised on semi-arid were lower than those recommended by NRC (2007) for local or meat goats. Funded by CNPq and FACEPE.

Key words: comparative slaughter, Caatinga, maintenance

438 Effect of yeast culture and direct-fed microbes on the growth performance of lambs. S. P. Doto*, J. K. Wang, and J. X. Liu, *Institute of Dairy Science, College of Animal Sciences, Zhejaing University, Hangzhou 310029, P.R. China.*

An experiment was conducted to determine the effect of yeast culture and direct-fed microbes on the growth performance of weaned lambs. Thirty-two male lambs of Hu sheep with initial weight of 22.2 (±0.75) kg were fed on a basal diet with grass hay and concentrate at a ratio of 2:1, and randomly assigned to 1 of 4 treatments: (1) basal diet without additive (control), (2) added with yeast culture (YEC, Diamond V Mills, Inc., Iowa, USA), (3) yeast culture plus *Bacillus licheniformis* (YBL, Zhejiang Future, Hangzhou, China), and (4) yeast culture plus *Clostridium butyricum* (YCB, Zhejiang Future). The direct-fed microbes in powder form consisted of live microbes and their respective carrier fermentation media. Yeast culture was offered at a dose of 15 g per head per day, while *B. licheniformis* and *C. butyricum* were offered at 2.3 g per head per day. Average daily gain of growing lambs was 102, 114, 90, and 89 g/d in control, YEC, YBL, and YCB, respectively, with no significant difference ($P > 0.05$) among treatment, but the carcass weight was significantly higher ($P < 0.05$) in the YEC-added lambs than in other treatments. There were little differences in blood glucose and plasma urea-N concentrations among 4 treatments, while blood creatinine concentration (μmol/L) was significantly higher ($P < 0.05$) in YBL (97.9) and YCB-added lambs (92.1), compared with the control (77.3) and YEC (79.6). Solid-associated fungi population relative to total rumen bacteria 16S ribosomal DNA was significantly lower ($P < 0.05$) in the lambs on YBL (3.55) compared with those on YCB (23.12). From the results obtained in the current study, it is inferred that yeast culture can significantly improve growth performance of weaned lambs and that no additional advantage can be expected from combined addition with either B. licheniformis or C. butyricum. Further study is needed to investigate the effects of these additives using an adjusted diet formulation.

Key words: yeast culture, direct-fed microbes, growth performance

439 Mineral profile of lactating West African Dwarf ewe fed Mexican sunflower leaf meal based diets. A. H. Ekeocha*, *University of Ibadan, Ibadan, Oyo, Nigeria.*

A study was conducted to determine the mineral balance of lactating West African Dwarf (WAD) ewe. Sixteen lactating WAD ewes weighing between 22.80 – 26.03 kg on a basal diet of *Panicum maximum* were allotted into 4 treatment groups of 4 replicates each. The experiment was conducted using completely randomized design with 4 replicates. The Mexican sunflower leaf (MSL) replaced wheat bran (WB) gravimetrically at 0,15,30,45%. The control treatment (treatment A) had no MSL but treatments B, C and D had 15, 30 and 45% MSL

as graded replacement for WB. The experiment lasted for 13 weeks. Feed and water were provided ad libitum and routine vaccination and medication administered. Parameters measured include macro minerals i.e Calcium (Ca), Magnesium (Mg), Phosphorus (P), Potassium (K), Sulfur (S), Sodium (Na) in terms of apparent digestibility, balance and retention and micro minerals i.e Copper (Cu), Zinc (Zn), Manganese (Mn) in terms of apparent digestibility, balance and retention. Animals on treatments 0, 15 and 30% MSL were significantly higher ($P < 0.05$) than animals on treatments D in calcium and sulfur digestibility. Mineral balance were not significant ($P > 0.05$) among treatments. Animals on treatment D had less apparent sulfur digestibility and retention. Inclusion of up to 30% MSLM in the diets of lactating ewe appeared most beneficial to sheep as it had no negative effects on mineral profile.

Key words: mineral profile, lactation, West African dwarf ewe

440 Mineral profile of pregnant West African Dwarf ewe fed Mexican sunflower leaf meal based diets. A. H. Ekeocha*, *University of Ibadan, Ibadan, Oyo, Nigeria.*

Minerals are useful indicators of nutritional and physiological status. In view of this a study was conducted to determine the mineral balance of pregnant West African Dwarf (WAD) ewe. Sixteen pregnant WAD ewe weighing between 17.50 and 17.88 kg on a basal diet of *Panicum maximum* were allotted into 4 treatment groups A, B, C and D of 4 replicates each. The MSL replaced wheat bran (WB) gravimetrically at 0, 15, 30, 45%. Treatment A served as control, while animals in treatments B, C and D received Mexican sunflower leaf (MSL) at 15, 30 and 45% respectively. The experiment lasted 5 mo. Feed and water were provided ad libitum and routine vaccination and medication administered. Parameters measured were macro minerals such as Calcium (Ca), Magnesium (Mg), Phosphorus (P), Potassium (K), Sulfur (S), Sodium (Na) in terms of retention, balance and apparent digestibility and micro minerals such as Copper (Cu), Zinc (Zn), Manganese (Mn) in terms of retention, balance and apparent digestibility. The treatment effects on observed variations were not significant ($P > 0.05$) for mineral balance. Animals on treatments 0, 15, and 30% Mexican sunflower leaf meal (MSLM) were significantly higher ($P < 0.05$) in calcium, magnesium and sulfur retention than animals on treatments D (45% MSL). Animals on treatments 0, 15, and 30% MSLM were significantly higher ($P < 0.05$) in sulfur and magnesium apparent digestibility than animals on treatments D (45%MSL). Mineral balance were not significant ($P > 0.05$) among treatments. Inclusion of dietary Mexican sunflower leaf meal up to 30% improved the mineral digestibility, balance and retention of pregnant ewe.

Key words: mineral profile, pregnant ewe, Mexican sunflower leaf meal

441 Nutritive value of palm kernel cake-brewers dried grain (PKC-BDG) based diets supplemented with exogenous enzymes for growing-finishing pigs. A. O. K. Adesehinwa*[1], O. O. Obi[1], M. A. Adesina[2], B. A. Makanjuola[1], O. O. Oluwole[1], T. O. Olorungbohunmi[1], and O. Fagbiye[3], *[1]Institute of Agricultural Research and Training, Obafemi Awolowo University, Ibadan, Oyo State, Nigeria, [2]National Agricultural Extension & Research Liaison Services, Ahmadu Bello University, Zaria, Kaduna State, Nigeria, [3]Federal College of Animal Health & Production Technology, Ibadan, Oyo State, Nigeria.*

Forty-eight (48) growing pigs (averaging 41.20 ± 1.41kg initial body weight) were randomly assigned to 4 dietary treatment groups in a completely randomized design to determine the nutritive value of PKC-BDG based diets supplemented with either of 2 exogenous enzymes (Allzyme Vegpro 5X or Allzyme SSF) or their combination for growing-finishing pigs. The basal control diet was formulated to contain 10, 45, 30, 10 and 5% of maize, palm kernel cake, brewers' dried grain, groundnut cake and micro-nutrients respectively. Pigs were provided ad-libitum access to the diets and water throughout the 56-d duration of the study. Record of weekly weight gain and feed intake was taken and used to compute all the data generated. All the data obtained were subjected to ANOVA and where statistical significance were observed, the means were compared using the Duncan's Multiple Range (DMR) test (Steel and Torrie, 1980). The SAS Computer software package (1988) was used for all statistical analyses. The result of the proximate analysis of the basal diet revealed that the diet contained 7.9, 17.3, 7.5, 6.8 and 9.2% moisture, crude protein, ether extract, crude fiber and ash contents respectively. The feed intake, weight gain, feed conversion ratio and dressing percentage (%) of the pigs were neither significantly ($P > 0.05$) affected by the individual nor combination of the enzymes. The rate of growth of the pigs on the diet supplemented with Allzyme SSF was significantly ($P < 0.05$) superior to that of pigs on the other 3 diets over the 8-week experimental period. However, final weights of the pigs were not significantly ($P > 0.05$) different across the groups. Hence, since there was no superiority in the performance of pigs fed diets containing either or combination of Allzyme Vegpro 5X and SSF relative to the control diet (without enzyme inclusion), it could therefore be concluded that there was no advantage derived from using either or combination of the enzymes in this PKC-BDG based diet for growing-finishing pigs.

Key words: agro-industrial by-product, enzyme utilization, pig feed

442 The influence of low and standard energy diets on efficiency, carcass value, and pork quality in Berkshire swine. M. J. Bishop*[1], H. N. Zerby[1], S. J. Moeller[1], P. S. Kuber[1], J. M. DeRouchey[2], and K. S. Betts[1], *[1]The Ohio State University, Columbus, [2]Kansas State University, Manhattan.*

The present study addressed the influence of dietary-induced, reduced growth rate in purebred Berkshire pigs (n = 140) on subsequent daily growth rate (ADG), pen gain:feed ratio (FC), ultrasonic backfat (BF) and loin area (LMA), and pork loin quality when fed to a target 113.6 kg live weight (LW). A randomized complete block design, conducted in 3 replications, assessed 3-phase dietary regimens fed at standard (SE; ME = 3234, 3243, 3247 kcal/kg, respectively) and low (LE; ME = 2857, 2864, and 2868 kcal/kg, respectively) energy content with TID lysine:ME ratios of 2.90, 2.37, and 2.06 g/Mcal in phases 1, 2, and 3, respectively. Dietary treatment resulted in harvest at 6 (6) and 7 (7) months of pig age. To avoid total confounding harvest date with pork quality assessment, litter-mate pigs were randomly assigned to one of 4 treatments (6LE, 6SE, 7LE, and 7SE), with 6LE and 7LE representing harvest weight outside of a desired packer range. Pig weight and pen FC were measured weekly. Loin quality data were collected at 24h postmortem. Data were analyzed using mixed model procedures with treatment as a fixed effect, litter within replication as a random effect for all traits, and a random harvest date effect for meat quality traits. As expected, 6LE (0.62 kg/d) and 7LE pigs (0.61 kg/d) grew at a reduced rate when compared with 6SE (0.82 kg/d) and 7SE (0.81 kg/d) ($P < 0.05$); however, 6LE and 7LE pigs consumed more feed and had poorer FC (0.19 kg/kg) when compared with 6SE (0.27 kg/kg) and 7SE (0.28 kg/kg) pens of pigs ($P < 0.05$). While 7LE pigs had less BF than 6SE pigs (20.3 vs. 22.8 mm, $P < 0.05$) at harvest, they also had less LMA (35.0 vs 37.5 cm2, $P < 0.05$), resulting in no difference in estimated lean (49.1 vs 49.2%, respectively). Loin color (3.09 vs. 3.09), L* (51.0 vs. 49.9), ultimate pH (5.91 vs. 5.91), marbling score (2.01 vs. 2.04) and slice shear force (12.9 kg vs. 12.1 kg) were not different between 7LE and 6SE, respectively. Feeding a lower energy diet reduced FC, and did not improve lean content or pork quality; therefore, SE diets offer the best economic return when feeding Berkshire pigs.

Key words: pork quality, swine, carcass composition

443 Effects of ractopamine on performance, carcass and meat quality in purebred Berkshire swine. K. S. Betts*[1], S. J. Moeller[1], H. N. Zerby[1], J. M. DeRouchey[2], M. D. Cressman[1], M. J. Bishop[1], A. S. Gress[1], and F. L. Fluharty[1], *[1]The Ohio State University, Columbus, [2]Kansas State University, Manhattan.*

The study evaluated the effects of a 28 d pre-harvest ractopamine (RAC) feeding program on average daily gain (ADG), feed conversion efficiency (FC), backfat (BF) and loin muscle area (LMA) and pork quality in purebred Berkshire pigs (n = 62) utilizing a randomized complete block design with 3 treatments (Control (C) 0 ppm; RAC5, 5.0 ppm; RAC10; 10 ppm) in 2 replicates. Litter-mate pigs were randomly assigned to each RAC treatment. Ultrasonic BF and LMA and pig weight were measured at 0, 7, 14, 21, and 28 d of the feeding period. Carcass composition and pork quality (NPPC, 2000; visual color (VC), marbling (M), firmness (F), wetness (W), ultimate pH, and Minolta L*, a*, b* were assessed at 24h post-harvest. Warner-Bratzler shear force (WBSF) was assessed on one chop after a 7 d aging period. Mixed model procedures were used in analyses with fixed effects of treatment and a random effect of litter within replicate. Live weight (93.5 kg) and BF (20 mm) were not different, while LMA was different (C = 32.3 cm2; RAC5 = 34.4 cm2, RAC10 = 33.1 cm2; $P < 0.05$) at 0 d. Daily gain was numerically greater from 0 to 7 d and significantly greater from 0 to 14, 0 to 21, and 0 to 28 d for pigs fed RAC when compared with pigs fed a C diet ($P < 0.05$). Pigs fed RAC10 had greater ADG than pigs fed RAC5 from 0 to 21 and 0 to 28 d. At 21 d, RAC5 and RAC10 pigs had greater LMA than C, at 28 d LMA of RAC5 was intermediate and not different from either C or RAC10 with C different from RAC10 ($P < 0.05$), and carcass LMA of RAC10 was greater than RAC5 and C. No differences were observed across treatments for ultrasonic or carcass BF. Trends for greater lean percentage (LP) ($P = 0.06$) and improved gain feed ratio (G:F) ($P = 0.11$), whereby RAC10 (49.8%, 0.31 kg/kg) carcasses had numerically greater lean LP and G:F than RAC5 (47.8%, 0.28 kg/kg) and C (47.8%, 0.26 kg/kg) carcasses. Neither RAC5 or RAC10 diets influenced fresh loin quality with no differences in VC, M, F, W, L* or WBSF, whereas ultimate

pH was greater (0.06 units, $P < 0.05$) for the RAC10 treatment when compared with C. Ractopamine improved value and efficiency without negatively influencing quality.

Key words: swine, ractopamine, meat quality

444 The effects of diet ingredients on gastric ulceration and salivary pH in gestating sows. S. L. Wisdom*[1], B. T. Richert[1], J. S. Radcliffe[1], D. C. Lay Jr.[2], and J. N. Marchant-Forde[2], *[1]Purdue University, West Lafayette, IN, [2]USDA-ARS-LBRU, West Lafayette, IN.*

Diet and stress are thought to have significant influence on the development of ulceration of the pars esophagea (UPE) region of the stomach in swine. The objective of this experiment was to determine the effects of diet ingredients on UPE and salivary pH in breeding sows. Forty-eight sows were randomly assigned to 1 of 4 treatment groups with parities (avg. 1.81 ± 0.21) balanced across treatments. Treatments were: 1) control, a commercial gestating sow diet; 2) proton pump inhibitor, a commercial gestating sow diet plus a single daily dose of 60 mg omeprazole; 3) sodium bicarbonate, a commercial gestating sow diet with sodium bicarbonate included at 2% of the diet; 4) roughage, a high fiber diet (25% SB hulls) fed at a higher feed intake to an equal total ME as control. Treatments began on d 30 of gestation and all diets were fed once per day. All sows underwent initial endoscopic evaluation at d 30 to assess UPE already present and initial salivary pH was measured. Salivary pH and UPE were also investigated at d 60 and d 90 of gestation. Ulcers were scored using a 7-point scale, ranging from 0, showing no visible lesions, to 6, showing deep ulcerations in > 20% of the pars esophagea. Salivary pH was measured 5 times throughout the day at 0700 h, 1000 h, 1300 h, 1600 h and 1900 h. Data were analyzed using mixed procedure of SAS. UPE differed between groups before treatment was applied ($P < 0.01$), but using initial UPE as a covariate, there were no effects of treatment on d 60 or d 90 (both $P > 0.05$). Treatment also had no effect on litter size, piglet weight, or lactation feed intake ($P > 0.05$). The average UPE score was 1.06 ± 0.23 ranging from 0 to 6, with the largest individual score difference changing from score 5 to 0. Salivary pH did not correlate with UPE and there was no treatment effect (both $P > 0.05$), but there was a change in salivary pH throughout the day ($P < 0.01$) with the highest pH (8.99 ± 0.05) at 0700 h and lowest pH (8.88 ± 0.02) at 1300 h. The results indicate that the selected treatments did not influence UPE. To evaluate the impact of natural changes in salivary pH, further investigations are needed.

Key words: swine, gastric ulcer, salivary pH

445 Effect of dietary glutamine supplementation on the apparent total tract digestibility of energy and nutrients and jejunal gene expression in weaned piglets. A. Chen*, Y. Xiao, T. Wu, Q. Hong, and C. Yang, *Zhejiang University, Hangzhou, Zhejiang, China.*

Glutamine plays essential roles in the beneficial function to improve nutrition status in young mammals. This study was conducted to examine the effect of dietary L-glutamine supplementation on apparent total tract digestibility (ATTD) of dietary energy and nutrients in 21-d-old weaned piglets, and the expression of jejunal gene related to intestinal health. A total of 128 piglets were blocked by litter and assigned to one of 2 group, representing supplementation with 1% L-glutamine (wt:wt) or isonitrogenous L-alanine (control) to corn- and soybean meal-based diets. After 10-d treatment, the fresh fecal samples were collected to determine apparent total tract digestibility of dry matter (DM), digestible energy (DE) crude protein (CP) and amino acid (AA), and jejunum were obtained to access the expression of peroxisome proliferator-activated receptor gamma (PPARγ), mammalian target of rapamycin complex 1 (mTORC1) and pyruvate kinase (PK). The results show that the apparent total tract digestibility of energy or nutrients was higher ($P < 0.05$) in dietary glutamine supplementation piglets. The total tract digestibility of DM, DE, and CP averaged 81.02, 82.18, and 86.73%, respectively, for glutamine treatment piglets and 74.29, 76.79, and 83.83%, respectively, for control piglets. A significant increase of AA digestibility was observed ($P < 0.01$) except for alanine which was reduced by 8.19% ($P < 0.01$). Besides, dietary glutamine supplementation resulted in increased expression of jejunal mTORC1 by 22.10% but decreased PK by 29.75% ($P < 0.05$). Jejunal PPARγ mRNA abundance was not affected by glutamine treatment. In conclusion, 1% L-glutamine supplementation to post-weaned piglet diet enhanced the apparent total tract digestibility of energy or nutrients and modified jejunal gene expression.

Key words: glutamine, digestibility, gene expression

446 Effect of feeding Bt (MON810) maize to pigs from 12 days post-weaning for 110 days on growth performance, body composition, carcass characteristics, organ weights and intestinal morphology. S. G. Buzoianu*[1,2], M. C. Walsh[1], G. E. Gardiner[2], M. C. Rea[3], R. P. Ross[3], and P. G. Lawlor[1], *[1]Pig Development Department, Moorepark Animal and Grassland Research and Innovation Centre, Teagasc, Fermoy, Co. Cork, Ireland, [2]Department of Chemical and Life Sciences, Waterford Institute of Technology, Waterford, Ireland, [3]Moorepark Food Research Centre, Teagasc, Fermoy, Co. Cork, Ireland.*

Increased use of genetically modified (GM) ingredients worldwide makes sourcing non–GM ingredients more difficult and expensive. The aim of this study was to assess the effects of feeding GM Bt (MON810) maize to pigs from 12 d post–weaning to slaughter for 110 d on growth performance, body composition, carcass characteristics, organ weights and intestinal health. Seventy 2 male pigs (10.7 ± 1.9 kg) were blocked by weight and litter and assigned to one of 4 treatments: T1: non-GM maize (nGMm) to slaughter; T2: GM maize (GMm) to slaughter; T: nGMm for 30 d followed by GMm to slaughter; T4: GMm for 30 d followed by nGMm to slaughter. Individual BW and feed disappearance were recorded on d 0, 30, 60, 100 and at slaughter. Body composition (fat %, bone mineral content and area bone mineral density) was determined by dual energy X-ray absorptiometry on d 80 of the study (n = 10/trt). On d 110 of the study, 10 pigs/trt were slaughtered and the heart, kidney, spleen, liver, stomach and small intestine (SI) were removed and weighed. Sections of SI were processed for histological examination of villus height, width, crypt depth and goblet cell number/villus. Carcass weight was also recorded at slaughter. All data were analyzed as a one-factor ANOVA using the GLM procedure of SAS. Organ weights were analyzed using body weight at slaughter as a covariate in the model. There was no treatment effect for body composition. Growth parameters (ADG, F:G and ADFI, BW at slaughter) were not influenced by treatment. Organ and carcass weight and kill-out percentage did not differ between treatments. Values for all parameters measured were within normal ranges for pigs of a similar age and weight. Intestinal morphology was not affected by treatment. In conclusion, feeding GM Bt maize from 12 d post weaning to slaughter had no adverse effect on pig growth performance, body composition, organ weights, carcass characteristics or intestinal morphology. This research will help assure both farmers and consumers as to the safety of GM Bt maize.

Key words: Bt maize, pig health, MON810

447 Effect of feeding genetically modified Bt (MON810) maize to pigs from 12 days post-weaning for 110 days on serum and urine biochemistry. S. G. Buzoianu*[1,2], M. C. Walsh[1], G. E. Gardiner[2], M. C. Rea[3], R. P. Ross[3], and P. G. Lawlor[1], *[1]Pig Development Department, Moorepark Animal and Grassland Research and Innovation Centre, Teagasc, Fermoy, Co. Cork, Ireland, [2]Department of Chemical and Life Sciences, Waterford Institute of Technology, Waterford, Ireland, [3]Moorepark Food Research Centre, Teagasc, Fermoy, Co. Cork, Ireland.*

Perceived health risks are among the main reasons for low acceptability of genetically modified (GM) feed ingredients. The aim of this study was to evaluate the effect of feeding GM maize to pigs from 12 d post-weaning to slaughter for 110 d on health as assessed by serum and urine biochemistry. Seventy-two entire male pigs (10.7 ± 1.9 kg live weight) were blocked by weight and litter and randomly assigned to 1 of 4 treatments (d 0); T1: non-GM maize (nGMm) in diet to d 110; T2: GM maize (GMm) in diet to d 110; T3: nGMm in diet for 30 d followed by GMm to d 110; T4: GMm in diet for 30 d followed by nGMm to d 110. Serum collected on d 0, 30, 60, 100 and 110 (n = 10/trt) was analyzed for liver and kidney health indicators (alanine aminotransferase, aspartate aminotransferase (AST), γ-glutamyl transferase, alkaline phosphatase, total protein (TP), urea (SU) and creatinine (SC). Creatinine and protein were measured in urine collected on d 110 to further assess kidney health. Statistical analysis was performed by a one–factor ANOVA using the GLM procedure of SAS. For serum biochemistry, d 0 values were used as a covariate in the model. On d 30, SU was lower for T3 compared with T1, T2 and T4 (2.9 vs 3.9, 4.7 and 4.2 mmol/L, respectively; SEM = 0.37; $P = 0.03$). On d 110, there was a higher concentration of SC in pigs fed T3 and T4 compared with T1 and T2 (181.5 and 177.6 vs 163.9 and 155.9 μmol/L; SEM = 5.63; $P = 0.001$). Serum TP was lower on d 110 in pigs fed T4 compared with T1, T2 and T3 (57 vs 60.5, 59.3, 61.1 g/L; SEM = 1.62; $P = 0.02$). On d 110, serum AST tended to be lower in pigs fed T2 compared with T1 (37.2 vs 53.5 units/L; SEM = 4.01; $P = 0.06$). Although statistically significant differences were found, values remained within the normal ranges for pigs of similar age and weight. No parameter was consistently affected throughout the study, therefore changes detected are unlikely to be of clinical importance. This study shows no adverse effects of feeding Bt GMm to pigs between weaning and slaughter on serum or urine biochemistry and should help to assure consumers as to the safety of Bt maize.

Key words: Bt maize, pig health, MON810

448 Supplementation of xylanase to improve DDGS and corn germ meal utilization by finishing pigs as measured by performance and carcass yield in a commercial environment. D. D. Hall*[1], M. U. Steidinger[2], J. C. Remus[3], M. Hruby[3], and A. J. Veldkamp[3], *[1]Hall Farms Consulting, LLC, Noblesville, IN, [2]Swine Nutrition Services, Anchor, IL, [3]Danisco Animal Nutrition, Waukesha, WI.*

Two experiments were conducted to test a hypothesis that dietary supplementation of xylanase (Danisco Porzyme 9302 @ 4,000 units/kg) improves nutrient utilization of commercially available corn co-products in diets consisting of 30% dried distillers grains and solubles (DDGS) or a combination of 30%DDGS and 20% corn germ meal (CGM) by growing-finishing pigs. In both experiments, pigs were housed at 30–32 pigs/pen with pen space at 6.75–7.4 sq.ft./pig. Each trial consisted of 8 reps (Exp. 1 initial wt. 26kg) or 7 reps (Exp. 2 initial wt. 33kg) Statistical analysis (SAS.JMP) was block design with block = (rep. initial wt.). All diets had equal phytase addition (Danisco Phyzyme XP@750 units/kg). Withdrawal of DDGS was tested in 2 × 2 factorial design with Xylanase in both experiments (Table 1). There were no differences in daily gain or feed intake in Exp. 1. In Exp. 2, addition of CGM reduced ADG compared with Control (DDGS) fed pigs (d43–97; 0.932 vs 0.841 kg/d;$P < 0.05$). Feed/gain ratio was improved in both Exp. 1 (d41–81;$P < 0.06$) and Exp. 2(d43–97;$P < 0.001$) by addition of xylanase to the corn co-product diets of DDGS or DDGS + CGM (Table 1). Supplementation of xylanase and DDGS withdrawal resulted in carcass yield equal to the corn-soy control fed pigs in both experiments (Table 1).

Table 1. Feed/gain and yield

Exp.1	Corn	DDGS	DDGS	DDGS	DDGS		DDGS	Xylanase
Xylanase			+		+			
(D82-MKT)	Corn	DDGS	DDGS	Corn	Corn	SEM	*P* <	*P* <
Feed/gain								
D0-41	2.40	2.32	2.34			0.026	0.10	
D41-81	2.96[a,b]	2.98[a]	2.88[b]			0.045		0.06
D81-104	3.26	3.45	3.36	3.39	3.43	0.070	0.10	
Yield,%	77.4[b]	76.6[c]	76.6[c]	76.8[c]	77.1[b,c]	0.20	0.02	
Exp.2	DDGS	CGM	CGM	CGM	CGM		CGM	Xylanase
Xylanase			+		+	SEM	*P* <	*P* <
(D76-mkt)	Corn	CGM	CGM	Corn	Corn			
Feed/gain								
D0-43	2.42[a]	2.51[b]	2.53[b]			0.025	0.01	
D43-97	3.26[a]	3.54[d]	3.38[b]	3.46[c]	3.38[b]	0.023	0.001	0.001
Yield,%*	76.7	75.5	76.6	76.2	77.4			

*At time of publication, yield (Exp. 2) = first cut 56 pigs/trt.

Key words: pigs, xylanase, corn germ meal

449 Monitoring muscle proteolysis in pig plasma. K. L. Price* and J. Escobar, *Virginia Polytechnic Institute and State University, Blacksburg.*

Nτ-methyl-L-histidine (NτMH, CAS number 332-80-9, archaic 3-methylhistidine) is released from skeletal muscle during proteolysis, cannot be reused for protein synthesis, and it is excreted from the body in urine. In humans, free NτMH is the main form found in plasma and urine. In healthy rodents NτMH is predominately found in the acetylated form (Ac-NτMH). Furthermore, changes in urinary Ac-NτMH, and not free NτMH, are associated with muscle breakdown during sickness. Our objective was to quantify free and Ac-NτMH in pig plasma during health and disease. We chose plasma over urine because blood samples are usually easier, more reliable, and faster to collect than urine samples. Plasma samples were subjected or not to acid hydrolysis (6 M HCl for 24 h at 110°C) to quantify total and free NτMH, respectively. Plasma samples were then subjected to pre-column derivatization with phenylisothiocyanate, and separation and quantification using HPLC. To determine how much NτMH was acetylated, free NτMH was subtracted from total NτMH. Pigs (33.41 ± 1.05 kg, n = 9) were fitted with indwelling jugular catheters. Blood samples were collected before ($t = 0$) and 12 h after a bolus of *E. coli*-derived lipopolysaccharide (LPS, 10 μg/kg BW i.v.). In healthy pig plasma ($t = 0$), the major representation of NτMH was in the acetylated form (71% Ac-NτMH). Plasma free NτMH was not different ($P = 0.490$) between $t = 0$ and $t = 12$ (30.60 ± 1.80 μM vs 29.14 ± 0.93 μM, respectively). Total plasma NτMH increased 39% ($P = 0.048$) from 86.4 ± 8.6 μM

at t = 0 to 120.2 ± 13.2 μM at t = 12. Ac-NτMH increased 56% (P = 0.0546) from 57.3 ± 9.2 μM at t = 0 to 89.6 ± 12.6 μM. Finally, plasma concentrations of 3-methyl-L-histidine (3MH, CAS number 368–16–1, archaic 1-methylhistidine) were not detected at either time point. In summary, our findings indicate that a) 3MH is not detectable in plasma; b) free NτMH remained unaffected after LPS treatment and hence may not be a reliable indicator of muscle proteolysis; and c) the majority of plasma NτMH is present in the acetylated form in health and sickness. Additionally, our results demonstrate that to accurately monitor NτMH fluctuations, pig plasma needs to be acid hydrolyzed.

Key words: methylhistidine, HPLC, acid hydrolysis

450 Effect of independent laboratory assessment, freezing volume, and other factors influencing post-thaw quality of frozen boar sperm. J. M. Ringwelski* and R. V. Knox, *Department of Animal Sciences, University of Illinois, Champaign-Urbana.*

Frozen boar sperm shows lower fertility compared with liquid semen. This has been partly classified based on post-thaw lab assessments. Experiment 1 was performed to evaluate effects of independent lab assessment of post-thaw motility following freezing in 5 mL (Lab 1) or 0.5 mL (Lab 2) straws. Ejaculates(n = 117) from 27 mature boars of Landrace(n = 5), Large White(n = 15), Duroc(n = 5), and Other(n = 2) breeds were collected and frozen across seasons (winter-summer) from Feb to Jun 2010. Ejaculates were collected, diluted 1:1 in Modena, and held at 17°C until processing(Lab 1) or upon arrival the next day(Lab 2). All samples were frozen within 24 h of collection. Once frozen, straws were stored at −196°C until analysis. Straws were thawed at 50°C for 45 s for 5 mL straws and 20 s for 0.5 mL straws and evaluated at 37°C upon thawing. Data were analyzed using SAS for the effects of lab and volume, breed and season. There was no effect (P > 0.05) of lab and volume(47.4 vs. 49.8%), breed or season on motility. Experiment 2 was conducted to determine the effect of independent lab on pre-freeze concentration and motility, and also effects of breed, season, and collection number on post thaw quality measures in 0.5 mL straws. Straws(n = 47) from 26 boars were thawed and evaluated for motility and membrane integrity using propidium iodide. Data were analyzed in SAS for effects of lab assessments on pre-freeze motility, concentration, and total sperm cells. Effect of breed, season, and collection number on motility and viability were also evaluated in 0.5 mL straws. Measures of concentration (0.82), motility (0.78), and total cells (0.67) were all positively related for independent lab assessments (P < 0.001). Motility (47%) and membrane integrity (51%) were not affected by breed, season, or collection number (P > 0.05). The results of these experiments suggest that independent lab assessments post-thaw can be highly related, and there is no significant difference related to freezing in 5 or 0.5 mL straws. In boars in active collection rotations, breed and season had no impact on post-thaw quality of frozen boar sperm.

Key words: boar, spermatozoa, cryopreservation

451 Characteristics of the work habits and demographics of caretakers on swine finishing facilities in Ohio. S. M. Crawford*[1], S. J. Moeller[1], P. H. Hemsworth[2], C. C. Croney[1], N. A. Botheras[1], and H. N. Zerby[1], *[1]Ohio State University, Columbus, [2]University of Melbourne, Melbourne, Victoria, Australia.*

Contract finishing farms representing 2 integrated swine entities (n = 32) within Ohio were observed to study daily work habits and characterize the demographics of the caretaker(s) (n = 40) working on the farms. The farms used in the research housed a minimum of 1000 pigs. A standard observer visited each farm for 2 consecutive days, at a time designated by the caretakers, and recorded human behaviors during the daily work. A questionnaire was administered to collect demographic data. Of the 40 persons observed, 33 completed the questionnaire. The data was summarized to characterize attributes that may influence animal care and caretakers attitudes and actions. On average, the caretakers were 41.2 yrs of age (range 21 to 60 yrs), had worked with pigs for 16.9 yrs (range 1 to 40 yrs; mode = 8 yrs), and worked in contract finishing for 7.4 yrs (range 1 to 20 yrs; mode = 1 yr). Males were the predominant gender (93.9% male; 6.1% female). Thirty caretakers indicated employment off-farm, including responses such as grain farming, dairy farming, beef feedlot manager, electrician, truck driver, postal worker, mechanic, seed sales, plumber, and financial services. When asked why they initiated a finishing production contract, responses included diversification, enjoyment, income, and risk reduction. Thirty-one of 33 caretakers had completed Pork Quality Assurance Plus® training. On observation days, caretakers spent 36.43 s per pen, with a wide range from 5.76 to 128.8 s. A significant association was observed between the time spent per pen and the number of words spoken (r = 0.71) and verbal sounds (whistles, hoots, etc) (r = 0.72). Salivary cortisol levels that were collected from 2 or 3 pigs in each pen, over a 2-d period, were different (P < 0.01) indicating different stress levels across farms. The summary results are indicative of the large variation that is observed within contract finishing farms within the given integrated system and suggest that caretakers may need additional training to improve animal well-being. Also, the knowledge of these variations can aid in determining training/education needs for the caretakers in the future.

Key words: pigs, caretaker

452 Survey of animal welfare and dairy management practices on 91 Organic Valley dairy farms. W. K. Fulwider*, *CROPP Cooperative, LaFarge, WI.*

The objective of this survey was to evaluate animal welfare on Organic Valley dairies across the United States. Cows were scored on 91 dairies between May 10, 2010 and January 20, 2011 in California, Indiana, Iowa, Michigan, North Carolina, Ohio, Oregon, Pennsylvania, Tennessee, Vermont, and Wisconsin. Dairies were selected from tight knit clusters in each area so the most farms possible would be surveyed in one week. All cows on each dairy were scored. Data were collected on body condition, locomotion, hygiene, hock lesions, broken and docked tails, hair coat, housing, and euthanasia. Body condition scores ranged from 1 to 5, with 1 being thin and 5 heavy. The percentage of cows with body condition score of 1 was 0.1, 2 was 69.1, 3 was 29.1, 4 was 4.8, and 5 was 0. Locomotion scores ranged from 1 to 5, with 1 being excellent and 5 unable to bear weight on at least one limb. Percentage of cows with locomotion score 1 were 97.0, 2 were 2.1, 3 were 1.0, 4 and 5 were 0. Hygiene scores ranged from 1 to 5, with 1 being clean and 5 soiled. Percentage of cows with hygiene scores of 1 were 67.2, 2.0 were 29.5, 3.0 were 1.9, 4.0 were 0.4, and 5.0 were 0. A tarsal score of 1 represented hair loss, 2 was moderate, and 3 indicated severe swelling. Percentages of cows with hock score 1 were 13.4, 2 were 1.1, and 3 were 0.1. A knee score of 1 represented hair loss, 2 swelling, and 3 severe swelling. Percentages of cows with knee score 1 were 2.0, 2 were 0.2, and 3 were 0. Percentage of cows with broken tails was 3.8. Percentage of cows with docked tails before organic transition or due to injury was 2.8. No bald spots, lice, or mange were observed on cow hair coats. Housing consisted of 32 farms with tie-stalls, 28 free-stalls, 18 bedded packs, 7 stanchion barns, and 4 other. Some farms had more than one housing type. Gun was the preferred euthanasia method (92.1), followed by i.v. (7.9). Bedding cows housed due to inclement weather on a daily basis may improve hygiene scores. Incidence of broken tails was higher on larger farms with hired milkers. This is the most comprehensive survey to date of animal welfare and management on US organic dairy farms.

Key words: dairy, organic, welfare

453 A dairy quality assurance program for New Mexico dairy producers. F. A. Rivera*[1], G. R. Hagevoort[1], M. L. Kinsel[2], and M. A. Smith[1], *[1]NMSU Ag Science Center, Clovis, NM, [2]Agricultural Information Management Inc., Ellensburg, WA.*

The New Mexico Dairy Quality Assurance program was developed to evaluate management practices on dairies including biosecurity, animal care, calf management, milking barn management, nutrition, reproduction and animal health management. Input was obtained through a combination of producer interviews and animal observations. The program was developed to be compatible with the NMPF's FARM program (Farmers Assuring Responsible Management), but additionally address particular issues facing New Mexico producers. To date, about 25% of New Mexico's dairy producers have participated in the program. Many of the interview questions refer to the use of protocols for standardization of management practices. Eighty-three percent of producers stated they do have a written form of a herd health plan. All participating producers stated they had protocols for fresh cows, udder health, worker training, and non-ambulatory animals; however, most these protocols are not in a written form indicating a high level of reliance on verbal training of employees on procedures and protocols. Thirty 6 percent of producers indicated written protocols for fresh cows, while 36% indicated written udder health protocols, 37% for worker training, and 39% for non-ambulatory animals. Less than one half of the producers indicated to have protocols directly pertaining to biosecurity. Ninety-four percent of producers record withdrawal periods: 60% of which utilize some computer software. Utilizing the FARM method to determine the number of observations required to observe animal management and welfare practices proved to be a challenge on the large dairies in New Mexico (average herd size 2200). Specifically, dairies with large heifer programs with limited body condition or locomotion score problems tend to mask issues apparent in the adult milking strings. Results on New Mexico dairies showed that including a large heifer program in the evaluation can cut the percentage of body condition or locomotion scores in half, to a level where it seems not to warrant any further action and may go unreported.

Key words: quality assurance program, animal welfare, biosecurity

454 Effect of prior grazing experiences on grazing behavior and performance of lactating cows. F. Lopes*[1], N. M. Esser[1], P. C. Hoffman[1], W. K. Coblentz[2], and D. K. Combs[1], *[1]Department of Dairy Science, University of Wisconsin, Madison, [2]USDA-ARS, Marshfield, WI.*

The impact of grazing experiences early in life on grazing behavior and performance of lactating dairy heifers was evaluated in a 3-year study. Sixty-four Holstein and Holstein x Jersey calves were randomly assigned to one of 4 treatments (n = 16) in 2008. Treatments were combinations of managing heifers in confinement or on pasture: T1, grazed 2008 and 2009; T2, grazed 2008 and confined in 2009; T3, confined in 2008 and grazed in 2009; T4, confined in 2008 and 2009. All animals grazed as lactating cows in 2010. In 2008, T1 and T2 heifers were on pasture from August through October, and T3 and T4 were housed in bedded pack pens. In year 2, T1 and T3 grazed from June–September, 2009, while T2 and T4 remained in confinement. All 4 treatment groups calved between January and April, 2010, and grazed as primiparous cows from May through July. In 2009 and 2010 grazing activities were assessed by visual observations (9h/d) and by measuring movements with GPS units attached to each animal. Daily milk was also recorded in 2010. All data were analyzed using proc mixed (SAS) as a completely randomized design, with treatment and day as fixed effects. Paddock was the random effect. In 2009 on d1, heifers that had grazed in 2008 spent more time grazing than heifers with no grazing experience (78 vs. 35% of the time, $P < 0.05$). In 2010 on d1, time spent grazing was 62, 59, 76, and 13% for T1, T2, T3 and T4, respectively, with T4 ranking lowest ($P < 0.05$). In 2009 and 2010 on d 1–3, experienced heifers walked a greater distance in the pasture than inexperienced animals. Milk production was lowest initially for cows with no previous grazing experience (T4). Animals that had not grazed in 2009 (T2 and T4) produced less milk than those that had grazed in 2009 (T 1 and T3) on d 1–3. However, average (61d) daily milk over the entire experiment was not significantly different ($P > 0.05$) (30.5, 30.1, 31.5 and 29.6 kg for T1, T2, T3 and T4). Results indicate that previous grazing experience can impact behavior and milk production during the first 3 d on pasture. After that, no behavioral differences ($P > 0.05$) were noted in after d-3 in either study.

Key words: heifers, behavior, grazing

455 Effects of acute and chronic stress on immune- and inflammatory-response gene expression in beef calves. C. Terrill*, T. Friend, J. Sawyer, P. Riggs, L. Berghman, S. Garey, D. Riley, A. Adams, and M. Carter, *Texas A&M University.*

Transport stress research has shown correlations between stress, morbidity, and mortality in calves subjected to the traditional US market system, indicating compromised immune function. The objective of this study was to determine if expression of specific immune- and inflammatory-response genes differed between calves that were subjected to an acute stress (AS, weaned and handled for 1.5 h) and a chronic stress (CS, weaned, handled and transported over 3–4 d. Two groups of 40 calves, *Bos taurus* (n = 20) and *Bos indicus* cross (n = 20), weighing 181 to 250 kg were used in this study. Jugular venipuncture blood samples (9mL) were collected from AS calves within 1.5 h of separation from their dam, and from CS calves upon arrival at a north Texas feed yard. For gene expression analysis, RNA was extracted from leukocytes obtained from blood samples by filtration. The remaining sample was then centrifuged for measurement of plasma cortisol. A diagonal covariance mixed model ANOVA was used to determine effects of treatment, breed, and breed by treatment interaction on cortisol concentrations. Mean cortisol did not differ significantly between AS (16.40 ± 1.08ng/ml) and CS calves (18.06 ± 1.14ng/ml) ($P > 0.296$). Expression values for each gene were analyzed using linear models that considered the effects of treatment (AS and CS) and breed (*Bos taurus* and *Bos indicus*). An interaction of effects was detected for 3 genes ($P < 0.029$). Breed was influential for 5 genes ($P < 0.046$). After adjustment for multiple comparisons in expression values for AS and CS, significant differences were found in relative quantification for 33 genes ($P < 0.047$), with mean treatment differences ranging from 0.309 – 913.19. Similar cortisol concentrations in both the AS and CS calves indicate that both groups experienced significant stress. However, the gene expression differences show a greater immune response in the calves subjected to CS, indicating that these measurements may be more useful than cortisol for identifying detrimental long-term stress.

Key words: transport, cortisol, gene expression

456 Estimation of genetic parameters for gait in Canadian Holstein cows. N. Chapinal*[1,2], F. Miglior[3,4], A. Sewalem[3,4], A. M. de Passille[5], J. Rushen[5], M. A. G. von Keyserlingk[2], and D. M. Weary[2], *[1]Department of Population Medicine, University of Guelph, Guelph, ON, Canada, [2]Animal Welfare Program, University of British Columbia, Vancouver, BC, Canada, [3]Guelph Food Research Centre, Agriculture and Agri-Food Canada, Guelph, ON, Canada, [4]Canadian Dairy Network, Guelph, ON, Canada, [5]Agriculture and Agri-Food Canada, Agassiz, BC, Canada.*

Lameness is one the most important welfare and economic problems in modern dairy herds. No direct genetic selection for lameness resistance has been done so far. The objective of this study was to estimate the genetic parameters of gait for Holstein cows from a research farm in British Columbia. A total of 265 cows had their gait assessed from 1 to 26 times (mean ± SD = 7 ± 5 times) throughout their productive lives. Data were collected in different experimental studies, but only cows assigned to control groups, or data collected before treatments were applied were used. Overall gait was assessed using a 1-to-5 scale with half-integers where 1 = not lame and 5 = severely lame, based on 6 different gait components (head bob, back arch, asymmetry of the steps, tracking-up, joint flexion and reluctance to bear weigh in a particular limb). A linear animal model was used to analyze overall gait. The statistical model included the fixed effects of parity (1 to 9), the interaction between year and season of calving (2001 to 2009, 2 seasons/yr), the interaction between experiment and observer (11 experiments and 6 observers), the linear and quadratic regression of time at gait assessment (expressed as number of days before or after calving, if in dry or lactation period, respectively). The random effects of the model included animal, permanent environment and residual. Variance components were estimated with REML procedure using a DMU software package. Estimate of heritability for overall gait was 0.09. Research is in progress to estimate variance components of individual gait components.

Key words: lameness, heritability, linear animal model

457 Automatic estimation of body condition score from digital images. M. Caccamo*[1], G. Azzaro[1], G. Gallo[2], G. C. Guarnera[2], J. D. Ferguson[3], and G. Licitra[1,4], *[1]CoRFiLaC, Regione Siciliana, Ragusa, Italy, [2]IPLAB, Catania University, Catania, Italy, [3]University of Pennsylvania, PA, [4]DISPA, Catania University, Catania, Italy.*

Body condition score (BCS) is an indicator of cows' health status based on visual or tactile inspection. The human intervention in assessing BCS is the main limiting factor since it is subjective and requires time and well-trained experts. For these reasons, to fully automate scoring, or at least to assist the human expert in this task, state-of-the-art computer vision is an important application that can reduce subjectivity and speed the scoring process. The objective of this study was to explore the possibility to efficiently automate the process of quantitatively estimating the BCS of cows using images acquired by commercial low-cost digital cameras. Images were acquired using 2 cameras at 3 m from the ground placed above an exit alley from the milking robot in such a position to allow capturing images of the dorsal area of cows. The BCS of each cow was estimated on site by 2 technicians and properly associated to the cows' images. A statistical region merging algorithm was applied to the H channel of the hue, saturation and value (HSV) color space to segment images. Cows' shapes were extracted from the binarized images, cleaned from noise and aligned in a unique reference frame. The standardized contours were described then in terms of arc-length parameterization with a uniform sampling. A standard principal component analysis was applied to determine the components describing the many ways in which the body shape of different cows tend to deviate from the average shape. This mathematical representation allowed a mapping of cow's shapes into a vector space, whose metric was used for automatic estimation of BCS through regression approach. The proposed method was tested on a benchmark data set containing 148 images available through the Internet (www.corfilac.it/bcs) by means of the leave one out cross validation procedure and the regression error characteristic curves. Experimental results confirmed the effectiveness of the proposed technique (mean error 0.26) that outperformed other state-of-the-art approaches proposed in the context of dairy cattle research.

Key words: body condition score, digital imaging, body shape

458 Use of infrared thermography to identify thermoregulatory differences between heat-sensitive and heat-tolerant breeds of *Bos taurus* cattle. R. E. Chaffin[1], K. J. Hoernig[1], J. S. Johnson[1], J. K. Bryant[1], B. Scharf[1], D. K. Kishore[1], P. A. Eichen[1], E. S. Dierenfeld[2], and D. E. Spiers*[1], *[1]University of Missouri, Columbia, [2]Novus International, Inc., St. Charles, MO.*

Previous studies have shown that a breed of heat-tolerant *Bos taurus* cattle (i.e., Romosinuano; RO) maintain a lower core temperature than more heat-sensitive Angus cattle (ANG) even with a lower respiration rate during heat stress. A new study was performed to further identify regional skin differences between RO (Florida-derived; n = 5) and ANG (Missouri/Oklahoma-derived; n = 10). Animals were tested in the Brody Environmental Chambers (University of Missouri), with an adjustment period of 8 d at thermoneutrality (TN; 19–22°C), followed by 2 weeks of cycling heat stress (HS; 26–36°C). A thermal imaging camera (Fluke Corp., Everett, WA) was used to create thermal images of hooves, legs, rump, and shoulder areas during TN, early HS (HS1; d 10) and late HS (HS2; d 21) periods. Measured skin sites were shaved before the study, with rump and hoof sites being ~10x10cm. Only maximum values from each site were used to avoid wet areas. Temperature of all sites increased in the heat, with no shift from HS1 to HS2. Rump and hoof sites showed no differences across breed. ANG shoulder temperature was 1.9°C higher ($P < 0.05$) than ROMO in the heat. In contrast, overall leg temperature of RO was 1.9°C higher ($P < 0.05$) than ANG, with greater breed differences ($P < 0.05$) at TN and HS1 (2.3 and 2.0°C respectively), and no difference after adaptation at HS2. These results suggest that increased heat dissipation through the leg at all air temperatures may be a major avenue by which the heat-tolerant breed may efficiently radiate excess heat to the environment and maintain a lower core body temperature.

Key words: radiant, breed, heat stress

459 Effect of climatic on body temperature of dairy cows. J. C. Lees* and J. B. Gaughan, *The University of Queensland, Australia.*

It is generally accepted that body temperature (BT) is a reliable indicator of heat load status. However the effects of previous heat load on BT have not been determined. The aim of this study was to determine the effect of climate on BT, and to establish if BT lags changes in climatic conditions. BT of lactating Holstein-Friesian cows (n = 83) were collected at 10 min intervals over 5 to 7 d using temperature loggers (HOBO Pro V2) placed in the vagina. Cows had access to a feed pad and pasture and were kept outside in a sub-tropical environment. Ambient temperature (TA), black globe temperature (BG), and relative humidity (RH) were obtained every 10 min from an on-site weather station. Data were obtained during summer Jan/Feb (E), winter Jul/Aug (M) and summer Nov/Dec (L). Hourly means for BT, THI, BG, TA and RH were calculated for E, M and L. Multivariate ANOVA was used to determine residual correlations using partial correlation coefficients between BT and the climate variables. The lag effects of the variables on BT at h 0 were assessed by determining the relationships at −1, −2 and −3 h before 0 h. There were moderate correlations between BT, THI (0.51; $P < 0.001$) and TA (0.48; $P < 0.001$) at 0 h during E; and between BT, THI (0.47; $P < 0.001$) and TA (0.49; $P < 0.001$) at 0 h during L. There were weak correlations ($\leq$-0.07; $P > 0.05$) at 0 h between BT, THI, TA and BG during M. At 0 and – 1 h, the relationship between BT and BG was moderate during E (0.41 and 0.42 respectively; $P < 0.001$), whereas during L there was a stronger association at 0 h (0.42; $P < 0.001$), and at −1 h (0.40; $P < 0.001$). There was a weak relationship between BT and RH at 0 h during E (−0.14; $P < 0.001$), a moderate relationship during L (−0.35; $P < 0.001$), and a weak relationship during M (−0.06; $P > 0.05$). The lack of correlation between BT and climatic variables during M confirms that there was no adverse heat load during winter. It appears that BT is primarily driven by current or at the most the previous h ambient conditions during summer, at least on a herd basis. The relationship between BT and climate variables, in low, moderate and high production cows needs to be determined.

Key words: body temperature, dairy cows, heat load

460 Repeatability of subjective and objective measures of exit velocity as an indicator of temperament in feedlot cattle. M. D. D. Vetters*, T.E. Engle, J.K. Ahola, and T. Grandin, *Colorado State University, Fort Collins.*

Observations were collected for the purpose of comparing exit velocity evaluation; including a subjective rank scoring system (walk, trot, or run) and an objective measurement, to determine the repeatability of each measurement over time. Squeeze chute exit velocity was obtained for 1,100 crossbred yearling steers using a subjective (Sub) and objective (Obj) temperament scoring system. The Obj scoring system utilized infrared sensors to determine the time taken for an animal to traverse a fixed distance of 1.83 m, immediately after exiting the squeeze chute. The Sub temperament scoring measurement of: 1 = walk, 2 = trot, or 3 = run was assigned by 2 different observers when each steer crossed a fixed point between the infrared sensors. Observers also noted any incidence of jumping or falling by each steer. All animals were scored for each system (Sub and Obj) simultaneously upon exiting the squeeze chute on d 0 and d 21 of the experiment. The Sub score between observers on a single day showed considerable agreement (weighted Kappa 0.60) indicating the system is repeatable between different observers. However, the agreement for a single observer between d was only moderate (weighted Kappa 0.40) indicating a d effect for Sub score. In addition, although the mean velocities for d were not different ($P > 0.18$; 2.98 and 3.02 ± 0.04), the consistency of Obj exit velocity for each animal between the 2 weighing events was low (Spearman rank correlation coefficient = 0.25). These data indicate that the Sub and Obj measurement systems used in this experiment are reliable instruments for assessment on a given day; however, substantial variation exists for Sub and Obj temperament scoring across days. If this variation can be accounted for it could be possible to more accurately compare these systems of temperament assessment.

Key words: beef cattle, exit velocity, temperament

461 Group pasture versus stall housing effects on cortisol and DHEA concentrations in young Quarter Horses. S. M. Garey*, T. H. Friend, L. R. Berghman, J. E. Sawyer, M. M. Vogelsang, A. L. Adams, C. L. Terrill, and M. J. Carter, *Texas A&M University, College Station.*

Individual stall housing of horses is common in the US Whether horses are able to adapt to the stress of isolation, or if this type of housing presents a long-term stress for the animal is unclear. 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. Fourteen 2 to 3 year-old Quarter Horses were randomly assigned to either stall or pasture housing for 28 d. The 3.66 × 3.66 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 7 pasture horses were in one group on a novel 0.2 km^2 pasture. All horses were fed concentrate 2 times per day, while pastured horses had coastal grass, and stalled horses had coastal hay. 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 20 d. Plasma was analyzed by ELISA to determine cortisol and DHEA concentrations, and all samples were normalized against pre-treatment concentrations. A mixed model repeated measures ANOVA with unstructured covariance determined effects of treatment, sample time and sample time by treatment interaction. Stalled horses had significantly higher cortisol concentrations (4.62 ± 0.43 ng/ml) than pastured horses (3.27 ± 0.46 ng/ml, $P = 0.05$), although no significant differences were observed in DHEA ($P = 0.34$). There was no sample period by treatment interaction ($P = 0.55$). Plasma cortisol differences between treatment groups decreased in the final 4 d of the study, becoming equal by d 28. In conclusion, differences in cortisol concentrations between the treatment groups were significant, but diminished toward the end of the study. These results suggest that horses housed in an individual stall over an extended period of time may acclimate to the stress of isolation.

Key words: housing, stall, cortisol

462 Cortisol and DHEA concentrations in foals identified as high versus low behavioral responders during weaning. S. M. Garey*, T. H. Friend, L. R. Berghman, J. E. Sawyer, M. M. Vogelsang, A. L. Adams, C. L. Terrill, and M. J. Carter, *Texas A&M University, College Station.*

Weaning of young animals from their dams has been shown to induce stress. Frequent whinnying and increased movement displayed by foals are common behavioral indicators of distress. The objective of this study was to determine if cortisol or dehydroepiandrosterone (DHEA) differed among foals identified as high versus low behavioral responders during weaning. Fifteen 5 to 6 mo-old Quarter Horses were weaned by removal and relocation of their dams. Post-separation, the foals were housed in groups of 3 to 4 with ad libitum coastal hay and water. Jugular vena puncture blood samples were collected from the foals at 24 h and 0.5 h before separation, then every 24 h for 3 d and a final sample on d 5. To minimize stress during blood sampling, foals were handled and restrained in familiar stocks, with 2 foals per stock. Scan sampling at 2-min intervals for 30 min per day was done for 3 d post-separation to record movement, activity and number of vocalizations. Three observers also ranked the foals' display of distress relative to other foals in the study. Behavioral data were analyzed to rank and identify the 5 most distressed (MD) and 5 least distressed (LD) foals. A mixed model repeated measures ANOVA with unstructured covariance was used to determine differences in plasma cortisol and DHEA concentrations between MD and LD foals as well as sample time effects, and a Spearman correlation was used to identify associations between rank and average cortisol and DHEA. Cortisol ($P = 0.262$) and DHEA ($P = 0.298$) did not differ between MD and LD foals pre-weaning, and no interaction was found between the behavioral groups and sample time ($P = 0.167$). Overall, cortisol and DHEA did not differ between MD foals (9.97 ± 1.66 ng/ml, 3.39 ± 1.17 ng/ml) and LD foals (7.29 ± 1.66 ng/ml, $P = 0.287$; 0.38 ± 1.17 ng/ml, $P = 0.110$), respectively. Average DHEA was correlated with rank (r = 0.661, $P = 0.038$), however average cortisol was not (r = 0.071, $P = 0.80$). This study suggests that high responding and low responding foals may be experiencing similar distress during weaning.

Key words: weaning, behavior, cortisol

463 Preference for condensed tannins by sheep in resoponse to challenge infection with *Haemonchus contortus*. J. Juhnke[1], J. Miller[2], F. Provenza[1], J. Hall[3], and J. Villalba*[1], *[1]Utah State University, Department of Wildland Resources, Logan, [2]Louisiana State University, Department of Pathobiological Sciences, Baton Rouge, [3]Utah State University, Department of Animal Dairy and Veterinary Sciences, Logan.*

We determined the ability of parasitized lambs to modify their preference for a condensed tannin (CT)-rich feed after they experience the antiparasitic effects of CT. Twenty 2 lambs were familiarized with beet pulp (BP) and beet pulp + 8% quebracho tannins (BP+CT) and then given choices between the 2 feeds (before a parasitic infection). Subsequently, each animal was dosed with 10,000 infective larvae of *Haemonchus contortus*, and 22 d later they were exposed to BP (Control group; n = 11) or BP+CT (Treatment group; n = 11) for 24 d. After this exposure, animals in both groups were given a choice between the 2 feeds for 14 d. Feed intake, preference for BP+CT, fecal egg counts (FEC), and blood parameters were analyzed as a split-plot design with lambs (random factor) nested within group and day as the repeated measure. All lambs preferred BP to BP+CT throughout the study ($P < 0.001$) and no difference in preference for BP+CT was detected between groups before a parasitic infection ($P > 0.10$). However, during a parasitic infection, intake of and preference for BP+CT was higher for the Treatment than for the Control lambs ($P < 0.05$). When parasitic infections were terminated by chemotherapy, differences between groups in preference for BP+CT disappeared ($P > 0.05$). Preference for BP+CT by the Treatment group was higher during a parasitic infection than after chemotherapy ($P < 0.05$). Treatment lambs had lower FEC ($P < 0.05$), and red cell parameters indicated a lower degree of anemia in the Treatment than in the Control group ($P < 0.09$), suggesting tannins attenuated parasitic burdens. Thus, lambs needed to experience the beneficial antiparasitic effects of CT (Treatment) to increase their preference for the CT-containing food, indicating this behavior was learned. Preference for CT in the Treatment group was a function of parasitic infection as it subsided after chemotherapy. It may be possible through management programs to enhance utilization of tannin-rich forages and feeds by parasitized animals.

Key words: diet selection, endoparasites, foraging

464 Lack of acclimation in Holstein calves exposed to repeated transport. A. L. Adams*, T. H. Friend, G. A. Holub, S. M. Garey, C. L. Terrill, M. J. Carter, and A. J. Krenek, *Texas A&M University, College Station.*

Little is known about the adaptation of livestock to repeated transport stress. This study determined how repeated transport affected plasma cortisol (CORT) concentrations and post-transport calf behavior. Thirty-six 4-mo-old Holstein steer calves were housed in groups of 6 with each group randomly assigned to either transport (T) or control (C) treatments. T calves were transported for 6 h in their groups in a 7.3 m x 2.4 m goose-neck trailer divided into 3 compartments, at an average density of 0.87 m^2/calf, every 7 d for 5 consecutive wk. Location of groups within the trailer rotated. Simultaneous blood samples were obtained in the trailer or home pen via jugular venipuncture before loading, and after 2, 4, and 6 h of transport. Behavior was recorded for transported calves at 5-min intervals for 1 h after return to their home pens. CORT was analyzed as a repeated measure in a mixed model ANOVA. Latency to eat and lie down were analyzed in a mixed model ANOVA. Spearman rank correlations showed no association between CORT and behavior. The location of the calves in the trailer did not significantly affect CORT and basal CORT concentrations did not differ significantly for T calves. CORT during transit increased with each repeated transport, except during wk 5 ($P = 0.043$). CORT

concentrations peaked after 2 h of transit (11.17 ± 0.84 ng/ml) and decreased after 4 and 6 h of transit (4 h: 8.21 ± 1.17 ng/ml, 6 h: 5.73 ± 0.74 ng/ml, $P < 0.0001$). T calves had higher CORT concentrations than C calves after 2 h (C: 6.98 ± 0.86 ng/ml) and 4 h (C: 6.94 ± 1.2 ng/ml) of transit, but had lower CORT than C calves after 6 h of transit (C: 7.28 ± 0.76 ng/ml, $P < 0.0001$). Calves transported in the rear of the trailer were the first calves to lie down when returned to their pens ($P = 0.0008$) and the last calves to attend the feed bunk ($P = 0.022$). As temperature-humidity index increased, calves located in the rear of the trailer began to lie down sooner post-transport ($P = 0.018$). These results suggest that calves did not start to acclimate after being transported 5 times and that calves transported in the rear compartment of the trailer were the most fatigued.

Key words: calves, cortisol, transport

Bioethics Symposium: The Ethical Food Movement: What Does it Mean for Animal Agriculture?

465 Food production using animals: The roles of media coverage and societal values in shaping opinions about ethics. S. Priest*, *University of Nevada, Las Vegas.*

While the news media may set the agenda for public debate about science, they rarely cover ethics in any depth, and yet much news about science is fraught with ethical implications. Social amplification theory argues that media accounts can help amplify, as well as attenuate, risks. However, news producers do not create these effects independent of other influences. Both information subsidies and levels of cultural resonance are also important, and the technical definition of risk is not the only determinant of public opinion. Expectations and beliefs, including non-risk-related concerns such as perspectives on ethics, come into play. This is illustrated by data from a pilot study using student subjects that looks at initial reactions to the use of nanotechnology, genetic engineering, and synthetic biology with respect to genetic alteration of either cattle or bacteria; the results show that the type of organism involved is more important than the technology, indirectly suggesting the relevance of ethical considerations. While this small study may not be generalizable to a different population, it serves to remind us that public thinking is not solely a function of scientific understanding. The agricultural community could benefit by being more responsive to public (that is, consumer) opinion. Science itself cannot resolve what are essentially disagreements about values. When agriculturists and scientists blame the news media for negative public reactions, this can become a rationale for disregarding popular criticisms rather than taking them seriously. Not only is this ethically questionable, it is not necessarily in the strategic interests of the scientific and agricultural communities. Arguably, the GM food controversy arose in part because agriculture initially ignored the views of the public, including their ideas about ethical agricultural practices. It is a basic tenet of progressive public relations practice that communication should be 2-way and take public opinion into account.

Key words: animal agriculture, media role, bioethics

466 The (mis)appropriation of science in framing the ethics of animal production: Environmental issues. J. L. Capper*, *Washington State University, Pullman.*

Today's consumer has a heightened awareness of environmental issues relating to animal production. All foods have an environmental impact, yet the desire to "know where your food comes from" and idealistic views of "traditional" or "natural" production systems have led to product differentiation based on environmental claims. Various niche markets have reported that extensive systems are more environmentally sustainable. This exacerbates the challenge faced by the conventional livestock industry in providing sufficient milk, meat and eggs to feed the growing population while maintaining environmental stewardship. Yet low productivity within extensive systems significantly increases resource use per kg of milk or meat produced. For example, grass-based beef finishing systems require 77% more animals, 83% more land, 326% more water and emit 74% more greenhouse gases (GHG) per kg beef than corn-based systems using modern technologies. Scientific results are also being inappropriately used to further the agendas of anti-animal agriculture groups. A recent report from the FAO concluded that improved productivity and intensification are necessary to reduce livestock's environmental impact, yet these recommendations were overshadowed by the widely-reported (and since disproved) conclusion that animal agriculture accounts for 18% of global GHG emissions. This figure has since been incorrectly applied as representative of animal agriculture's impact in all regions, regardless of variations in efficiency. International averages have also been used to represent regional systems in media reports of comparative water use for animal production, leading to misinformation and consumer confusion. The popular assumption that transportation is a major contributor to the environmental impact of food production has furthered interest in "local food" and "food miles," despite the increased fuel costs of individual vs. mass food transport. Scientific principles and logic must be used to communicate with the consumer and improve their understanding of environmental issues, while maintaining respect for social and personal belief systems.

Key words: environmental impact, beef, local food

467 What did they just say? Science, politics, and animal welfare. J. A. Mench*, *University of California, Davis.*

Scientific information is becoming increasingly important not only in framing the debate about farm animal welfare but in propelling significant changes in public policy. The media, often unfamiliar with animal production practices, rely on scientific reports as critical background for their stories. Multi-national retailers use scientific information when they develop their animal welfare programs and farm auditing standards, and in making purchasing decisions. So that's a good thing, right? But hold on. Why does there seem to be so much confusion about what the science, and the animal welfare scientists, are saying? Of course, disagreement in science is normal, expected, and healthy. In any socially relevant field of science value judgments inevitably come into play when scientists attempt to reconcile the incomplete, complex and often contradictory information that results from research. As long as the values underlying these differences of opinion are transparent, both science and the public dialog about contentious issues are well served. Unfortunately, it seems instead that the contradictions and complexities inherent to farm animal welfare research are increasingly being ignored, or even worse skillfully (mis)appropriated, to advance particular agendas. This has ramifications for the credibility of animal welfare science, and also suggests that a new tack needs to be taken in communicating with the public about animal welfare issues and the role that science plays in addressing them.

Key words: animal welfare, science, ethics

468 The (mis)appropriation of science in framing the ethics of animal production: The use of antibiotics. M. D. Apley*, *Kansas State University, Manhattan.*

At the scientific levels of regulatory agencies, such as the Food and Drug Administration Center for Veterinary Medicine (FDA/CVM), the agricultural antimicrobial use debate revolves around risk assessments, surveillance data, movement of resistance genetics, and antimicrobial selection pressures. Unfortunately, we are sometimes hampered by data-gathering abilities that are more advanced than our interpretive skill sets. An example of a regulatory challenge is eliminating most of the uses of antimicrobials for improvement in rate of gain or feed efficiency as proposed in FDA/CVM Draft Guidance 209 (2010). This

action assumes that the lowest, longest antimicrobial exposures are a primary driver for resistant subpopulation selection in food animals. Without evidence for this assumption, the danger in this approach is that the precedent for the future regulation of prevention, control, and therapeutic uses of antimicrobials is not based on scientific evaluation of risk and benefit. Current FDA/CVM thinking related to microbial safety is outlined in Guidance Documents 152 and 159. But as the debate moves upward in the regulatory environment and spills over into the political arena, these scientific principles tend to be reduced to sound bites augmented by agenda-related dips into selected data. Additional key debates subject to scientific horseplay include the impact of modern production methods on disease incidence, the quantity of antimicrobials used in animal agriculture, transfer of resistant bacteria and resistance genetics between animals and humans, and in vivo vs. in vitro pharmacodynamic properties of antimicrobials. Oversimplification of the resistance issue is also used to mislead the public. But even with all of the scientific shortcuts in the public arena, the food animal industry cannot act as if we do not cause changes in susceptibility profiles with our antibiotic use; we can affect antimicrobial populations, and bacteria can transfer through the food chain. The challenge is keeping all parties on the high road when deciding the actual effects and what to do about them.

Key words: antibiotics, resistance, ethics

Breeding and Genetics: Dairy Cattle Breeding I

469 Assessing accuracy of heat detection in dairy herds. H. Seegers*[1], D. Billon[1], E. Bossard-Apper[2], C. Ponsart[3], B. Grimard[4], and N. Bareille[1], *[1]Research Group Epidemiology and Risk Analysis Oniris-INRA, Nantes, France, [2]Agriculture School, Angers, France, [3]UNCEIA, Maisons-Alfort, France, [4]Veterinary School, Maisons-Alfort, France.*

Herd reproductive performance depends on accuracy of heat detection and conception rate. Assessing the accuracy of the detection practices on a farm is a quite difficult exercise. Therefore, the objective was to provide a method to estimate the accuracy of heat detection in dairy herds, using quite only data available in fertility reports (mainly information about calving and insemination dates). A first step relied on the development of a simulation model to represent the biological processes (cyclicity resumption, detectability of ovulation, conception rate, embryonic and fetal deaths) and managerial processes (detection, submission rules, culling decisions) involved. This simulation tool was then used to generate fertility reports for 384 scenarios with known levels in sensitivity and specificity of heat detection, in combination with different levels for other parameters (especially herd size, milk yield, conception rate and managerial rules). At second step, the simulation outcomes were analyzed with stepwise multiple regression models to obtain prediction equations for the accuracy criteria, using as predictors the criteria present in a classical fertility report. Accuracy criteria were the % detected within detectable heats (separating 2 periods: until 1st AI and After 1st AI) and the % of AIs outside an ovulation period. At third step, these prediction equations were applied to a data set of 40,000 yearly fertility reports to obtain the distribution of estimated accuracy criteria in a population of 10,000 French farms with Holstein herds. Raw estimates calculated from the data set were almost considered plausible by authors and external experts. The % of detection averaged 55.3% (Q1 = 40.1; Q2 = 58.2; Q3 = 73.7) until the 1st AI and 50.1% (Q1 = 38.2; Q2 = 50.1; Q3 = 63.4) later. The % of AIs done outside an ovulation period averaged 6.3% (Q1 = 2.9; Q2 = 5.7; Q3 = 9.1). A test of the method is ongoing, based on confrontation with AI technicians guesses for a sub-sample of farms. If consistency reached is deemed sufficient, a use on a semiquantitative scale (very good, good, intermediate, low and very low) seems to be an acceptable way to express the results for farmers and advisors.

Key words: dairy cow, estrus, detection

470 Heritability and repeatability estimates for twinning rate in the Irish dairy and beef cattle. A. M. Doyle[1], R. D. Evans[2], and A. G. Fahey*[1], *[1]University College Dublin, Belfield, Dublin [4], Ireland, [2]Irish Cattle Breeding Federation, Bandon, Co. Cork, Ireland.*

Twinning rate is a complex threshold trait with a binary phenotype (1 = single, 2 = twin) and a quantitative phenotype. Increasing the twinning rate in beef cattle and decreasing twinning rate in dairy cattle could have positive economic effects for both industries. In beef cattle twinning can increase the rate of production if problems associated with twinning such as dystocia, longer rebreeding and retained placentas can be overcome. Decreasing twinning in dairy cattle would be beneficial as although twinning can increase milk production, fertility problems and the occurrence of freemartins make it disadvantageous. The objective of this study was to estimate the heritability and repeatability for twinning rate in 6 dairy (n = 1,070,457) and 10 beef (n = 83,476) breeds in Ireland using SAS 9.1 Software and DMU Animal Breeding Software. Heritability and repeatability estimates were analyzed using a linear animal model with fixed effects for herd-year-season, parity, age, heterosis and recombination; while sire and dam were included as random effects. Heritability was estimated to be between 0.002 and 4.0% and 0.0–4.1% for dairy and beef breeds respectively, and repeatability was estimated to be between 0.002 and 6.1% and 0.002–8.1% for dairy and beef breeds respectively. Twinning rate increased as parity increased. A comparison of gestation length between single and twin births found gestation length of twins to be significantly ($P < 0.05$) shorter than single births. The analysis suggests that there is a genetic component to twinning rate in dairy and beef breeds and this trait could be included in national selection index to reduce the incidence of twinning in dairy cattle and increase the rate of twinning in beef cattle due to a cumulative effect over time.

Key words: twinning, repeatability, heritability

471 Genetic analysis of ovulatory disorders in Austrian Fleckvieh cows: A comparison between linear models and survival analysis. A. Koeck*[1,2], B. Fuerst-Waltl[2], J. Sölkner[2], C. Egger-Danner[3], and G. Meszaros[2], *[1]Department of Animal and Poultry Science, University of Guelph, Guelph, ON, Canada, [2]Division of Livestock Sciences, University of Natural Resources and Life Sciences, Vienna, Austria, [3]ZuchtData EDV-Dienstleistungen GmbH, Vienna, Austria.*

The aim was to compare linear models and survival analysis for genetic analysis of ovulatory disorders, which included veterinary treatments of silent heat/anestrus and cystic ovaries. Data of 23,450 daughters of 274 Austrian Fleckvieh sires were analyzed. For linear model analyses, ovulatory disorders were defined as a binary response (presence or absence) in the time periods from calving to 150 d after calving and from calving to 300 d after calving. For survival analysis, ovulatory disorders were defined either as the number of days from calving to the day of the first treatment for an ovulatory disorder (uncensored record) or from calving to the day of culling, or the last day of the period under investigation (until 150 or 300 d after calving; censored record). Estimates of heritability were very similar (0.016 to 0.020) across methods and periods. Correlations between sire EBV from linear model and survival analysis were 0.98; whereas correlations from different time periods were slightly lower (0.95 and 0.96).

Key words: ovulatory disorder, linear model, survival analysis

472 Montbeliarde-sired crossbred cows compared to pure Holstein cows for production, SCS, days open, and survival during their first three lactations. A. R. Hazel*, L. B. Hansen, B. J. Heins, and J. G. Linn, *University of Minnesota, St. Paul.*

Montbeliarde × Holstein crossbred cows (MH, n = 58) and Montbeliarde × Jersey/Holstein crossbred cows (MJH, n = 78) were compared with pure Holstein cows (HO, n = 122) for 305-d milk, fat, and protein production, SCS, days open (DO), and survival during the first 3 lactations. Cows were in 2 research herds of the University of Minnesota and calved from October 2005 to June 2010. Best Prediction was used to calculate production for 305-d lactations with adjustment for age at calving, and records less than 305 d were projected to 305 d. Cows were required to have at least 250 DIM for DO, and cows with DO greater than 250 d were truncated to 250 d. For production, SCS, and DO, independent variables for statistical analysis were the fixed effects of herd, parity group (primiparous or multiparous), breed, interaction

of herd and parity group, lactation number (2 or 3) nested within multiparous parity group, herd-year of calving nested within interaction of herd and parity group, interaction of herd and breed, interaction of lactation number nested within parity group and breed, interaction of herd, lactation nested within parity group, and breed, and random cow nested within breed. The MH, MJH, and HO, respectively, were not significantly different ($P > 0.05$) for fat plus protein production during first lactation (503 kg, 496 kg, 514 kg), second lactation (605 kg, 604 kg, 605 kg), or third lactation (675 kg, 645 kg, 656 kg). The MH (2.11) had lower SCS ($P < 0.05$) than MJH (2.57) and HO (2.70) during second lactation, and MH (2.67) had lower SCS ($P < 0.05$) than HO (3.39) during third lactation. The MH (133 d) and MJH (122 d) had fewer DO ($P < 0.01$) in first lactation than HO (170 d). During second lactation, MH (141 d) and MJH (140 d) had fewer DO ($P < 0.05$) than HO (179 d). The MH had higher survival rates ($P < 0.01$) than HO to third (62% vs. 39%), fourth (44% vs. 16%), and fifth (32% vs. 8%) calving. The MH (4%) and MJH (4%) had lower mortality rates ($P < 0.05$) than HO (17%) within 3 years of first calving.

Key words: crossbreeding, heterosis, Montbeliarde

473 Joint estimation of genetic parameters for test day somatic cell count and mastitis using a random regression model in the United Kingdom. R. Mrode*, T. Pritchard, M. Coffey, and E. Wall, *Scottish Agricultural College, Penicuik, Midlothian, UK.*

Genetic parameters were estimated in a joint analysis of log-transformed somatic cell count (SCC) and mastitis (MAS) in Holstein/Friesian cows for the first 3 parities using a random regression model. There were 67175, 30,617 and 16,366 cows with records for SCC in parities 1, 2 and 3 respectively. Corresponding numbers for MAS were 9070, 6009 and 4012 respectively. The percentage incidence for MAS was 14, 20 and 25% in parities 1, 2 and 3 respectively. The model for SCC included herd-test-day, fixed lactation curves nested with calving year-groups, age and month at calving, random regressions with Legendre-polynomials of order 2 for animal and permanent environmental (PE) effects. The model for MAS included fixed herd-year-season, age and month of calving, random animal and PE effects. Two separate analyses were implemented with MAS analyzed as binary trait or as number of infections in the lactation. The analyses were carried out using Gibbs sampling with a chain length of 120,000, of which the first 40,000 were discarded as burn-in period. Estimates of heritability were 0.11, 0.14 and 0.15 for SCC in parities 1, 2 and 3 respectively. Corresponding estimates for MAS were 0.05, 0.07 and 0.09 as a binary trait. Estimates for MAS using number of infections were similar at 0.06, 0.07 and 0.12. Posterior standard deviations were about 0.01 for all estimates. The genetic correlation of 0.75 estimated between parities 1 and 2 for SCC was lower than the 0.92 between parities 2 and 3. The corresponding estimates for MAS were 0.54 and 0.89 respectively from the binary analysis. SCC in the first 3 parities had genetic correlations of about 0.55 with MAS in the first parity but this increased to about 0.63 with MAS in parity 2. However, the genetic correlations between SCC in parities 1 and 2 with MAS in parity 3 were about 0.48 while it was 0.68 between SCC and MAS in the third parity. It is intended that the new parameters will be used in setting up a national evaluation system for the joint analysis of SCC and MAS.

Key words: somatic cell count, mastitis, genetic parameters

474 Estimation of genetic parameters for health and survival in Canadian Holstein calves. C. E. McCorquodale*[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, [2]Guelph Food Research Centre, Agriculture and Agri-Food Canada, Guelph, Ontario, Canada, [3]Canadian Dairy Network, Guelph, Ontario, Canada, [4]Department of Animal and Poultry Science, University of Guelph, Guelph, Ontario, Canada.*

The objective of this study was to estimate the genetic parameters of calf survival and health in a population of Ontario Holsteins. Heifer calves on 16 south-western Ontario dairy farms were followed from time of birth to approximately 4 mo of age. Visits were made at 1–8 (T1), 14–22 (T2), 35–43 (T3) and 90–120 (T4) days of age. At each visit, the height, weight, temperature, and a health score were collected. A blood sample was taken at T1 to measure serum total protein using refractometry. Details of birth events and colostrum feeding information were recorded on individual birth records. Information on treatment for illness events and death information was collected for the duration of the study. In total 1,462 calves, sired by 246 different bulls were included in the study. Two linear animal models were used to analyze survival and treatment separately. Survival of calves was measured as a binary trait (0 = survived to T4; 1 = dead before T4) and treatment of calves at T1, T2 and T3 was recorded as a binary trait (0 = not treated; 1 = treated). Both models included the fixed effects of herd, season of birth with 4 classes, calving ease score with 4 classes, type of birth with 2 classes (1 = single birth and 2 = twin), and weight group with 5 classes. Fixed regressions included the total volume of colostrum consumed during the first 24 h and the serum total protein score. The random effects of the models included animal and residual. Estimates of heritability for treatment during T1, T2 and T3 were 0.11, 0.05 and 0.09, respectively. The heritability estimate for survival was 0.05. Similar to recently published data from Norway and New York State, heritability estimates for calf survival and health in Ontario calves give additional reason to consider routine genetic evaluation for these traits.

Key words: Canadian Holstein, calf health and survival, genetic parameters

475 Genetic parameters of lactation yield in the tropical carora breed with random regression test-day models. E. Tullo*[1], S. Biffani[2], C. Maltecca[3], and R. Rizzi[1], *[1]University of Milan, Faculty of Veterinary Medicine, Department of Veterinary Science and Technology for Food Safety, Milan, Italy, [2]Parco Tecnologico Padano, Lodi, Italy, [3]Department of Animal Science, North Carolina State University, Raleigh, NC, USA.*

In tropical environments, lactation curves with lower peaks and higher persistencies might be desiderable from both an economical and a physiological standpoint. The objective of this study was to obtain genetic parameters for test day yields (TD), and persistencies (P) for the tropical breed Carora and to compare these with results from a standard 305-yield animal model. A random regression animal model (RR-AM) was employed for the analysis of 181,810 test day records collected in the west-central part of Venezuela from 1992 to 2009, and belonging to 7,075 Carora cows, daughters of 436 sires. Milk TD yields (kg), comprised between 5 and 305 DIM, were analyzed with a model that included fixed effects of class of age, year and month of calving, herd and third order Legendre polynomials of days in milk. Random effects were fitted for the interaction herd-year-month-of-test and for the additive genetic and permanent environmental effects. Third order Legendre polynomials were applied as random regression covariates for both additive genetic and permanent environmental effects. Estimated daily

heritabilities for milk yields ranged from 0.15 to 0.25, with the lowest values around the peak of the lactation. Within lactation repeatabilities ranged from 0.39 to 0.48. Genetic correlations among test days within lactation ranged from −0.20 to 0.99. To investigate differences among models, the re-ranking between EBVs for 305d yield, obtained with Lactation Animal Model (L-AM) and RR-AM was investigated. For the top 100 sires a rank correlation of 0.54 was found. The average re-ranking among sires was of 21.9 ± 16.93. Correlations between persistency and 305d milk yield EBV ranged from 0.06 (P as a deviation from the peak) to 0.32 (P as production difference between the first and the second stage of lactation). Understanding persistency trends with respect to milk yield, in tropical enviroment should allow selecting individuals able to express their potential genetic values without incurring in excessive heat stress losses.

Key words: random regression test-day model, tropical dairy cattle, persistency

Breeding and Genetics: Quantitative Animal Breeding

476 Cooperation under directional selection with kinship-based groups. F. Siewerdt*[1], A. D. Franklin[1], J. A. Carrillo[1], A. K. Sasikala-Appukuttan[1], A. S. Schierholt[2], T. E. Callicrate[1], M. A. Campbell[1], and H. L. M. Moreira[3], *[1]University of Maryland, College Park, MD, [2]Universidade Federal Rural da Amazônia, Belém, PA, Brazil, [3]Universidade Federal de Pelotas, Pelotas, RS, Brazil.*

The goal of this selection experiment was to determine if the accumulation and expression of genes with associative genetic effects is dependent on selection being performed in the presence of closely related individuals. Laboratory colonies of *Tribolium castaneum* were assigned to 3 selection lines and 3 replications. A selection line consisted of 64 demes of 16 adults, placed in small glass jars with a small amount of medium (95% flour and 5% yeast) in a walk-in incubator with controlled temperature and humidity. The medium was a limiting factor for census growth of the deme, creating competition between individuals and the opportunity for reduction in reproductive activity and manifestation of cannibalism. Two lines were group selected for increased number of adults at 35 d after establishment of the demes. The best demes were used to place as many demes in the following generation as possible. In one selection line kinship structure was preserved in consecutive generations by placing new demes only with beetles from the same original deme. In the other selection line the deme structure was disrupted at each generation by placing the new demes with beetles coming from 16 different demes in the previous generation. A randomly selected control was kept; adult counts were expressed as deviations from this line. Each selected line was split into 2 lines at generation 11. One newly formed line was kept on the original selection strategy and the other was placed on the competing selection strategy. After 16 generations of selection, genetic gains suggest that accumulation and expression of associative genetic effects may be dependent on the presence of kin. Average cumulative genetic gains in the selected lines with intact deme structure and with disrupted deme structure were, respectively, 49.8 ± 10.1 and 28.9 ± 2.7 adults. Between-deme variability was 5.5 times higher in the lines with intact deme structure. Swapping selection strategies at generation 11 had no effect on genetic progress measured at generation 16. There may be latency in the expression of accumulated associative genetic effects, which could only occur in the presence of close kin.

Key words: *Tribolium castaneum*, Associative genetic effect

477 A recursive binomial model for piglet mortality. L. Varona*[1] and D. Sorensen[2], *[1]Unidad de Genetica Cuantitativa y Mejora Animal, Universidad de Zaragoza, Zaragoza, Spain, [2]Department of Genetics and Biotechnology, University of Aarhus, Tjele, Denmark.*

Several interesting traits in animal production do not follow a Gaussian distribution. Statistical procedures based on Bayesian analysis allows to model successfully unconventional distributions of data. However, sometimes is not clear how to model environmental correlation between traits. Structural models may provide a useful alternative to model this relationship. In this study, we have developed a recursive procedure between a linear (litter size) and a binomial trait (number of piglets born dead) and we have tested the procedure with data from 2 Danish pig breeds: Landrace and Yorkshire. The Landrace data set included 5178 litter size records and a pedigree file of 8800 individuals, whereas the Yorkshire data set consisted of 3938 litter size records and a pedigree file of 7143 individuals. The posterior mean (and standard deviation) estimates of the recursive parameter of litter size on the logit-transformation of the probability of born dead were 0.094 (0.005) and 0.121 (0.007) for Landrace and Yorkshire, respectively. These results indicate that as litter size increase, the probability of a piglet to born dead also does. Moreover, the procedure provides a useful alternative to model non genetic relationship between traits. The adequacy of the model was tested by the logarithm of the conditional predictive ordinate of data, showing that the proposed model improves the predictive ability over the one that does not include the recursive relationship with litter size.

Key words: recursive models, pig, Bayesian analysis

478 Genetic correlation between purebred piglet birth weight and crossbred performance. C. Y. Chen*[1,2], I. Misztal[1], S. Tsuruta[1], J. Holl[3], W. O. Herring[3], and M. Culbertson[3], *[1]Department of Animal and Dairy Science, University of Georgia, Athens, [2]Newsham Choice Genetics, Chesterfield, MO, [3]Smithfield Premium Genetics Group, Rose Hill, NC.*

The objective was to estimate the genetic correlation between purebreds and crossbreds for several weight traits. Data consisted of 157,600 purebreds (Durocs) and 94,185 crossbreds (Duroc x (Large White x Landrace). Traits were purebred birth weight (PBWT), crossbred birth weight (CBWT), crossbred carcass weight per day of age (CWDA), and binary crossbred hot carcass weight (CHCW) with cutpoint at 75 kg. Two linear 3-trait models (PBWT, CBWT, and CWDA) and one linear-threshold 3-trait model (PBWT, CBWT, and CHCW) were used. Fixed effects included sex, parity, and litter size for all models with age at slaughter for CHCW. Contemporary groups were fitted differently for linear traits (fixed) and CHCW (random). Random effects of litter and residual were included for all models. Genetic effects were fit differently for purebreds (animal additive) and crossbreds (animal or sire additive). A dam effect (composed of genetic and environmental) was also evaluated for crossbreds. Heritability was 0.18 for PBWT with all models. For CBWT, estimates of heritability were 0.07 with the animal model and from 0.03 to 0.05 with the sire models. For CWDA, same estimates were 0.17 and 0.12 for animal additive and sire genetic effects, respectively. Heritability was 0.08 for CHCW. Estimates of genetic correlations ranged from 0.77 to 0.89 for PBWT-CBWT, 0.16 to 0.30 for PBWT-CWDA, 0.13 to 0.56 for CBWT-CWDA, 0.45 for PBWT-CHCW, and 0.13 for CBWT-CHCW. The selection for birth weight in purebreds is efficient for selection of birth weight in crossbreds. Such a selection is also useful in achieving market weight in crossbreds.

Key words: birth weight, crossbreds,, genetic correlation, pigs

479 Construction of individual breeding values for feed intake of Piétrain boars based on mean pen feed intake, weight and weight gain test station records. M. Dufrasne*[1], V. Jaspart[2], J. Wavreille[3], and N. Gengler[1,4], *[1]Animal Science Unit, University of Liege, GxABT, Gembloux, Belgium, [2]Walloon Pig Breeders Association, Ciney, Belgium, [3]Walloon Agricultural Research Centre, Gembloux, Belgium, [4]National Fund for Scientific Research, Brussels, Belgium.*

The aim of this study was to predict genetic merit of Piétrain boars for feed intake by constructing an index combining individual residual feed intake (RFI), average daily gain (ADG) and live weight (LW) of their progeny. Reliabilities of estimated breeding values (EBV) of 50

recently tested boars for individual Estimated Feed Intake (EFI) and for Index Feed Intake (IFI) were compared. Data were collected on pigs in test station in context of the genetic evaluation system of Piétrain boars for crossbred performances in the Walloon Region of Belgium. Because there were no facilities to record individual feed intake, individual EFI was computed as the total pen feed intake divided by number of individuals per pen. Data file contained 1 397 records of individual EFI. Model developed was an animal model with sex and pen as fixed effects. EBV for ADG between 100 and 210 d and for LW at 100 d were defined as linear covariables, therefore EBV are expressing RFI. Mean EFI was 1 876.8 g/d with a SD of 177.5 g/d. Heritability for EFI considered without regressions on ADG and LW was 0.08 and mean reliability of EBV was 0.16 which was low to base selection decision. Coefficients of linear regression estimated were used to estimate IFI as followed: IFI,g/d = RFI,g/d + 2.61 LW,kg + 214.37 ADG,kg/d. Heritability for RFI was 0.06 and was low compared with literature. Heritability for IFI was 0.09 which was more consistent with literature values. Mean reliability for RFI was 0.13 and mean reliability for IFI was 0.35. Therefore, thanks to combining RFI with EBV for ADG and LW which have high mean reliabilities (0.71 for ADG and 0.72 for LW) accuracy of EBV for individual feed intake was increased. These results show that with index combining genetic values of growth and live weight with RFI, genetic potential for individual feed intake of boars could be estimated more accurately than with only individual EFI.

Key words: feed intake, index, reliability

480 Genetic correlations between purebred Limousin and F1 Limousin*Angus. R. Davis*[1], I. Misztal[1], M. Lukaszewicz[1,2], S. Tsuruta[1], and J. K. Bertrand[1], *[1]University of Georgia, Athens, [22] Polish Academy of Sciences, Institute of Genetics and Animal Breeding, Jastrzębiec, Poland.*

The purpose of this study was to estimate correlations between purebred and crossbred animals to verify efficiency of current models used in crossbreeding selection. Records on 3 weight traits: birth weight (BW), weaning weight (WW) and post-weaning gain (PW) from a purebred Limousin line (L) and a crossbred line made of Limousin*Angus F1 progeny (F1), were used to estimate correlations between crossbred and purebred animals as well as other genetic parameters using single trait models (ST; weights are the same traits in both populations) and a multiple trait crossbred model (MT; weights are different traits). For BW there were 148,647 records for L and 17,981 for F1, for WW 81,585 for L and 21,778 for F1, and for PW 37,687 for L and 11,021 for F1. Fixed effects in all models for L and F1 animals were contemporary group and month. Random effects for L animals in both models were direct genetic, maternal genetic and maternal permanent environment. Random effects for F1 were sire genetic and dam environmental. The pedigree for Angus dams was unavailable and therefore these dams were assumed unrelated. In the ST model, direct heritability estimates for purebred animals were 0.38, 0.22 and 0.31 for BW, WW and PG, respectively. For F1, the same estimates were 0.21, 0.34 and 0.34. Genetic correlations estimates between purebreds and crossbreds were 0.4, 0.6 and 0.3 for BW, WW and PG, respectively. The purebred selection in is only partially effective on crossbreds, especially for BW and PG. The selection is effective for WW where the lower genetic correlation is compensated by higher heritability. Estimates in this study may be biased by the ignoring of maternal pedigrees in F1.

Key words: crossbreeding, F1, correlation

481 The heritability of lean color and its influence on beef tenderness. P. Johnson*[1], D. Moser[2], and M. Miller[1], *[1]Texas Tech University, Lubbock, [2]Kansas State University, Manhattan.*

The objective of this study was to determine heritability estimates of lean color, as measured by subjective scoring and Hunter Colorimeter readings, and its phenotypic and genetic correlation with tenderness in beef. Data were collected over 5 years on the longissimus dorsi muscle of 1,277 head; 12 different breeds were represented. Tenderness was measured by Warner-Bratzler shear force (WBSF) and quantitative ratings were given for initial tenderness and sustained tenderness by trained sensory panelists. Phenotypic correlations were found using the GLM procedure of SAS and variance and covariance components were obtained using MTDFREML. Lean color was found to be moderately heritable (0.34 ± 0.122) while the heritability estimates of Hunter colorimeter readings varied; 2 were moderately heritable: a* (0.29 ± 0.115) and b* (0.28 ± 0.120), while the third was lowly heritable, L* (0.09 ± 0.087). Phenotypic correlations found to be significant ($P < 0.01$) were: lean color and WBSF, a* value and WBSF, L* value and WBSF, lean color and initial tenderness, L* value and initial tenderness, lean color and sustained tenderness, L* value and a* value, L* value and b* value and a* value and b* value. Both a* and b* values were found to be highly and negatively correlated genetically with WBSF (−0.71 and −0.72, respectively). The genetic correlation between lean color and WBSF was −0.46. The genetic correlations of a* value and b* value with WBSF were both high, −0.71 and −0.72, respectively. The genetic correlation between lean color and initial tenderness was also high, 0.56, while that between a* value and initial tenderness was 0.43; similar to that found between b* value and initial tenderness, 0.44. The genetic correlations between lean color and sustained tenderness, a* value and sustained tenderness and b* value and sustained tenderness were all found to be high at 0.58, 0.70 and 0.58, respectively. The genetic correlation between a* value and b* value was also found to be high, 0.63. In conclusion, regardless of how lean color is measured, it is not only heritable, but has also been shown to be moderately and highly correlated with measurements of tenderness in beef.

Key words: beef, tenderness, color

482 Multivariate characterization of morphological traits in Nigerian sheep. A. Yakubu[1], M. Okpeku[2], M. Wheto[3], S. Amusan[3], B. O. Agaviezor[4], M. A. Adefenwa[5], B. M. Ilori[3], O. Ajayi[3], G. O. Onasanya[3], J. Ekundayo[3], T. Sanni[3], C. O. N. Ikeobi[3], M. I. Takeet[6], and I. G. Imumorin*[7], *[1]Dept of Animal Science, Nasarawa State University, Lafia, Nigeria, [2]Department of Livestock Production, Niger Delta University, Amassoma, Nigeria, [3]Department of Animal Breeding and Genetics, University of Agriculture, Abeokuta, Nigeria, [4]Dept of Animal Science and Fisheries, University of Port-Harcourt, Port-Harcourt, Nigeria, [5]Dept of Cell Biology and Genetics, University of Lagos, Lagos, Nigeria, [6]Dept of Veterinary Microbiology and Parasitology, University of Agriculture, Abeokuta, Nigeria, [7]Dept of Animal Science, Cornell University, Ithaca, NY.*

Principal component and discriminant analyses were performed to investigate distinction and patterns of morphological variation among 4 indigenous sheep breeds sampled from all over Nigeria. Body weight and 9 linear type traits (withers height, rump height, body length, ear length, fore cannon bone length, tail length, chest girth, chest depth and rump width) were measured in 402 randomly selected West African Dwarf (WAD), Yankasa, Uda and Balami sheep, respectively. The morphometric traits of Uda and Balami sheep were significantly ($P <$

0.05) higher than those of Yankasa sheep, which in turn had a comparative advantage over their WAD counterparts. There was variation in the pattern of the loading traits of the principal components (PCs) of each sheep breed. This was further revealed by the differences in the degree of accuracy when body weight was predicted from the scores derived from the PCs of each genetic group. Based on Mahalanobis distances, the least differentiation was observed between Uda and Balami sheep (0.298) while that between WAD and Balami sheep was longest (18.004). While 93.33% of WAD sheep were correctly assigned into their source genetic group, 63.93% of Yankasa, 45.16% of Uda and 61.15% of Balami sheep were classified into their source population in the nearest neighbor discriminant analysis. The present phenotypic information could be exploited in designing appropriate management, conservation and breeding programs for Nigerian indigenous sheep.

Key words: multivariate analysis, sheep, Nigeria

483 Multivariate analysis of morphological differentiation in Nigerian goats. A. Yakubu*[1], M. Okpeku[2], M. Wheto[3], S. Amusan[3], B. O. Agaviezor[4], M. A. Adefenwa[5], B. M. Ilori[3], O. Ajayi[3], G. O. Onasanya[3], J. Ekundayo[3], T. Sanni[3], C. O. N. Ikeobi[3], M. I. Takeet[6], and I. G. Imumorin[7], *[1]Dept of Animal Science, Nasarawa State University, Lafia, Nigeria, [2]Department of Livestock Production, Niger Delta University, Amassoma, Nigeria, [3]Department of Animal Breeding and Genetics, University of Agriculture, Abeokuta, Nigeria, [4]Department of Animal Science and Fisheries, University of Port-Harcourt, Port-Harcourt, Nigeria, [5]Dept of Cell Biology and Genetics, University of Lagos, Lagos, Nigeria, [6]Dept of Veterinary Microbiology and Parasitology, Abeokuta, Nigeria, [7]Dept of Animal Science, Cornell University, Ithaca, NY.*

The objective of the study was to morphologically characterize Nigerian indigenous goats using multivariate statistical analyses. Body weight and 9 biometric traits were measured in 352 randomly selected West African Dwarf (WAD), Red Sokoto (RS) and Sahel (SH) goats of both sexes categorized into 3 age groups from across Nigeria. The univariate analysis showed that breed, sex and age of the animals significantly ($P < 0.05$) affected the body parameters. The principal component analysis revealed variation in the morphometric characters of the goats. Stepwise discriminant analysis showed chronologically that tail length, rump width, rump height, ear length and body length were the most discriminating variables among different pair-wise breeds' comparisons. In the canonical discriminant analysis, the first canonical variate was significant and accounted for 95.5% of the variability among the goat breeds. The longest Mahalanobis distance was that between WAD and SH goats (11.44; $P < 0.001$) while the shortest was recorded for RS and SH goats (1.50; $P < 0.01$), respectively. The dendrogram showed 2 large clusters indicating that WAD and the 2 other goat breeds are separate genetic entities. Discriminant functions correctly allocated 65.79% of individual goats to their a priori breeds, although a sort of genetic introgression was observed between RS and SH goats. The present findings combined with molecular characterization could aid the formulation of management, breeding and conservation strategies for Nigerian indigenous goat resources.

Key words: multivariate analysis, goats, Nigeria

484 Searching for causal relationships among five traits of European quails. B. D. Valente*[1,2], G. J. M. Rosa[1,3], M. A. Silva[2], R. B. Teixeira[4], and R. A. Torres[4], *[1]Department of Animal Sciences, University of Wisconsin, Madison, [2]Departamento de Zootecnia, Universidade Federal de Minas Gerais, Belo Horizonte, Minas Gerais, Brazil, [3]Department of Biostatistics and Medical Informatics, University of Wisconsin, Madison, [4]Departamento de Zootecnia, Universidade Federal de Viçosa, Viçosa, Minas Gerais, Brazil.*

Structural equation models (SEM) allow modeling multiple traits expressing casual links among them. The number of different causal structures that can be used for fitting a SEM is typically huge, even when only a few traits are studied. In recent applications of SEM in mixed model settings, causal structures were pre-selected based on prior beliefs alone. Alternatively, causal structure spaces can be explored using algorithms that search for structures that are compatible with the joint distribution of the traits. However, in mixed models settings, the search cannot be performed directly on the joint distribution of the phenotypes as causal relationships are possibly masked by genetic covariances. In this context, it has been proposed that such search could be performed by applying the Inductive Causation (IC) algorithm to the joint distribution of phenotypes conditionally to unobservable genetic effects. Here, we applied this approach to a data set of 5 traits of European quails: birth weight (BW), weight at 35 d of age (W35), age at first egg (AFE), average egg weight from 77 to 110 d of age (AEW), and number of eggs laid in the same period (NE). We focus the discussion on the challenges and difficulties resulting from applying this method to field data. Statistical decisions were based on different Highest Posterior Density (HPD) interval contents (70, 75, 80, 85, 90, and 95%). Resulting causal structures were fitted and models were compared using the Deviance Information Criterion (DIC). In addition, we used temporal information to perform additional edge orienting, overriding the algorithm output when necessary. As a result, the final causal structure consisted of 2 separated substructures: BW→AEW and W35→AFE→NE.

Key words: causal relationships, European quails, structural equation models

485 Withdrawn

Companion Animals Symposium: Living Beyond 20: Discoveries in Geriatric Companion Animal Biology

486 Living beyond 20: Discoveries in geriatric companion animal management, nutrition and behavior. C. L. Morris*, *Omaha's Henry Doorly Zoo, Omaha, NE.*

It has traditionally been the responsibility of the animal science community to develop management, nutrition, health and well-being protocols for animals raised for production purposes. The vast array of scientific inquiry dedicated to production livestock have been instrumental in the management of these animals to optimize a value-based end product. Within the last several decades however, the animal science landscape has changed and diversified to include companion and exotic animals. In contrast to production animals, companion and exotic animals typically are not managed for production purposes; therefore, shifting the goals of animal husbandry away from production and toward longevity. Companion animals are valued in the home for their companionship and service, while exotic animals are typically managed for exhibit, education, research, or species conservation programs. This diversification of species included within the scope of the Animal Science community has provided a new direction for research efforts as the majority of these animals should live healthy lives that allow them to reach their senior years. Approximately 25% of dogs and cats in the United States are over 7 years of age and a large number of captive zoo animals are considered geriatric. In fact, many exotic animal species live longer in captivity due to managed health practices, genetics, optimal nutrition, and appropriate husbandry. These are significant and growing animal populations with specialized needs regarding nutrition, veterinary care, and behavioral husbandry management. While research efforts have been invaluable in promoting the health and longevity of these aging animal populations, additional research efforts are still needed to better understand the physical, physiological, and cognitive changes of geriatric animals and how to apply those discoveries to animal husbandry. The objectives of this symposium are to explore the scientific discoveries specific to the quality of life, nutrition and well-being of geriatric companion and exotic animals and to encourage and promote future research related to these growing animal populations.

Key words: geriatric animals, husbandry

487 Longevity, not production: When rate of gain is not the focus. T. A. Faber and G. C. Fahey Jr.*, *University of Illinois, Urbana.*

Feeding companion animals involves a different focus and strategy than feeding livestock. Diets for companion animals must be designed to supply the nutrient needs of the animal not only for today but for years to come. Changes in health and appearance associated with animal aging are based on genetic control, gradual loss of homeostasis of physiological systems, accumulation of toxic compounds (i.e., lipofuscin and free radicals), or combinations thereof. To enhance longevity, the process begins in utero. Proper development is dependent on the nutritional status of the mother, as she is the sole source of nutrients. After birth until weaning, the animal is mainly dependent on mother's milk. The mother's diet influences the nutrient composition of her milk and, thus, the nutrients the offspring receives. Post-weaning, factors such as body weight gain, calcium:phosphorus ratio, and essential fatty acid intake, play a role in the physical and mental development of the animal. Promoting the proper development of these systems may prevent health issues that may occur later in life. As an adult, the animal's nutrient intake should allow maintenance of a healthy body weight and proper nutrient balance to limit stress on physiological systems. A healthy body weight alone has been shown to play an important role in longevity. As the animal enters a geriatric state, the body's physiological systems begin to slow and they lose the ability to replenish themselves. Energy requirements may decrease by 20%, while protein and essential fatty acid requirements increase. Feeding a highly digestible, highly nutrient bioavailable diet, may improve nutrient absorption and keep the body nourished. In addition, feeding supplements such as glucosamine and antioxidants may improve joint health and limit free radical damage, respectively. Targeted feeding strategies throughout life may enhance the longevity of the companion animal.

Key words: companion animals, health, longevity

488 Obesity: What is wrong with being fat? D. P. Laflamme*, *Nestle Purina PetCare Research, St. Louis, MO.*

Few diseases in modern pets are "diet-induced." One possible exception to this is obesity, which is ultimately caused by consuming more calories than needed by the dog or cat. While fat is the most concentrated and efficiently stored source of calories, and protein least so, an excess of calories from any source will contribute to adiposity. Obesity is an excess of body fat sufficient to result in impairment of health or body function. In people, this is generally recognized as 20–25% above ideal bodyweight. This degree of excess is important in dogs as well. A lifelong study in dogs showed that even moderately overweight dogs (mean body condition score [BCS] of 6.7 out of 9) were at greater risk for earlier morbidity and a shortened lifespan. In addition, these dogs required medication for chronic health problems sooner than their lean-fed siblings. The average difference in body weight between groups was approximately 25%. Obese cats also face increased health risks, including an increased risk of arthritis, diabetes mellitus, hepatic lipidosis and early mortality. The risk for development of diabetes increases about 2-fold in overweight cats and about 8-fold in obese cats. Altered adipokine secretion appears to be an important mechanism for the link between excess body weight and so many diseases. Adipose tissue, once considered to be physiologically inert, is an active producer of hormones such as leptin and resistin and cytokines, including many inflammatory cytokines such as tumor necrosis factor α (TNFα), interleukins 1β and 6, and C-reactive protein. The persistent, low-grade inflammation secondary to obesity is thought to play a causal role in chronic diseases such as osteoarthritis, cardiovascular disease, diabetes mellitus and others. TNFα, for example, alters insulin sensitivity by blocking activation of insulin receptors. In addition, obesity is associated with increased oxidative stress, which also may contribute to obesity-related diseases. Management of obesity involves nutritional modification as well as behavioral modification.

Key words: obesity, canine, feline

489 Cognition and behavior in geriatric animals: If they had Sudoku what would it look like? K. L. Overall*, *University of Pennsylvania, Philadelphia.*

Especially when it comes to pets, we often think that decrements in mental and physical acuity are "normal aging changes." What if such

changes are the result of an interaction of "lack of use" with physiological/molecular responses to a life of exposure to stressors? If this is true, and there is a now considerable evidence to suggest that it is, we may be able to ameliorate age-related cognitive changes through a series of interventions including medication, diet, exercise and targeted cognitive stimulation. The type of stressor may matter. Military working dogs who are deployed live longer than those who are not deployed: their world is stressful, but it also is stimulating. The trick may be to define "targeted cognitive stimulation" in non-humans. In short, what does Sudoku look like if you don't have written language? Problem solving can be tactile, olfactory, visual-spatial, social, et cetera, yet few of these avenues are pursued. New evidence from dogs suggests that there are creative interventions that can ensure that we may delay decrements in cognitive function in canines and other animals who depend on us. In turn, these animals may be excellent models for testing interventions for humans.

Key words: canine cognition, dog, brain aging

490 Skinny old critters: Managing diet and expectations. C. L. Morris[1] and J. Cline*[2], [1]*Omaha's Henry Doorly Zoo, Omaha, NE* [2]*Nestle Purina Petcare Product Technology Center, St. Louis, MO.*

There are significant unstoppable changes in multiple organ systems as animals age. The age at which visible or clinical signs of aging occur is dependent on species, genetics, lifestyle, environment and diet. Though aging is a natural progression of physiology, emerging research indicates that many changes may be delayed through appropriate dietary management and alterations in lifestyle and environment of geriatric animals. The aging process may impact diet palatability, intake and food preference in some geriatric animals as a result of physical changes in nasal epithelium, hyposmia, hypoguesia, or food fatigue/aversion. Additionally, a more serious "visible" sign of aging is the reduction in nutrient utilization along with energy demands that may be in conflict. For example, old dogs require about 40% more protein than young dogs of the same size (Wannamaker and McCoy 1966); however, energy demands in some animals may be elevated or reduced. Although obesity is a major concern in both pet animals and zoo animals, many pet cats and captive exotic felids lose body condition throughout the aging process. Up to 33% of cats over 11 have compromised fat digestibility and 25% of cats over 11 have decreased protein digestibility (Perez-Camargo 2010; Cupp 2010). With obesity being a major concern for companion and zoo animals, caloric restriction without malnutrition throughout the lifetime remains a proven method for extending lifespan and slowing the aging process in mammals (Anderson et al., 2009). During a 14 year study in dogs, it was concluded that age at which chronic disease required treatment could be delayed by about 2 years through calorie restriction during their lifetime. Most animals that live their natural lifespan will likely develop an age related disease. Prevalent "aging" diseases in companion and zoo animals include neoplasia, hypo/hyperthyroidism, diabetes, kidney, liver or heart disease. Management of animal's environments, diet, plane of nutrition, managing expectations of caregivers, and public perceptions will be discussed.

Key words: geriatric animal nutrition, companion animals, exotic animals

491 Bones and joints: Improving mobility in senior years. B. Lussier*[1,2], [1]*Department of Clinical Sciences, Faculty of Veterinary Medicine, University of Montreal, St-Hyacinthe, Quebec, Canada,* [2]*University Hospital Research Center, University of Montreal, Montreal, Quebec, Canada.*

Osteoarthritis (OA) is frequently encountered in small animal practices. It is a chronic, crippling disease. It has been reported to affect 20% of the canine population in the USA. It is a degenerative process invariably leading to joint effusion, fibrosis and pain thus reducing the quality of life of dogs. OA in dogs is secondary to conformational, hereditary, degenerative and traumatic diseases. The most frequent causes of OA in dogs are hip dysplasia, elbow dysplasia, osteochondrosis and rupture of the cranial cruciate ligament. Some of these are hereditary conditions, while the causes of others are unclear. It has been established that nutrition may play a role in modulating the occurrence or severity of these diseases. At a young age, nutrition is important to prevent or decrease the expression of developmental diseases of dogs. It has been reported that lifetime food restriction has a significant impact on the lifespan of dogs. It significantly increases median lifespan and decreases the prevalence and severity of OA in several joints. In the latter months or years, when dogs are clinically afflicted by OA, its treatment is multimodal. Management of OA consists of the following: surgically treating the primary cause if possible, reducing the patient's weight, using adapted activity combined with physical therapy, using therapeutic nutrition and finally using pharmacological therapy. The nutritional management of OA is 2 fold: weight management and therapeutic nutrition. It is well recognized that weight reduction can alleviate the clinical signs of OA in dogs and that a weight increase is detrimental to function in OA dogs. Therapeutic nutrition must thrive to provide nutrients that may help reduce inflammation and pain, support cartilage repair, slow the degenerative process, thus improving function of the patient. Specifically developed diets and supplements have been used. They contain: Ω-3 fatty acids, greenlipped mussels, L-carnitine, chondroitin sulfate, glucosamine, antioxidants, vitamins E and C. In conclusion, nutrition plays an important role in the prevention/delay of OA, in modulating the severity of OA and in the treatment of dogs clinically afflicted by OA

Key words: osteoarthritis, canine, nutrition

Dairy Foods Symposium: Innovations in Dairy Processing Unit Operations

492 Plate heat exchangers. J. C. Bohn*, *AGC Heat Transfer Inc., Bristow, VA.*

The role of the plate heat exchanger in pasteurization makes it arguably one of the most essential pieces of equipment in modern dairy operations. Plates designed specifically for sanitary applications have emerged with flow patterns that improve clean-in-place response, with pressing depths that cater to viscous flows, with surface finishes that enhance clean-ability, and with material thicknesses that yield improved mechanical strengths to withstand the process stresses as well as frequent opening and closing cycles. These plate characteristics have improved the overall operational efficiency of plate heat exchangers. The use of rheological data to characterize formulated dairy products, along with improved computational algorithms, has increased design accuracies of plate heat exchangers. The demand for increased production has forced plate manufactures to utilize various methods in designing units to accommodate extended run times as well as achieving good clean-in-place response. Ice pigging, using pump-able slurry, has been introduced as a new method of reducing product losses, improving cleaning times and reducing biological oxygen demand loads. Modern dairy operations have benefited from easily opened and closed hydraulically driven twin screw frames that improve worker safety while easing the burden of field inspecting the internal product contact surfaces at an appropriate frequency. Third party field inspection of plate heat exchangers has become a standard practice in most all dairy operations, is recommended by 3-A standard 11–09, and has proven to be a valuable tool in ensuring the operational readiness of dairy pasteurizers.

Key words: pasteurization, rheology, pasteurize

493 Dairy processing efficiency and safety gains from double-seat valve technology. L. W. Clem*, *Electrol Specialties Company, South Beloit, IL.*

Double-Seat or Mixproof valve technology has undergone design changes within the last few years that allow the US dairy processor to significantly benefit from their application. The valve design allows separation of 2 product streams or a product and cleaning solution stream in the space of a single hygienic valve all while under automatic control and position monitoring. The design improvements include technologies to further enhance the separation of liquid streams through specialized seat contours and/or the use of deflector discs to assure safety and complete separation of fluid streams. These new valve types are allowed specialized process operational consideration and are recognized by the Pasteurized Milk Ordinance as acceptable means to provide for separation of pipelines. The double seat valve can be applied without reservation in product receiving and storage, fluid batching and blending operations, thermal process systems, and everywhere there is a need to segregate products or cleaning solutions. Elimination of process openings or connection points reduce or eliminate potential product contamination and/or personnel exposure to fluids including hot or streams potentially containing chemical solutions for cleaning.

Key words: dairy processing, equipment, valves

494 Innovations in homogenizer and separator technology for the modern dairy plant. W. Rowlands*, *Rowlands Sales Co. Inc.*

Demand for improved shelf life, higher flow rates, and lower operating costs are affecting design and integration of homogenizers and separators in today's efficient dairy operation. Modern innovations must incorporate energy reduction and natural resource sustainability. Machinery longevity, possible negative product attributes, and additional maintenance burdens all need to be considered. Evolving trends in homogenizer design include noise and vibration reducing drives, energy conserving low pressure homogenizing valves, cylinder blocks with improved CIP path, water reclamation systems and hands free automation. Emerging separator technology includes enhanced cleanability, hermetic machine design, longer bowl shoot intervals and additional machine automation. All improve product quality, while some minimally increase certain product yields. Water saving technology increases natural resource sustainability. Energy efficient drivetrains lower electric consumption while reducing surrounding workplace noise and vibration.

Key words: homogenizer, separator

495 Filtration systems. D. Weber*, *Parker Hannifin Process Advanced Filtration, Oxnard, CA.*

This symposium presentation will provide updated information important to efficient operation of membrane filtration systems. An overview of filtration technology including new developments in dairy applications and membrane products will be provided. Element configuration including material limiting factors, trends in system configurations, and cost versus configuration options will also be discussed.

Key words: membrane, filtration

Dairy Foods: Microbiology and Probiotics

496 Use of high pressure processing to control *Listeria monocytogenes* in packaged Queso Fresco. P. Tomasula*[1], L. Leggett[1], R. Kwoczak[1], D. Van Hekken[1], M. Tunick[1], J. Renye[1], M. Toht[1], S. Mukhopadhyay[2], A. Porto-Fett[3], and J. Luchansky[3], *[1]USDA/ARS/ERRC/Dairy and Functional Foods Research Unit, Wyndmoor, PA, [2]USDA/ARS/ERRC/Residue Chemistry and Predictive Microbiology Research Unit, Wyndmoor, PA, [3]USDA/ARS/ERRC/Food Safety Interventions Research Unit, Wyndmoor, PA.*

Queso Fresco (QF), a fresh, Hispanic-style cheese, is manufactured using pasteurized milk; however, its high pH (>6) and moisture content (>50%) coupled with post-pasteurization labor intensive practices may lead to contamination with Listeria monocytogenes (LM). The objective of this study was to evaluate the effectiveness of high pressure processing (HPP) as an intervention applied to QF after packaging to control LM. QF was manufactured from pasteurized milk using a commercial-make procedure. In preliminary experiments, about 8 kg of the dry, finely milled and salted curd was packed into a mold and held at 4°C overnight before the mold was removed. QF was then cut into slices with dimensions of about 12.7 cm x 7.6 cm x 1 cm. QF slices were surface inoculated on both sides with 50 µL of a 5-strain LM cocktail (ca. 5.0 $\log_{10}$cfu/g), individually double vacuum-packaged and then cooled to 4°C. The slices were then warmed to either 22 or 40°C and treated using HPP at pressures of 200, 400, and 600 MPa for holding times of 0, 5, 10 or 20 min. Only HPP treatment at 600 MPa, at both temperatures and all holding times, reduced LM to below the detection level of ≤0.91 $\log_{10}$cfu/g. Processing at 40°C resulted in visible textural changes and significant "wheying-off" of the cheese and was not investigated further. In subsequent experiments, QF slices were treated at 22°C and 600 MPa at holding times of 0, 3, 10 and 20 min and then stored at 4 and 10°C for 7 d. For the 3 min holding time, LM populations increased to 2.65 ± 0.92 and 4.50 ± 0.50 $\log_{10}$cfu/g, when QF was stored at 4 and 10°C, respectively. For the 10 min holding time, LM populations in QF remained below the detection level when stored at 4°C but increased to 2.00 ± 0.00 $\log_{10}$cfu/g when stored at 10°C. For the 20 min holding time, LM populations were not evident in QF when stored at 4°C but approached the detection level at 10°C. These results show that HPP was most effective when conducted at 600 MPa for 20 min, but HPP pressures >600 MPa, pulsed HPP, or addition of antimicrobials, may be necessary for ultimately controlling this pathogen.

Key words: *Listeria monocytogenes*, high-pressure processing, cheese

497 High-pressure processing of lowfat Cheddar cheese. M. Ozturk*[1], S. Govindasamy-Lucey[2], J. J. Jaeggi[2], K. Houck[2], M. E. Johnson[2], and J. A. Lucey[1], *[1]University of Wisconsin, Madison, [2]Wisconsin Center for Dairy Research, Madison.*

A major problem with lowfat cheese is the difficulty in attaining a strong flavor that is typical of full fat versions. Some studies have suggested that the use of high hydrostatic pressure (HHP) can accelerate cheese ripening by increasing starter lysis. Our objective was to investigate the use of HHP on lowfat Cheddar cheese with the goal of improving or accelerating flavor and texture development. To study the impact of pressure and holding time on the rheological, physical, chemical and microbial characteristics of lowfat Cheddar cheese, we used a central composite rotatable design with response surface methodology. A 2–level factorial experimental design was chosen to study the effects of the independent variables (pressure and holding time) with 2 star points (α = 1.414) and 2 replicates of the center point. Pressures varied from 50 to 400 MPa and holding times ranged from 2.5 to 19.5 min. We performed the design in 2 blocks (i.e., replicated the design), and validated its predictions with another trial. HHP was applied one week after cheese production, and analyses were performed at 2 wk, and 1, 3, and 6 mo. With an increase in pressure, cheeses had higher pH and residual lactose levels, and lower starter and non-starter bacteria counts. Compared with untreated cheeses, all HHP-treated cheeses had lower acid/base buffering areas due to solubilization of residual insoluble calcium phosphate. Cheeses treated with higher pressures were softer and had more homogeneous texture. Pressure had a larger impact on cheese properties than holding time. Several conditions exhibited buttery flavor notes in cheeses that were perceptible within a few weeks of HHP treatment. High pressure treated cheeses also had "sweet" notes due to their high pH. We did not observe any significant difference in proteolysis rates. This study indicates that holding times of around 5 min and pressures of ≥300 MPa could potentially be used to improve excessive firm textured cheese or reduce unwanted microbial activity.

Key words: high-pressure processing, lowfat cheese

498 The effect of UV light treatment and processing method on the microbial reduction of pasteurized whole milk. J. Tharani*, A. Laubscher, A. M. Lammert, and R. Jimenez-Flores, *Dairy Products Technology Center, California Polytechnic State University, San Luis Obispo.*

UV (UV) irradiation does not involve heat to kill microorganism. Therefore, it is of interest to the dairy food industry as a potential low cost non-thermal method of preservation. The objective of this study was to determine the impact of UV treatment immediately before or after pasteurization on microbial reduction in whole milk. A total of four controls and four test variables were produced. The controls were single or double pasteurized milk with or without the UV equipment. The test variables were UV light followed by pasteurization or pasteurization followed by UV at either 138 J/L or 920 J/L. Raw whole milk was standardized to 3.5% fat and each variable thermally processed at 166°F for 16 seconds and homogenized at 500/2000 psi. A Sure Pure Photo-Purification unit was used for UV treatment. Microbial testing was completed every 3 d until 21 d post processing. All variables were replicated 5 times. The results show that the reduction in microbial load was from 91,000 cfu/ml to 20 cfu/ml, 16 cfu/ml, 13 cfu/ml and 19 cfu/ml for the controls of single pasteurized with UV, single pasteurized without UV, double pasteurized with UV and double pasteurized without UV respectively. Alternatively, the reduction in microbial load was from 91,000 cfu/ml to <10 cfu/ml, 13 cfu/ml, <10 cfu/ml and 14 cfu/ml for UV treatment at 920 J/L followed by pasteurization, UV treatment at 138 J/L followed by pasteurization, pasteurization followed by UV treatment at 920 J/L and pasteurization followed by UV treatment at 138 J/L respectively. At the end of three weeks, the microbial load increased for all controls and test variables except for UV treatment at 920 J/L followed by pasteurization where the microbial population was still below 10 cfu/ml. After 3 d, differences were found in cardboard, fruity, and light oxidized flavors. Results indicate that when raw whole milk is treated with UV light at 920 J/L followed by pasteurization, there is a reduction in microbial load and the low microbial load is maintained throughout 21 d.

Key words: fluid milk, UV light

499 Tina wooden vat biofilms used in Sicilian PDO Ragusano cheese provide a new cluster of *Streptococcus thermophilus* strains. V. Florence[1,2], C. Delorme[3], C. Pediliggieri[4], M.-N. Madec[1,2], V. Chuat[1,2], S. Parayre[1,2], S. Carpino[4], P. Campo[4], P. Renault[3], S. Lortal*[1,2], and G. Licitra[4], *[1]INRA, UMR1253, STLO, Rennes, France, [2]Agrocampus Ouest, UMR1253, STLO, Rennes, France, [3]INRA, Micalis, Jouy en Josas, [4]CoRFiLaC, Ragusa, Sicily, Italy.*

Ragusano cheese (PDO) is a brine-salted pasta filata cheese from Sicily. Raw milk is directly placed in the traditional wooden vat (tina) for cheese making. The biofilm present on this tina was shown to be a safe and very efficient lactic acid bacteria delivering system. Depending on the farm, the biofilm exhibited 2 to 10 co-dominant species, thus representing a valuable source of biodiversity. In this work, *S. thermophilus* was shown, by RT-PCR-TTGE, to be the more active species in 3 different tinas over a 2 years period. To explore the biodiversity within *S. thermophilus*, 25 clones per tina and per year were isolated from M17 plates and analyzed by Pulsed field gel electrophoresis (PFGE) and multi locus sequence typing (MLST). Many different PFGE profiles were obtained highlighting the strain biodiversity within each tina. Some of the profiles were highly related suggesting clones from the same initial strain derived by minor variations; however, each tina contained at least 4 co-dominant strains of *S. thermophilus*. From the cheese at d 1, 22 clones were also isolated and analyzed by PFGE. Most of the profiles were similar to the one of the biofilm, confirming the crucial role of the tina in inoculating *S. thermophilus* for the acidification step. A MLST analysis was applied on 50 strains of *S. thermophilus* isolated from the biofilm using the 6 following genes glck, ddlA, tkt, proA, ptsi, serB. Seven completely new sequence types were found. When compared with 170 other strains of *S. thermophilus* coming from all over the world analyzed by MLST in the same conditions, strains isolated from Tina whatever the year and the farms formed a completely separated group, a new cluster. Special phenotypic traits of these new strains of *S. thermophilus* are under investigation.

Key words: cheese, *Streptococcus thermophilus* biodiversity, biofilm

500 Molecular identification and characterization of *Lactococcus lactis* ssp. *lactis* and *Lactococcus lactis* ssp. *cremoris* by FTIR and its utilization for Cheddar cheese production. H. U. Rehman*[1], M. Nasir[1], S. U. Rehman[2], M. A. Jabbar[1], and M. A. Ali[1], *[1]University of Veterinary & Animal Sciences, Lahore, Punjab, Pakistan, [2]University of Agriculture Faisalabad, Faisalabad, Punjab, Pakistan.*

Cheese starter cultures are expensive and precarious in subcontinent countries like Pakistan. Hence, it is imperative to isolate and characterize indigenous cultures for sustainable and low priced cheese production in the country. The present study was designed to isolate, identify and characterize the *Lactococcus lactis* ssp. *lactis* and *Lactococcus lactis* ssp. *cremoris*, from milk samples. The cultures were isolated through agar media, from milk samples collected from different locations of Faisalabad, Pakistan and then identified on morphological basis by Gram staining, sugar fermentation and catalase tests. Phenotypic characterization of commercial and local made cultures was done by FT-IR spectroscopy; a rapid and novel phenotypic finger printing method, that creates holistic biochemical profile of microorganisms by developing spectra in a specific range. The preservation of isolated bacterial cultures was done at 4°C, which decreased significantly ($P \leq 0.05$) with time but the viability was non-significant compared with commercial culture. Isolated and commercial culture were used at 1% to produce Cheddar cheese for physico-chemical and sensory evaluation. The texture of test cheeses produced with local culture was less elastic compared with control cheese sample produced with commercial culture. The color, flavor and overall acceptability scores of cheese samples with different cultures were not significantly different ($P \geq 0.05$). It is concluded that cheese prepared from indigenous isolated culture was comparable with that of commercial culture cheese and therefore, further studies should be carried out for commercial production of various cheese cultures.

Key words: Cheddar cheese, starter culture, FTIR

501 Transcriptional and physiological responses of *Bifidobacterium animalis* ssp. *lactis* strains to hydrogen peroxide stress. T. S. Oberg*[1], R. E. Ward[1], J. L. Steele[2], and J. R. Broadbent[1], *[1]Utah State University, Logan, [2]University of Wisconsin, Madison.*

Consumer interest in probiotic foods containing bifidobacteria is increasing, but industry efforts to secure high cell viability in foods is undermined by the sensitivity of these anaerobes to oxidative stress during food production or storage. To address this limitation, we investigated transcriptional responses of 2 fully sequenced *Bifidobacterium animalis* ssp. *lactis* strains, BL04 and DSM10140, to hydrogen peroxide (H_2O_2) exposure. Although the genome sequences for these strains are virtually identical, they display different levels of intrinsic and inducible H_2O_2 resistance. For transcriptomics, late log phase cells were exposed to a sub-lethal H_2O_2 concentration for 5 or 60 min, then mRNA was isolated, converted to cDNA, and hybridized to an Affymetrix microarray. Data analysis by the limma/eBayes method found significant ($P < 0.05$) changes in 158 genes in BL04 after 5 min, and 30 differentially expressed genes after 60 min. Surprisingly, no significant changes in gene expression were detected in DSM10140 at either time. Examination of genomic data for each strain suggested differences in H_2O_2 stress resistance might be related to membrane lipid composition, due to genetic mutations in genes for long chain fatty acid-coA ligase. To address this hypothesis, membrane fatty acids were isolated and analyzed by GC-MS. Results confirmed the 2 strains had significantly different lipid profiles. In particular, the BL04 membrane contained higher percentages of C14:0 and C16:0, and lower percentages of C16:1n7 and C18:1n9. These differences could affect membrane fluidity and, potentially, transduction of stress signals, either of which could explain the observed contrasts in H_2O_2 stress resistance.

Key words: *Bifidobacterium*, stress response, hydrogen peroxide

502 Fresh cheese containing higher inoculation of *L. acidophilus* and its effect on the functionality and metabolism of probiotic culture. A. Cruz, J. Faria*, W. Castro, R. Cadena, and H. Bolini, *University of Campinas (UNICAMP).*

This work aimed to evaluate the effect of supplementation with increasing *L. acidophilus* counts on the physicochemical parameters and functionality of fresh Minas cheese. Probiotic fresh cheese (Minas cheese) was supplemented with *L. acidophilus* La-14 (0, 0.4 or 0.8 g/L milk) being submitted to physico-chemical analysis (pH, proteolysis and organic acids levels) and microbiological analysis (probiotic and starter viable count) for 21 d refrigerated storage. In addition, conventional and probiotic commercial cheese supplemented with *Bifidobacterium animalis* Bi-07 were submitted to the same analysis. It was observed an effect of the storage time on the physical-chemical parameters and the microbiological counts ($P < 0.05$). Probiotic cheeses inoculated with increasing concentrations of *L. acidophilus* and the

commercial probiotic cheese presented lower pH values, greater proteolysis level and organic acids production along the refrigerated storage. *L. acidophilus* ranged from 9.42 to 9.11 log cfu/g, maintaining the functionality of the product throughout the shelf life. *B. animalis* counts ranged from 8.36 and 8.91 log cfu/g, while *Lactococcus lactis* count ranged from 8.93 to 7.49 log cfu/g. Additional consumer test should be performed to evaluate the changes due the supplementation of higher *L acidophilus* counts during the fresh cheese processing.

Key words: probiotic cheese, *L. acidophilus*, functionality

503 Microbiological and physico-chemical properties of probiotic whey beverages processed with different whey concentrations. W. Castro, A. Cruz, J. Faria*, M. Bisinotto, and R. Celeghini, *University of Campinas (UNICAMP).*

The use of whey in probiotic beverage formulations can be an option to address environmental challenges faced by the dairy industry. This work aimed to evaluate the microbiological and physico-chemical properties of probiotic whey beverages processed with increased whey concentrations. Whey probiotic beverages were manufactured with 0, 20, 35, 50, 65 and 80% (w/w) liquid sweet whey (pH = 6.48, Minas fresh cheese whey) concentrations and were subjected to physico-chemical analysis (pH, proteolysis, color values) and microbiological count (*Streptococcus thermophilus*, *Lactobacillus bulgaricus*, and *Lactobacillus acidophilus*). The whey concentration had an effect on all parameters analyzed. The pH values ranged from 4.07 to 4.14 ($P > 0.05$), while proteolysis was inversely proportional to the whey concentration. The color values (Hunter Lab Color, Minolta) were inversely proportional to the whey concentration, without difference between samples except for 65 and 80% whey ($P > 0.05$). *S. thermophilus* counts ranged from 8.37 to 9.05 log cfu/mL ($P > 0.05$), while *L. bulgaricus* count ranged from 8.01 to 8.31 log cfu/mL ($P < 0.05$). Regardless of the whey concentration, all products presented high values for *Lactobacillus acidophilus* count (minimum value of 8.1 log cfu/mL; $P > 0.05$), suggesting that the whey beverage was an adequate food matrix to be supplemented with probiotic bacteria. The findings indicate that increased whey concentrations had and effect on the physico-chemical parameters of whey probiotic beverages. Additional consumer testing is needed to evaluate their acceptance.

Key words: whey probiotic beverage, functionality, stability

504 A dairy safety program: Considering human and animal safety. M. A. Smith*, G. R. Hagevoort, and F. A. Rivera, *NMSU Ag Science Center, Clovis.*

The dairy industry in the Southwest has experienced a decade of expansion in regards to the number of milking cows and concomitant number of employees. In this process, a new management structure, historically absent from dairy farms with fewer employees, is being developed. It has been recognized that there is a need for middle management positions, responsible for training and supervising employees, much like positions established within other similar sized industries. In the past, the task of training and supervision of employees typically was that of upper management. With increasing employee numbers, this task is often delegated to employees with seniority. NMSU Dairy Extension was asked by producers to assist in providing training tools for large open lot dairies, permitting room for inclusion of dairy particular protocols. This has led to the development of a dairy safety training program consisting of a DVD and a manual (in English and Spanish) for on dairy training purposes entitled Considering Human and Animal Safety: Dairy Safety Training for New Mexico Dairy Producers. The format allows supervisors and managers the opportunity to establish safety protocols within their individual farms. The program is based on the notion that well trained workers have high regards for their own safety as well as that of the safety of others and the safety and well-being of the animals they provide for. The program can be regarded as an essential part of an overall Quality Assurance Program. The program raises awareness of unsafe or potentially harmful working conditions, which with early detection may take minimal correctional action. By presenting guidelines on how to safely handle dairy cows in various common situations on the dairy farm, as well as how to work with heavy equipment in a safe manner, management can train both new and current employees. Emphasis is put on understanding animal behavior as the basis for safely working with and around animals. Part II is currently being developed and will specifically focus on individual positions on the dairy such as: milkers, outside caretakers, feeders and calf raisers.

Key words: animal well-being, dairy quality assurance, employee safety training

505 Assessing a comprehensive dairy cattle economic program for practicing dairy veterinarians. G. M. Schuenemann*, D. Shoemaker, D. Breece, S. Bas, and J. D. Workman, *Department of Veterinary Preventive Medicine, 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 economic information to dairy veterinarians. A comprehensive dairy cattle economic program 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, participated in the advanced dairy cattle economic modules (2 d each, ~40 h of learning). Financial statements (balance sheet, profit and loss); production and financial factors that affect business performance; financial ratios and business analysis; net farm income per cow (cost of production), milk pricing, economic decision tools (value of a pregnancy, number of milking times, income over feed cost, borrowing money); economics of uterine diseases and mastitis; grains and biofuels outlook; and transitioning the dairy farm to the next generation were discussed. Educational materials were delivered through in-class lectures followed by case-based learning, group discussions, and participant presentations of out-of-class assignments. Attendees were assessed using pre- and post-tests of knowledge to determine the level of knowledge gained in both modules. Participants evaluated the program and provided feedback at the conclusion of each module. Veterinarians reported that the overall program, presentations and discussions were useful and of great immediate use to them. The presented materials and the educational delivery methods substantially increased the knowledge level of the attendees (18% increase from pre- to post-test scores; $P < 0.05$). Importance of knowing the costs of production, costs of diseases, business objectives (profitability, liquidity, and solvency), written record-keeping for small dairies, regular meetings with the production team, and the use of computerized decision-making tools were listed as learned concepts that participants can apply in their practices. Results suggested that both economic modules were relevant and effective; offering practical economic information with immediate field application.

Key words: dairy cattle economics, education, veterinary

506 III. Dairy calving management: Assessment of a comprehensive program for dairy personnel. G. M. Schuenemann*, S. Bas, E. Gordon, and J. Workman, *Department of Veterinary Preventive Medicine, The Ohio State University, Columbus.*

The purpose of the study was to assess the effectiveness of a comprehensive educational program (CEP) designed to improve calving management practices of calving personnel and communication within the farm team. Calving personnel (n = 47), attending an estimated of 13,100 cows from 12 Ohio dairies, attended the calving management program (~2 h of training and ~1 h of demonstration). Bovine reproductive anatomy, behavioral signs of normal parturition (stages 1–3), dystocia (presentations and positions), hygiene practices during the assistance procedure, strategies for intervention (when and how to intervene), record-keeping, communication (when to call for help), and newborn care were discussed. Post-training follow ups (2 per yr) were available for participating herds. The impact of the CEP on stillbirth was assessed in 1 herd (292 births). Educational materials were delivered through lectures followed by group discussions and hands-on demonstrations. Attendees were assessed using pre- and post-tests of knowledge to determine the level of knowledge gained during the training program. Participants evaluated the program and provided feedback at the conclusion of the program. Dairy personnel reported that the overall program, presentations, and discussions were useful. The presented materials and demonstrations substantially increased the knowledge level of the attendees by 16.1 percentage points from pre- to post-test scores ($P < 0.05$). Identification of cows in need of calving assistance, hygiene practices at calving, record-keeping, and communication with the farm team were reported as learned concepts. The follow-up assessment with participant herds revealed that they were able to implement the learned skills, communicate calving records with the farm team, and have written calving protocols. The incidence of stillbirth was reduced by 9 percentage points (from 15.5% to 6.5%; $P < 0.05$). Results suggested that the CEP was relevant and effective, offering information with immediate field application. Impact outcomes such as calf-dam survival, herd performance (fertility), and long-term adoption of practices need further investigation.

Key words: calving management, education, stillbirth

507 Virtual town hall meetings as a method for engaging the public and dairy industry on contentious topics: The case of tail docking. D. M. Weary*, C. Schuppli, and M. A. G. von Keyserlingk, *University of British Columbia.*

As dairy farm numbers decline and the general population becomes increasingly urbanized, there is increasing scope for producer practices to fall out of step with public values. One method to engage producers and the public is through virtual town hall meetings where participants can state their views and see the perspectives of others. Here we report on the results of our 'Cow Views' on-line engagement designed to create discussion on tail docking and document the reasons participants put forward for and against the practice. A total of 178 people participated; 30% were producers, 23% were veterinarians, 25% had no experience with the dairy industry and 22% included a mixture of teachers, students and industry professionals. Approximately 79% of participants were opposed to docking. Responses varied with participant demographics (e.g., females were more likely than males to oppose docking), but in every demographic sub-group (e.g., by sex, age, country of origin and dairy production experience) the majority of respondents were opposed to tail docking. Common reasons for opposition to docking included the lack of scientific evidence that docking improves cleanliness or udder health, that docking is painful for cows, that docking is unnatural and that tails are important for controlling flies. Some respondents in favor of docking also cited cow cleanliness as an issue, as well as concerns about milker comfort. These results can be used to better target extension efforts (e.g., improving producer education on the lack of positive effects of docking on cleanliness and udder health, and design features of milking parlor that prevent contact with the tail). More generally, the results illustrate the use of this type of on-line discussion in providing a safe and productive format for producers, industry professionals and the public to share perspectives on contentious topics.

Key words: animal welfare, attitudes, survey

508 The Missouri Show-Me-Select Replacement Heifer Program. D. A. Mallory*, J. M. Nash, M. F. Smith, S. E. Poock, and D. J. Patterson, *University of Missouri, Columbia.*

The Missouri Show-Me-Select Replacement Heifer Program was designed to improve reproductive efficiency of beef herds in Missouri and increase individual farm income. The program objectives include: 1) a total quality management approach for health and management of heifers from weaning to late gestation; 2) increased marketing opportunities for and added value to Missouri raised heifers; and 3) the creation of reliable sources of quality commercial and purebred replacement females. The program was initiated as a pilot project in 2 regions of Missouri in 1997 with 33 farms and 1,873 heifers. During the past 14 years, 703 farms enrolled 91,776 heifers in the program. Regional extension livestock specialists serve as coordinators of the program locally and work closely with the 205 veterinarians involved with the program state wide. State specialists provide program support to regional extension field staff and participating veterinarians. The reproductive goals for heifers enrolled in the program are aimed at improving breeding performance during the heifers′ first breeding period, minimizing the incidence and severity of dystocia, with the resulting delivery of healthy, vigorous calves, and successful rebreeding of heifers during the subsequent breeding season. Heifers are now eligible to qualify as Tier 2 replacements on the basis of minimum accuracies of the heifer′s sire for specified traits at the time of sale. The marketing component of the program facilitated the sale of 22,807 heifers in 107 sales across Missouri from 1997 through the fall sales in 2010. These sales generated interest from 7,063 prospective buyers that formally registered to buy heifers, and 2,560 individuals that purchased heifers from the various sales. Heifers from the program have now sold to farms in AR, AZ, CO, FL, GA, IA, IL, IN, KY, KS, LA, MO, NE, OK, SC, TN, and TX. Collectively, 107 sales have generated $25,406,700 in gross sales. The program is estimated to have contributed $50 million to Missouri′s economy. The Missouri Show-Me-Select Replacement heifer Program is the first statewide on-farm development and marketing program of its kind in the US

Key words: beef cattle, heifer development, reproductive management

509 Enhancing knowledge and technology adoption in a misunderstood discipline: The weight trait project. M. L. Spangler*[1], E. J. Pollak[2], G. L. Bennett[2], K. J. Hanford[1], S. D. Kachman[1], L. A. Kuehn[2], W. M. Snelling[2], and R. M. Thallman[2], *[1]University of Nebraska-Lincoln, Lincoln, [2]US Meat Animal Research Center, Clay Center, NE.*

Currently several commercial DNA marker panels are available for complex traits. In the fall of 2009, the American Angus Association integrated the results of an Angus-specific marker panel into their national cattle evaluation for carcass traits. Despite this advancement, there still exists tremendous confusion by producers as to the efficacy of DNA diagnostics. The Weight Trait Project (WTP) began in the summer of 2009 and was designed to address issues associated with creating and implementing DNA-based selection in conjunction with Expected Progeny Differences (EPD). The WTP is an ongoing unified effort among researchers, breed associations (n = 7), and seedstock producers (n = 20) to improve the process of developing and validating DNA tests and to investigate the infrastructure necessary for the flow of information required to deliver Marker-Assisted EPD to producers. The objectives of the current study were to illustrate methodology for incorporating DNA marker information into EPD predictions for the trait of weaning weight and develop mechanisms for disseminating this information to producers. To gauge changes in knowledge, practices, and behavior, a survey was sent to participants. The 17 respondents (85% return rate) indicated that collectively they own 20,125 beef cows. Increases in knowledge were rated from 0 (none) to 4 (significant). Mean survey results were 1.5, 2.8, 2.0, 3.4, 2.4, 2.7, 2.8, and 2.9 for EPD, genomics terminology, parentage verification, marker assisted selection, across breed genomic predictions, whole genome selection and panel development, test validation, and accuracy improvement of EPD, respectively. Producers indicated adoption of methods to improve the following production practices: making mating decisions (40%), efficient use of DNA technology (75%) and selection (bull buying) decisions (47%). Mean responses for changes in behavior (1 = none; 5 = very likely) were 3.9, 3.8, 4.3, and 4.6 for making more informed selection decisions, better educating their clientele, feeling comfortable with terminology, and desiring to stay abreast of DNA technology, respectively.

Key words: beef cattle, genomics, producer education

510 Evaluating cow efficiency at the producer level: The Northwest Minnesota Beef Improvement Program. R. S. Walker*[1], S. L. Bird[2], G. I. Crawford[3], and A. DiCostanzo[4], *[1]LSU AgCenter, Homer, LA, [2]University of Minnesota North Central Research & Outreach Center, Grand Rapids, [3]University of Minnesota Extension, Hutchinson, MN, [4]University of Minnesota, St. Paul.*

Measuring cow efficiency through cow size and calf weaning weight may provide opportunities to cull more strategically to improve herd efficiency. With the increase in production cost, cow size, and depressed cattle markets, profitability is narrow for the cow/calf producer. In Northwest Minnesota, bovine tuberculosis (TB) was recently detected in 12 beef herds. This resulted in a downgrade in Minnesota′s TB status, which significantly impacted movement and testing regulations and caused additional costs for marketing animals. The Northwest Minnesota Beef Improvement Program was developed to provide assistance for producers by evaluating cow size and calf performance and develop strategies for improving cow efficiency. In addition, information gained would be used as educational tools for enhancing producer awareness on the impacts of cow efficiency on profit margins. Cow and calf production and BW data were collected from each herd and summarized with a follow-up consultation with each participating producer by the University of Minnesota Beef Team. In the evaluation process for measuring cow efficiency, adjustments (ADJ) were made for cow BW (BCS 5.0 and age 5.0 yr) and calf BW (205 d of age) at weaning. In the fall of 2009, 9 beef producers and over 1,250 beef cow-calf pairs among 5 breeds were represented. Breeds consisted of Angus, Angus cross, Hereford, Gelbvieh, and Simmental. Means ± SD from all herds combined for cow age, cow ADJ BW at weaning, cow BCS at weaning, calf ADJ BW at weaning, and calf ADJ BW as a percentage of cow ADJ BW at weaning were 5.5 ± 2.8 yr, 626 ± 57.3 kg, 5.3 ± 0.7, 266 ± 35 kg, 0.43 ± 0.06, respectively. Mean cow and calf ADJ BW at weaning varied among herds ranging from 593 to 675 kg and 227 to 289 kg, respectively. Ranges in cow and calf ADJ BW means for cows with ADJ BW above the herd average compared with cows with ADJ BW below the herd average were 68 to 124 kg and –3 to 11 kg, respectively. Variations observed in calf weaning weight based on cow size across all herds indicate opportunities for commercial producers to improve herd efficiency through cow efficiency.

Key words: body weight, cow size, herd efficiency

511 The benefits of using StockPlan to assist producers make management decisions before and during dry spells or drought. M. J. McPhee*[1], M. B. Whelan[2], B. L. Davies[3], G. P. Meaker[4], P. Grahman[5], and P. M. Carberry[6], *[1]Industry and Investment NSW, Armidale, NSW, Australia, [2]Southern Cross University, Lismore, NSW, Australia, [3]Industry and Investment NSW, Paterson, NSW, Australia, [4]Industry and Investment NSW, Goulburn, NSW, Australia, [5]Industry and Investment NSW, Yass, NSW, Australia, [6]Formerly Industry and Investment, Cala, NSW, Australia.*

The StockPlan workshop assists cattle, sheep meat, and wool producers explore the financial consequences of management options before and during dry spells or drought. An independent survey of 345 properties in the central western area of New South Wales, Australia was conducted. The survey found that 195 properties participated in a StockPlan workshop. The benefits achieved from the 195 properties indicated that 75% of respondents received at least one benefit from the StockPlan workshop: 63% improved ground cover, 25% reduced stress, 24% increased productivity, and 15% maintained or increased stocking capacity. The StockPlan workshop demonstrates how to use Drought Pack, Feed Sell Agist (FSA) Pack, and ImPack. Two case studies illustrate the assistance that producers receive. FSA Pack was used to assist cattle producers determine whether they should "feed," "sell," or "agist" cattle. A sensitivity analysis of the buying and selling options was performed. FSA Pack assisted the beef producers decide that the "sell" option had the lowest associated risk. The second case study used ImPack to evaluate 3 options: "sell 10% of stock"; "keep and feed all stock"; or "sell progeny as weaners and keep and feed cows" for a mixed cropping and beef enterprise. A -year breeding herd re-structure was performed for each of the 3 options. The ImPack analysis based on a cash-flow analysis indicated that "sell 10% of stock" was a better option because it reduced interest payments early in the planning period and therefore assisted in reducing the overall debt.

Key words: case study, cash flow, sensitivity

512 Carcass and meat quality characteristics of exhibition swine. S. J. Moeller*, H. N. Zerby, K. S. Betts, M. J. Bishop, S. M. Crawford, M. D. Cressman, and A. S. Gress, *The Ohio State University, Columbus.*

The objective was to characterize performance and pork quality of barrows exhibited at the Ohio State Fair (OSF) from years 2000 to 2010. Data set one (MQP; n = 181 Duroc, n = 553 crossbred pigs) pigs were weighed (~20.5 kg), placed on test (~102 d) at the exhibitor's operation, and exhibited at the OSF based on start weight. Data set 2 (CH) included 419 grand- and reserve-champion barrows (n = ~42 annually) from 10 purebred and one crossbred population, and pigs were exhibited based on live weight. Carcass backfat (BF), loin area (LMA) and loin quality (visual color (C), marbling, firmness (F), and wetness (W) and Minolta L*) were recorded. Mixed models for MQP and CH included breed and year fixed effects for production traits. Year was included as a random effect for measures of pork quality. In the MQP, live weight (116 kg), average daily gain (0.94 kg/day), and BF (20 mm) were not different between Duroc and crossbred pigs; however, crossbred carcasses had greater LMA (48.3 vs. 45.3 cm2; $P < 0.001$) and percent carcass lean (53.5 vs. 53%; $P < 0.05$) resulting in a greater rate of lean growth per day on test (0.40 vs. 0.39 kg/day; $P < 0.01$) than the Duroc. Loins from MQP Duroc carcasses were darker based on visual color (2.7 vs. 2.3; $P < 0.001$) and L* (55.2 vs. 56.3; $P < 0.001$) measurements and had a firmer visual appearance (2.2 vs. 1.9; $P < 0.001$) with a less exudative appearing surface (2.2 vs. 1.9; $P < 0.001$). Lean growth rate of MQP barrows, after the first year (0.32 kg/day) were variable, ranging from 0.38 to 0.42 kg/day, likely an indication of year-to-year variation in both genetics and weather conditions. In the CH group, LMA of crossbred (57.9 cm2) and Hampshire (56.7 cm2) barrows were greater ($P < 0.01$) resulting in a greater percentage carcass lean (57.3 and 56.6%, respectively) when compared with the other breeds. Carcasses in MQP and CH competitions with visual scores of 1 for C, F, or W were disqualified, resulting in 29 and 30% of MQP and CH loins, respectively, disqualified across the period. Results indicate that exhibition swine represent a significant challenge for packers due to the high proportion of pale, soft and or exudative pork produced.

Key words: exhibition, pork quality, swine

513 SowBridge: A breeding herd distance education program allowing on-farm delivery. M. H. Whitney*, *University of Minnesota Extension, Mankato.*

The US pork industry has changed significantly the past 30 years. Small farrow-finish operations have been largely displaced by larger specialized production systems. While decision makers still attend educational events, employees often have few opportunities to increase their educational level. SowBridge was designed for owners, managers, employees, and consultants involved with breeding, gestation, and farrowing operations. The program is coordinated through the extension programs of U of Minnesota, U of Iowa, U of Nebraska, South

Dakota State U, Ohio State U, Purdue U, U of Illinois, Kansas State U, Michigan State U, U of Nebraska, and North Carolina State U. Participants in the program receive a CD in the mail 1 week before each monthly session, containing a slide set of the presentation and supporting materials. Presenters are from participating universities as well as industry. Participants call at 11:30am CT to a toll-free telephone number. A moderator introduces the topic and speaker, then 30 min are designated for the presentation, followed by time for questions. During the presentation, the speaker explains the material while participants follow along on their own computers. A total of 167 participants from 19 states and 4 other countries have participated in the program the past 3 years. Participants include animal caretakers, breeding technicians, managers, owners, veterinarians, consultants, students, and ag educators. Number of participants per site has ranged from 1 to 12. When asked to provide a monetary value of the program for their production units, responses were: $200 - $500 (27%), $500 - $1000 (46%), and $1000+ (27%). The most cited positive aspects of the program were the ability to receive information without travel and ability to use as quality training for employees. SowBridge is a distance education program that is effective in providing information directly to employees and managers in swine breeding and farrowing units, and can be utilized to reach individuals both nationally and internationally.

Key words: breeding, education, swine

514 Content appraisal: A tool for analyzing web content and its effectiveness. J. Nadeau*[1], N. Heidorn[2], and N. Broady[3], *[1]University of Connecticut, Storrs, [2]Louisiana State University, Baton Rouge, [3]University of Kentucky, Lexington.*

Effective website content that keeps clientele engaged includes short, concise snippets of information supplemented with pictures, videos, and related websites including links to related social media outlets such as YouTube, Facebook and Twitter. Translating research-based information into web based searchable content can be challenging for the traditionally trained research/extension professional. Content appraisal is a way to make your web information relevant and useful to clientele. This simple, qualitative content appraisal system will identify easy modifications to make website material more effective. This system provides a thorough evaluation of content and results in a report that focuses on key aspects of content strategy, identification of trouble spots, and provides recommendations for improvement. The criteria examined include knowledge level, interrelatedness, relevance, usability, actionability, and differentiation. Updates to improve impact may include linkages to relevant topics on other websites or social media, keeping items current, search engine optimization, increasing online discoverability, changes in formatting and writing style to increase overall readability, a clear call to action, and the incorporation of items that fill a unique need. eXtension (pronounced e-extension)'s first Community of Practice (CoP), HorseQuest, recently applied a content appraisal process in an attempt to document the efficacy and impact of their web content. HorseQuest has produced approximately 1,277 articles, 495 news items, 1,130 published answers to ask-an-expert questions, 13 learning lessons, and 21 videos. Since its launch, there have been 1,658,539 total views. HorseQuest is the first CoP to implement the content appraisal system. This appraisal resulted in immediate and simple improvements to our web content, increasing the site′s potential impact.

Key words: content appraisal system, extension, internet based learning

515 Challenges and benefits of the participation of youth in creating youth-friendly material: Horses and Humans for a Healthy Habitat. M. Philbrick, J. Nadeau*, and T. Hoagland, *University of Connecticut, Storrs.*

As a part of the program Horses and Humans for a Healthy Habitat, youth were recruited to evaluate if creating a youth-friendly brochure intended to instruct youth in good environmental practices with horses was beneficial to the youth. The youth worked with a knowledgeable environmental coordinator to create fact sheets and learning activities. They based their work on the adult version of the Horse Environmental Awareness Program in CT (HEAP). They meet in focus groups of 5–6 interested youth. To determine if these activities were educational for the youth, the youth (n = 30) were surveyed before the activities began and after they completed the teaching material. The survey consisted of groups of questions which covered 4 sections of HEAP and were answered on a Likert 5 class scale. The majority of participants were grade 7 or higher, however they ranged from grade 3 to 12. The majority of the youth (58%) owned horses and managed them at their own homes. Eighty-eight % of the youth participated in horse care. The greatest challenge was attendance due to lack of interest and busy school and horse schedules. Each youth did not answer each question, therefore the response numbers for each question varies. The distribution of the responses was evaluated by chi-squared analyses to see if the response distributions were different from random. In most cases, (10 out of 19 questions) the youth answered the questions in a distribution that would indicate they already knew something about the topic. Yet in all cases (19 questions), after developing the learning material the youth responded with a distribution of responses that clearly indicated that they had learned from the activity and more of the distributions were found (18 out of 19 questions) to be significantly different from random at $P < 0.003$ and clearly in the correct (increased knowledge of practice or increased environmental awareness) direction. Youth participating in focus groups to increase environmental awareness for a targeted group results in increased knowledge for the participants and generates useful products.

Key words: environment, extension, youth

Growth and Development Symposium: Understanding and Mitigating the Impacts of Inflammation on Animal Growth and Development

516 Containing inflammation is essential for animal growth and health. T. A. Niewold*, *Nutrition and Health Unit, Department of Biosystems, Faculty of Bioscience Engineering, Katholieke Universiteit Leuven, Heverlee, Belgium.*

It is well established that infection leads to inflammation and release of pro-inflammatory cytokines. Cytokines activate immune cells and have a profound effect on growth by reducing intake and increasing catabolism of muscle tissue. Less is known about the postprandial (low-grade) inflammatory response in the intestines, a normal physiological response, called metabolic inflammation (MI). The extent of MI is related to energy value and glycemic index of feed as well as specific (e.g., fatty acid) constituents in the feed. To maintain integrity in the body, MI is tighly regulated. The host benefits from downregulation of inflammatory responses directly (e.g., tissue integrity, nutrient transport, and energetically) and indirectly (e.g., Lawsonia and Clostridium benefit from inflammatory responses). Tight control of MI is often disrupted due to the regulatory mechanisms being overwhelmed by high-energy feed intakes fed in production settings. Moreover, feed may also contain pro- and anti-inflammatory components. Prime examples of the latter are the antimicrobial growth promoters (AGP). Initially, beneficial effects of AGP were attributed to their antibiotic characteristics; however this is highly unlikely for a variety of reasons. A prime reason is the sub-therapeutic concentrations in commercial rations. Thus, AGP are much more likely to work as growth permitters as direct inhibitors of intestinal inflammatory responses. This theory is corroborated by the good correlation between the (in vitro) direct anti-inflammatory effect of certain antibiotics, and their effectiveness as AGP. It also explains why non-antibiotic anti-inflammatory compounds like acetylsalicylic acid have a similar effect. It is concluded that effective growth promoters are inhibitors of the intestinal inflammatory response. Their proximal intestinal uptake should be low to maintain effective concentrations in the distal small intestine. Inflammation, whether it results from feed or disease, is inversely related to growth and health. Therefore, research should focus on anti-inflammatory compounds and anti-inflammatory feed composition.

Key words: inflammation, anti-inflammatory, antimicrobial growth promoter

517 Impacts of inflammation on cattle growth and carcass merit. C. R. Krehbiel*, C. L. Maxwell, C. A. Gifford, and R. L. Mills, *Oklahoma State University, Stillwater.*

Inflammation caused by bovine respiratory disease (BRD) continues to be one of the greatest challenges facing beef cattle producers and feedlot managers. Inflammation decreases DMI, ADG, and G:F in feedlot calves decreasing rate of growth and increasing days on feed which results in performance based economic losses during the feeding period. In the past decade, marketing of feedlot animals has drastically switched from selling cattle on a live basis to a grid-based marketing system. When cattle are marketed on a live basis, the economic effects of BRD stop at decreased feedlot performance, carcass weight and death loss. However, when cattle are marketed in a grid-based system, inflammation has the potential to also affect carcass cutability, quality, and consumer acceptability. The effects of inflammation on feedlot cattle in regards to performance are well understood; however, effects on cattle growth and ultimately carcass merit are not as well described. Recent studies in feedlot cattle have suggested that the incidence of BRD decreases both HCW and marbling. Research in other species has demonstrated that during the acute phase response, pro-inflammatory cytokines promote skeletal muscle catabolism to supply amino acids and energy substrates for immune tissues. Further, during this early immune response, the liver changes its metabolic priorities to the production of acute phase proteins for use in host defense. Together these dramatic shifts in systemic metabolism may explain the detrimental effects on performance and carcass traits commonly associated with BRD in feedlot calves. Moreover, recent studies relative to human health have revealed complex multilevel interactions between the metabolic and immune systems and highlighted inflammation as being a significant contributor to major metabolic diseases. The objective of this paper is to gather recent data to help explain the economical and physiological effects of inflammation on cattle growth and carcass merit.

Key words: bovine respiratory disease, carcass merit, cattle growth

518 Endotoxin, inflammation, and intestinal function in swine. N. K. Gabler*, L. H. Baumgard, and V. Mani, *Iowa State University, Ames.*

Circulating endotoxin or lipopolysaccharide (LPS) can stimulate localized or systemic inflammation via activation of toll-like receptors (TLR) and the immune system. This may partition energy away from growth and toward immune system requirements. Furthermore, inflammation can regulate intestinal epithelial function by altering intestinal integrity and nutrient transport. The gastrointestinal tract is a large reservoir of both gram-positive and negative bacteria in which bacterial populations gradually increase from approximately 0 to 10^3/mL of luminal contents in the duodenum to 10^{11}/mL in the colon. Thus, gram-negative bacteria serve as a source of endotoxin in the intestine, which can enter the systemic circulation, resulting in localized or systemic inflammation. Inflammation can alter feed intake, small intestinal nutrient transport, and growth. Furthermore, environmental factors can modulate intestinal endotoxin transport via altering either: 1) nonspecific paracellular transport through the tight junctions or 2) transcellular transport, potentially through lipid raft membrane domains via TLR4-mediated endocytosis. Paracellular endotoxin transport occurs through reduced tight junction integrity, which may be a result of enteric disease, inflammation, or stress, causing a dissociation of tight junction protein complexes. Lipid rafts involved in transcellular transport are specialized membrane regions rich in glycolipids, sphingolipids, cholesterol, and saturated fatty acids. Endotoxin-related signaling proteins such as TLR4, CD14, and MD2 assemble in the lipid raft, which permits endotoxin signaling or endocytosis. Either transport pathway may be altered by dietary and membrane fatty acid composition or environmental stresses and inflammation. This presentation will discuss the role of endotoxin and inflammation in regulating intestinal function as it relates to pig growth performance.

Key words: endotoxin, lipid raft, intestine

519 The role inflammation plays during clinical mastitis on the performance and health of dairy cows. M. A. Ballou*, *Department of Animal and Food Sciences, Texas Tech University, Lubbock.*

Genetic selection for increased milk production in dairy cattle over the past half a century was not associated with an attenuated inflammatory response. The systemic and local inflammatory responses contribute to the altered metabolism, reduced production performance, and high cull rate of lactating dairy cows with clinical mastitis. More aggressive inflammatory responses were observed in early lactation when compared with late lactation following an intramammary challenge with purified endotoxin. The epidemiology of clinical mastitis indicates the highest incidence is observed during the peripartum period; therefore, an enhanced inflammatory response may be involved in the etiology and severity of the clinical mastitis observed during the peripartum period. Milk production losses and compositional changes are observed among all mammary quarters from a cow with clinical mastitis, but the responses are more severe and sustained among culture-positive quarters. The culture-positive mammary quarters reflect both the systemic and local reactions; whereas culture-negative quarters only represent the systemic response. The systemic effects of the inflammatory response include: reduced dry matter intake, hyperthermia, and changes in whole-body nutrient partitioning affecting mammary epithelial substrate availability; whereas the local inflammatory effects include: the energetic requirements of the increased inflammatory leukocyte pool, decreased synthetic capacity of mammary epithelium independent of substrate availability, and paracellular leakage of milk components from the alveolar lumen into the extracellular fluid. Research has focused on either improving other host immunological defenses or attenuating the inflammatory response to limit the deleterious effects during peripartum mastitis. This paper will highlight recent research on the production losses associated with the inflammatory response during mastitis as well as potential management strategies to reduce or prevent those losses.

Key words: dairy, inflammation, performance

520 Nutritional costs of inflammation and consequences for animal growth and production. K. C. Klasing*, *University of California at Davis, Davis.*

The pro-inflammatory response to microbes or trauma results in decreased growth, impaired efficiency of nutrient use, altered nutrient requirements, and a clear stress response. Pro-inflammatory cytokines (IL-1 and IL-6 in chickens and IL-1, IL-6, and tumor necrosis factor in mammals) mediate many of these changes, either by direct effects on cells or by altering the endocrine milieu (e.g., corticosteroids). Other cytokines, including interferon gamma and IL-18 may also contribute. Growth and efficiency of nutrient use are diminished by changes in food intake, nutrient absorption, metabolism, and tissue accretion. Decreases in intestinal absorption of nutrients are also important and are greatest for lipids (including fat-soluble vitamins) and some trace minerals. Metabolic inefficiencies caused by inflammation are due to increased turnover of muscle and bone. Skeletal muscle and bone accretion are impaired, but liver accretion is increased due to increased production of lipids and acute-phase proteins. In aggregate, these alterations change the requirements for many amino acids and trace nutrients. Although accommodating these proportional changes in nutrient needs via dietary adjustments improves feed efficiency, growth cannot be completely normalized by nutritional means. Dampening the acute-phase response to inflammation by nutrients with regulatory properties (e.g., n-3 PUFA) has some utility, but diminishing the frequency and intensity of inflammatory challenges is the most useful strategy. This can be accomplished by sanitation, vaccination, and feeding prophylactic antibiotics or other antimicrobials.

Key words: inflammation, acute-phase response, growth

521 Warner-Bratzler and slice shear force measurements of three beef muscles in response to various aging periods following anabolic implant and zilpaterol hydrochloride supplementation of finishing beef steers. A. J. Garmyn*[1], L. F. Hightower[1], J. C. Brooks[1], B. J. Johnson[1], S. L. Parr[1], R. J. Rathmann[1], J. D. Starkey[1], D. A. Yates[2], J. M. Hodgen[2], J. P. Hutcheson[2], and M. F. Miller[1], *[1]Texas Tech University, Lubbock, [2]Intervet/Schering-Plough Animal Health, DeSoto, KS.*

Our objectives were to determine the effects of zilpaterol hydrochloride (ZH) and the payout pattern of trenbolone acetate and estradiol-17β on Warner-Bratzler shear force (WBSF) and slice shear force (SSF) of longissimus lumborum (LL) and the WBSF of gluteus medius (GM) and psoas major (PM) in response to various aging periods. British × Continental steers (n = 168) were assigned to treatments in a 3 × 2 factorial. The main effects of treatment were implant [no implant (NI); Revalor-S (REV-S), Revalor-XS (REV-XS)] and ZH (0 or 8.3 mg/kg of DM for 20 d). Harvest group was included as a random effect to account for the variation in days on feed (153 or 174 d). Loins (n = 96) were fabricated to obtain strip loin, top sirloin butt, and tenderloin subprimals. Five 2.54-cm steaks were cut from each subprimal and assigned to 1 of 5 aging periods (7, 14, 21, 28, or 35 d postmortem). Feeding ZH increased ($P < 0.01$) LL WBSF and SSF values at each aging period compared with controls. Implanting increased ($P < 0.05$) LL WBSF values at 14 and 21 d, but did not affect LL SSF values ($P > 0.05$). Only REV-S increased WBSF values at 28 and 35 d compared with NI or REV-XS. The percentage of LL steaks with a WBSF value <4.6 kg did not differ ($P > 0.05$) between ZH supplementation or implant strategy at any aging period, and by d 28 over 99% of LL steaks registered WBSF values <4.6 kg. Feeding ZH increased ($P < 0.05$) GM WBSF values only on d 21. Implant had no effect ($P > 0.05$) on GM WBSF values. The percentage of GM steaks with a WBSF value <4.6 kg did not differ ($P > 0.05$) between ZH supplementation or implant strategy at any aging period. Neither ZH nor implant strategy affected PM WBSF values ($P > 0.05$). All PM WBSF values were <4.6 kg on d 7. The results of this study indicated feeding ZH increased WBSF and SSF of LL steaks, regardless of aging period; however, the percentage of steaks with WBSF <4.6 kg did not differ due to ZH or implant. Implanting increased LL WBSF, but not SSF values.

Key words: anabolic implant, shear force, zilpaterol hydrochloride

522 The effects of anabolic growth implant and restricted feed intake on proliferation of bovine primary skeletal muscle cells. T. L. Lee*, D. U. Thomson, B. W. Wileman, L. K. Mamedova, B. J. Bradford, and C. D. Reinhardt, *Kansas State University, Manhattan.*

Sixteen crossbred steers (BW 293 ± 19.3 kg) were used to evaluate the impact of a steroid implant and nutrient intake on nutrient metabolism and muscle cell growth of steers. Steers were trained to Calan gates and randomly assigned to 1 of 4 groups: (1) implant (Revalor XS; 200 mg trenbolone acetate, 40 mg estradiol), high intake (2 × ME for maintenance); (2) implant, restricted intake (1 × ME for maintenance; (3) no implant, high intake; and (4) no implant, restricted intake. Serum was collected on d 0, 14, and 28 for application to satellite cells (previously isolated from non-study steers and frozen). Satellite cells were incubated with serum treatments (20% of total media) for 72 h. Protein abundance of myosin heavy chain (MYH; d 0, 14, and 28), phosphorylated extracellular signal related kinase (pERK; d 0 and 28), and phosphorylated mammalian target of rapamycin (pmTOR; d 0 and 28) were analyzed in differentiated satellite cells to determine effects of implant, intake, and their interaction (applied via the serum). MYH is used as a marker of myotube formation, and pERK and pmTOR are growth factor protein indicators of cell proliferation. Intake had no effect on MYH but implant increased MYH abundance ($P < 0.01$). There was no interaction between intake and implant on MYH abundance. Implant increased the abundance of pERK ($P < 0.01$), but intake had no effect, and there was no interaction between intake and implant on pERK. At high intake, implant increased abundance of pmTOR ($P = 0.02$) but implant had no effect on pmTOR at restricted intake ($P = 0.21$, interaction $P < 0.01$). These results demonstrate that a circulating factor in implanted cattle promotes satellite cell differentiation, possibly mediated by ERK phosphorylation.

Key words: implant, satellite cells, nutrient

523 Identification of tough beef carcasses from epigenetic changes detectable in blood. M. S. Updike*, C. Zhao, Y. Yu, F. Tian, and J. Song, *University of Maryland, College Park.*

For decades, inconsistency in beef tenderness has been a major problem identified by consumers. Currently a variety of methods to segregate palatable carcasses from unpalatable carcasses such as quality grade and camera technologies are used. Much of the research has focused upon changes in the muscle as this will become the beef. By taking a step back and asking what are some of the reasons that muscle can turn into tough beef, other methods may be identified. One factor that has previously been identified as causing tougher beef is stress on the live cattle such as that from hardware disease. To mimic hardware disease in this study, yearling Wye Angus cattle were surgically implanted with cannulas into the rumen. The cattle were fed a pelleted forage diet sufficient for maintenance, but not growth. Two months after the surgery, the cattle were serially slaughtered. Blood was collected during exsanguination and longissimus dorsi samples were collected 24 h after harvest, vaccum packed, aged for 14 d and then frozen. The steaks underwent Warner Bratzler shear force (WBS) analysis. The blood was used to detect epigenetic changes in the CpG islands of promoter regions of selected genes. As expected, the steaks from the negative control were more tender than the steaks from the treatment group. However, of greater interest was the bimodal distribution of tenderness within the stress group. Some stressed cattle were relatively tender while other stressed cattle had very tough beef. We also found that the methylation levels of NAALAD2, a member of the N-acetylated α-linked acidic dipeptidase (NAALADase) gene family, significantly increased in stress groups in blood samples ($P < 0.05$), compared with the non-stress group, although the methylation change is higher in the tender-stress group than in the tough-stress group, indicating that the methylation variation of the gene in blood mainly relates to stress stimuli.

Key words: epigenetics, stress, tenderness

524 Carcass and production characteristics of grass-fed Angus cattle through spring, summer, winter and fall. C. Zhao, J. Song, B. Bequette, and M. S. Updike*, *University of Maryland, College Park.*

Consumers are demanding that grass fed beef be available year round. This can pose challenges for grass fed beef producers as feeding harvested forages is one of the most expensive aspects of grass fed beef

production. Some producers choose not to finish cattle on forages over the winter due to increased costs. To examine the effects of seasonal effects, including feeding harvested forages during the winter, the production and carcass characteristics of Angus cattle finished on grass were examined. The Wye Angus based Angus cattle were rotationally grazed on 100% Alflalfa pasture, when available, during the spring, summer and fall. During the winter, the cattle were fed ad libitum alfalfa baylage. Cattle were harvested based upon both demand for additional beef and visual appraisal for degree of finish. Longissimus dorsi samples were aged for 14 d and then frozen before Warner Bratzler shear force (WBS) analysis. Season had no effect on any of the production or carcass characteristics of these grass fed Angus cattle ($P > 0.5$). The mean age at slaughter was 22.5 mo, the mean carcass weight was 291.3 kg, 62% of the carcasses graded choice, and the mean WBS was 2.9 kg.

Key words: grass-fed, beef, tenderness

525 Withdrawn

526 Effect of castration and slaughter ages on animal performance and meat quality of Holstein bulls fed high-concentrate diets. S. Marti*[1], C. E. Realini[2], A. Bach[3,1], M. Perez-Juan[2], and M. Devant[1], *[1]Department Ruminant Production, IRTA, Barcelona, Spain, [2]Carcass Quality Subprogram, IRTA, Girona, Spain, [3]ICREA, Barcelona, Spain.*

The aim of this study was to evaluate the effect of castration and slaughter ages on performance and meat quality of Holstein bulls fed a high-concentrate diet. One hundred and 20 4 animals (97 ± 2.4 d of age) were randomly allocated in 6 pens following a 3x3 factorial arrangement of treatments. Three castration ages (bulls: INT, 116 ± 3.7 kg; castration at 3 mo: CAS3, 115 ± 3.7 kg; and castration at 8 mo of age: CAS8, 117 ± 3.7 kg) and 3 slaughter ages (10, 12, and 14 mo of age) were evaluated. Animal intake was recorded daily using a computerized concentrate feeder, and BW was recorded every 14 d. The 9–10–11th rib section was removed at 24 h post-mortem and dissected into lean, fat and bone, and meat quality evaluated on the Longissimus thoracis. Data were analyzed using a mixed-effects model including castration and slaughter ages and their 2-way interaction as fixed effects, and initial BW as a covariate. Castration, at 3 or 8 mo of age, reduced animal growth and muscle pH, and increased marbling, and tenderness ($P < 0.001$). As slaughter age increased, feed efficiency was reduced ($P < 0.001$), and carcass weight, marbling and tenderness increased ($P < 0.001$). An interaction ($P = 0.01$) between castration and slaughter ages affected percentage of subcutaneous fat. The percentage of subcutaneous fat was greater in castrated animals and increased between 10 (INT: 3.7 ± 0.75%; CAS8: 5.7 ± 0.75%; CAS3: 7.6 ± 0.75%) and 12 mo at slaughter age (INT: 8.3 ± 0.75%; CAS8: 10.9 ± 0.75%; CAS3: 13.2 ± 0.75%). However, subcutaneous fat percentage decreased in animals slaughtered at 14 mo of age (INT: 7.0 ± 0.75%; CAS8: 9.7 ± 0.75%; CAS3: 7.5 ± 0.75%) and was similar for rib-sections from INT and CAS3. Interactions between castration age and slaughter age tended to be significant for intermuscular ($P = 0.07$) and intramuscular fat ($P = 0.06$). Castration at 3 or 8 mo of age reduces ADG and improves meat tenderness. As slaughter age increases feed efficiency decreases and carcass weight and meat tenderness increases, and depending on castration age increases or decreases subcutaneous, intermuscular and intramuscular fat percentages.

Key words: beef, castration, meat quality

527 Establishing a molecular fingerprint of high versus low-quality beef carcasses. K. J. Thornton*, K. Chapalamadugu, and G. K. Murdoch, *University of Idaho, Moscow.*

Beef cattle raised in the US exhibit undesirable carcass variability, despite similar production practices. Given that "uniformity" is one of the primary areas of improvement identified by the NCBA Beef Quality Audit, carcass characteristic variability observed in the northwest is less than ideal. In accordance with improved uniformity, producers are driven to select for less variance and higher quality animals. Therefore, it is important that underlying physiological causes for carcass quality differences are identified. To address this, post-mortem longissimus dorsi samples were collected from a random population of 500 cattle from different producers in the northwest, for the purpose of identifying key carcass characteristics that vary across this population. The whole transcriptome and proteome of the top 5% (high quality carcass grade) and bottom 5% (low quality carcass grade) of samples were analyzed using custom Nimblegen bovine microarrays and 2D proteomics, respectively. A total of 48 samples were evaluated representing 4 different groups: high-quality steers (HS, n = 12), low-quality steers (LS, n = 12), high-quality heifers (HH, n = 12), and low-quality heifers (LH, n = 12). The protein samples were pooled by group for proteome analysis, whereas microarray studies were conducted using individual samples balanced across the 12-plex microarray. When HS and LS were compared, 52 unique proteomic features differed by at least a 1.25 fold change in protein expression. Similar analysis between HH and LH showed that 61 proteins differed by at least a 1.25 fold change of expression. Differentially expressed proteins between the high and low quality groups are involved in pathways that regulate anabolism such as myogenesis and adipogenesis. Protein and mRNA differences between the 2 groups will provide insight into the molecular pathways contributing to high-quality cattle. In conclusion, we are generating a combined transcriptome and proteome fingerprint for high vs. low-quality beef carcasses. This may allow producers to employ altered management and genetic selection practices that promote greater uniformity with respect to carcass quality.

Key words: beef quality, proteome, muscle

528 Localization and abundance of DLK1 in skeletal muscle of cattle. E. Albrecht*[1], J. Kuzinski[1], T. Gotoh[2], and S. Maak[1], *[1]Leibniz Institute for Farm Animal Biology, Muscle Biology and Growth, Dummerstorf, Germany, [2]Kyushu University, Kuju Agricultural Research Center, Kuju-cho, Oita, Japan.*

The delta-like 1 homolog (DLK1), also known as preadipocyte factor 1 (PREF1), is a transmembrane protein involved in the differentiation of several cell types including adipocytes. Cell culture models demonstrated high expression in preadipocytes and complete disappearance during differentiation to adipocytes. Consequently, it can be expected that DLK1 expression decreases during life of cattle with increasing fat deposition. Furthermore, cattle which exploited their full potential for intramuscular fat (IMF) deposition are expected to have low DLK1 expression, independent of the final IMF content. We therefore investigated the localization and protein abundance of DLK1 in skeletal muscle of steers, known to have different capabilities to store IMF, in comparison with newborn calves and fetal muscle tissue. Six Japanese Black (JB), 5 Holstein (HS), and 6 Charolais (CH) steers were fed a high energy diet to maximize IMF deposition. When slaughtered at 26 mo of age, the IMF content in longissimus muscle was 34.3%, 20.4%, and 6.4% for JB, HS, and CH, respectively. Immunohistochemistry showed that DLK1 was localized in the cytoplasm of cells in muscle

perimysium. Many DLK1-positive cells were detected in fetal and newborn calf muscles, but only few in adult muscles. The abundance of DLK1 protein, determined by Western blot analysis, was accordingly lower in adult muscle tissue. A specific ~50 kDa band showed high variability between animals and reflected well the immunohistochemical results. The protein abundance and the number of DLK1-positive cells in a muscle cross section were highest in HS ($P < 0.05$), but similar in JB and CH ($P > 0.05$). Differences in mRNA abundance were not significant between breeds. According to our hypothesis, the results suggest that JB and CH, rather than HS steers, have widely exhausted their potential to generate new adipocytes or clusters of adipocytes growing to visible marbling flecks. This may indicate a more advanced maturity state of intramuscular adipose tissue in JB and CH steers at 26 mo of age.

Key words: intramuscular fat, cattle, preadipocyte

Nonruminant Nutrition Symposium: Nutrient and Neuroendocrine Regulation of Gastrointestinal Function

529 Involvement of gut neural and endocrine systems in pathological disorders. J. B. Furness*, *Department of Anatomy and Cell Biology, University of Melbourne, Melbourne, Australia.*

The gastrointestinal tract depends on a complex, integrated neural and endocrine control which has major influences on its functions, particularly on the secretion of water and electrolytes, motility, blood flow and mobilisation of digestive juices. Pathologies involving the enteric nervous system can be life threatening, including diarrheas in which toxins, such as cholera toxin, massively excite secretomotor neurons and Chagas' disease, in which trypanosomes cause degeneration of enteric neurons. Gut endocrine cells are involved in serious pathologies, including in the acute effects of gluten challenge in celiac disease, Zollinger-Ellison syndrome and watery diarrhea syndrome. There are also important interactions between the immune system and enteric neural and endocrine control systems, that are manifested in inflammatory bowel diseases and in ischemia/ reperfusion injury to the intestine, for example. The enteric nervous system is also a conduit for the transmission of infective prions. This is important for major commercial herd animals, such as sheep and cattle, in which the enteric nervous system may have a role in sporadic prion disease becoming endemic. There is now a comprehensive knowledge of the organization and functioning of the neural and endocrine control systems of the healthy digestive tract, with some exceptions, such influences on nutrient absorption being under researched. In contrast, in many cases there is very poor understanding of the changes in enteric neurons and endocrine cells in disease states, to the extent that it may not be clear whether changes that are observed are causes or consequences of the disorder. There has been a corresponding failure to identify suitable therapeutically-relevant molecular targets within the enteric nervous system and entero-endocrine cells. A new approach to digestive disorders that is being investigated is the use of neural stem cells. It has recently been shown that neural stem cells that are transplanted into the region of enteric ganglia can proliferate, differentiate into several appropriate phenotypes, and can integrate into existing nerve circuits.

Key words: enteric neurons, entero endocrine cells, digestive diseases

530 Neurogastroenterology and food allergies. J. D. Wood*, *Department of Physiology & Cell Biology and Internal Medicine The Ohio State University, Columbus.*

Neurogastroenterology is a subspecialty encompassing relations of the nervous system to the gastrointestinal tract. The central concept is emergence of whole organ behavior from coordinated activity of the musculature, mucosal epithelium and blood vasculature. Behavior of each effector is determined by the enteric nervous system (ENS). The ENS is a minibrain positioned close to the effectors it controls. ENS neurophysiology is in the framework of neurogastroenterology. The digestive tract is recognized as the largest lymphoid organ in the body together with a unique compliment of mast cells. In its position at the "dirtiest" of interfaces between the body and outside world, the mucosal immune system encounters food antigens, bacteria, parasites, viruses and toxins. Epithelial barriers are insufficient to exclude fully the antigenic load thereby allowing chronic challenges to the immune system. Our observations in antigen-sensitized animals document direct communication between the mucosal immune system and ENS. Communication is functional and results in adaptive responses to circumstances with the lumen that are threatening to the functional integrity of the whole animal. Communication is paracrine and incorporates specialized sensing functions of mast cells for specific antigens together with the capacity of the ENS for intelligent interpretation of the signals. Immuno-neural integration progresses sequentially beginning with immune detection followed by signal transfer to the ENS followed by neural interpretation and then selection of a neural program with coordinated mucosal secretion and a propulsive motor event that quickly clears the threat from the intestinal lumen. Operation of the defense program evokes symptoms of cramping abdominal pain, fecal urgency and watery diarrhea. Our approaches to immuno-ENS interactions merge the disciplines of mucosal immunology ENS neurophysiology into the realm of neurogastroenterology.

Key words: enteric neurons, entero endocrine cells, food allergies

531 Nutrient and neuroendocrine regulation of intestinal glucose absorption. S. P. Shirazi-Beechey*[1], A. W. Moran[1], D. M. Bravo[2], and M. Al-Rammahi[1], *[1]University of Liverpool, Liverpool, United Kingdom, [2]Pancosma, Geneva, Switzerland.*

The intestinal Na^+/glucose cotransporter, SGLT1, is the major route for the transport of dietary sugars from the lumen of the intestine into enterocytes. Regulation of this protein is essential for the provision of glucose to the body and avoidance of malabsorption. Data produced in various laboratories have suggested that the intestinal lumenal sugar concentration, the gut hormone, GLP-2, and the enteric nervous system participate in pathways regulating SGLT1 expression. To this end, it has been shown that i) expression of SGLT1 is upregulated in response to increased dietary sugars, ii) the serosal application of GLP-2 enhances SGLT1 expression, iii) raised lumenal glucose concentrations in the ileum results in SGLT1 upregulation in more proximal regions and iv) the upregulation of SGLT1 in response to high lumenal glucose is only achieved in intact mucosa and not in isolated enterocytes. However detailed network of pathways by which the lumenal sugar, gut hormones and the enteric nervous system interact to regulate SGLT1 expression has not been known. Experimental evidence in our laboratory has shown that the intestinal glucose sensor, the taste receptor1 subunit heterodimers, T1R2+T1R3, expressed on the luminal membrane of endocrine cells, senses lumenal glucose concentration. Lumenal glucose when above a threshold activates in endocrine cells, a signalling pathway involving T1R2+T1R3, the transducer G-protein, gustducin, and other signalling elements, resulting in secretion of GLP-1, GLP-2 and GIP. Binding of GLP-2 to its receptor on enteric neurons elicits a neuronal response which is transmitted to subepithelial regions evoking the release of a neuropeptide. Binding of the neuropeptide to its receptor on the basolateral membrane of absorptive enterocytes enhances intracellular cAMP, thereby increasing the stability of SGLT1 mRNA and levels of functional SGLT1 protein. The identification of molecular and cellular processes controlling SGLT1 expression will assist recognition of targets for modulating the capacity of the gut to absorb dietary sugars. This has important nutritional and clinical implications.

Key words: enteric neurons, entero endocrine cells, glucose absorption

532 The role of GLP-2 in controlling intestinal function in human infants: Regulator or bystander? D. Sigalet*, *Alberta Children's Hospital / University of Calgary, Calgary, AB, Canada.*

The regulation of nutrient absorptive capacity is a critical factor in the normal growth and development of an infant. This is especially important following surgical resection; the process of adaptation, or upregulation of nutrient transport capacity is the physiologic process which allows patients to transition to enteral feeding. The specific mechanisms which control this are still relatively poorly understood. Many actions of the entero-endocrine hormone, Glucagon-like Peptide 2, suggest that it may be a key regulator both in regulating physiological nutrient absorptive capacity and the process of adaptative upregulation of nutrient absorption following resection. This talk will review the biology of GLP-2 including the production in the L cell, regulation of GLP-2 release, sites of action, which include the enteric neurons, and pericryptal myofibroblast, and the effects on the intestinal mucosa. We will examine ontogeny of this system in the developing human infant and the evidence that GLP-2 is pivotal in the regulation of adaptation, with the implications for clinical practice.

Key words: enteric neurons, entero endocrine cells, ontogeny

Physiology and Endocrinology Symposium: Factors Controlling Puberty in Beef Heifers

533 Management implications associated with the onset of puberty and persistence of estrous cycles in beef heifers. G. C. Lamb*[1], K. M. Bischoff[1], T. E. Black[1], V. R. G. Mercadante[1], G. H. L. Marquezini[1], R. F. Cooke[2], and N. DiLorenzo[1], *[1]North Florida Research and Education Center, University of Florida, Marianna, [2]Eastern Oregon Agricultural Research Center, Oregon State University, Burns.*

For optimal economic return and lifetime productivity, replacement beef heifers need to attain puberty and conceive early during their first breeding season. Significant costs are associated with development and management of replacement beef heifers; therefore, management strategies that maximize the number of replacement heifers attaining puberty before their first breeding season are vital for the efficiency of cow-calf operations. We demonstrated that fertility in replacement beef heifers was not compromised by delaying the majority of weight gain until the last third of the developmental period before the onset of the breeding season, and BW at the onset of the breeding season and weight at puberty were not compromised compared with heifers on a constant rate of gain during the developmental period. Periods of reduced nutrient intake are analogous with losses in BW, BCS, decreases in luteal activity, and cessation of estrous cycles. Persistence of estrous cycles after establishment of puberty are affected by dietary energy restriction and repletion, but may be activated gradually in response to dietary manipulation, unrelated to many metabolite changes. Reproductive development also may be accelerated with the use of exogenous hormones such as progestins for synchronization of estrous and/or ovulation. The use of protocols containing progestins initiate estrous cycles of prepubertal heifers and results in pregnancy rates that are 15% greater than untreated controls. Acclimation of heifers to human handling after weaning may also be an alternative to hasten puberty attainment and improve pregnancy rates. In both *Bos taurus* and *B. indicus* heifers, the use of acclimation techniques reduced stress-related physiological responses and increased the percentage of replacement heifers that were pubertal at the initiation of the breeding season. Incorporation of nutritional, reproductive, and stress management during the development of replacement beef heifers increases the percentage of heifers that reach puberty at the onset of the breeding season and enhances overall reproductive performance of beef cattle operations.

Key words: puberty, beef heifer, management

534 How SNP chips will advance our knowledge of factors controlling puberty and aid in selecting replacement females. W. M. Snelling*[1], R. A. Cushman[1], G. L. Bennett[1], J. W. Keele[1], L. A. Kuehn[1], T. G. McDaneld[1], R. M. Thallman[1], and M. G. Thomas[2], *[1]USMARC, USDA-ARS U.S. Meat Animal Research Center, Clay Center, NE, [2]New Mexico State University, Las Cruces.*

The promise of genomic selection is that genetic potential can be accurately predicted from genotypes. Simple DNA tests might replace low accuracy predictions based on performance and pedigree for expensive or lowly heritable measures of puberty and fertility. The promise is greatest if the DNA variants affecting puberty and other measures of fertility are known with some certainty. Several of the 50,000 SNP in a standard assay have tentatively been associated with age at puberty, antral follicle count, pregnancy and related traits measured on different sets of heifers. At best, these SNP may be imperfectly correlated with causal variants and indicate genomic regions affecting puberty, but sample sizes are too small and SNP density too sparse to be definitive. Associations between individual SNP and similar phenotypes are inconsistent across data sets, and genomic predictions do not appear applicable to unrelated cattle. Discrepancies may be a result of different QTL segregating in the sampled populations, differences in linkage disequilibrium (LD) patterns so the same SNP are not correlated with the same QTL, and spurious correlations with phenotype. Larger samples and denser SNP will increase power to detect real associations with SNP having more consistent LD with underlying QTL. Meta-analysis combining results from different studies will effectively increase sample size. High-density genotyping with heifers pooled by early and late puberty, or extremes for quantitative indicators of puberty, can be a cost-effective means to sample large numbers. Networks of genes, implicated by associations with multiple traits correlated with puberty and fertility, could provide insight into the complex nature of these traits, especially if corroborated by functional annotation, established gene interaction pathways, and transcript expression. Integrating information about gene function and regulation with statistical associations from whole-genome SNP genotyping assays will enhance knowledge of genomic mechanisms affecting puberty, enabling development of more reliable DNA tests to guide heifer selection decisions.

Key words: genomics, puberty

535 Nutritional aspects of developing replacement heifers. R. N. Funston*, *University of Nebraska West Central Research and Extension Center, North Platte.*

Studies in numerous species provide evidence that diet during development can partially control physiological changes necessary for puberty. Numerous studies have reported inverse correlations between postweaning growth rate and age at puberty and pregnancy rates in heifers. Thus, rate of postweaning growth was determined to be an important factor affecting age of puberty, which influenced pregnancy rates. This and other research conducted during the late 1960s through the early 1980s indicated puberty occurs at a genetically predetermined size, and only when heifers reach their target weight can high pregnancy rates be obtained. Guidelines were established indicating replacement heifers should achieve 60 to 65% of their expected mature body weight by breeding. Traditional approaches for postweaning development of replacement heifers used during the last several decades have primarily focused on feeding heifers to achieve or exceed an appropriate target weight, and thereby maximize heifer pregnancy rates. Intensive heifer development systems may maximize pregnancy rates, but not necessarily optimize profit or sustainability. Since inception of target weight guidelines, subsequent research demonstrated the pattern of growth heifers experience before achieving a critical target weight could be varied. Altering rate and timing of gain can result in periods of compensatory growth thereby providing an opportunity to decrease feed costs. Recent research from our laboratory has demonstrated feeding replacement heifers to traditional target weights increased development costs without improving reproduction or subsequent calf production relative to development systems where heifers were developed to lower target weights ranging from 50 to 57% of mature BW.

Key words: beef cattle, heifer development, target weight

536 Harnessing basic knowledge of factors controlling puberty to improve synchronization of estrus and fertility in heifers. G. A. Perry*, *South Dakota State University, Department of Animal and Range Sciences, Brookings.*

The development of replacement heifers is a major economic investment for all beef and dairy operations. The costs associated with heifer development cannot be recovered if heifers do not conceive and remain productive in the herd; therefore, heifers need to conceive on schedule or risk being culled from the operations. Previous research has reported up to a 21% increase in fertility from a heifer′s pubertal estrus to the third estrus. The use of reproductive tract scores to determine pubertal status has demonstrated that peripubertal and pubertal heifers have an increased pregnancy success to synchronization protocols compared with heifers that were prepubertal. The development of radioimmunoassays has allowed for accurate measurement of changes in hormone profiles to characterize the pubertal process and determine when puberty occurs. This basic knowledge has increased our understanding of the mechanisms that control puberty and sexual development in heifers. In addition, understanding the hormonal changes that occur during the estrous cycle has allowed for the development of estrous synchronization protocols that result in increased control of follicular growth, regression of luteal tissue, and ovulation. Transrectal ultrasonography has resulted in an increased understanding of the endocrine regulation of follicular waves and development of methods to synchronize follicular waves for purposes of fixed-time AI. Current topics of research include the affect of antral follicle count on fertility and the affect of maternal nutrition (on the fetus in utero) on subsequent reproductive potential of a heifer (e.g., fetal programming). Advancements in genomic technologies will likely provide a powerful tool for selecting heifers at birth that will have a high probability of being reproductively successful if managed correctly. Therefore, the basic knowledge gain through research has improved and will continue to improve heifer development and pregnancy success.

Key words: heifer development, estrous synchronization, puberty

537 Estimation of heritability and non-genetic factors influencing calf temperament. A. N. Loyd*[1,2], D. G. Riley[1], D. A. Neuendorff[2], A. W. Lewis[2], R. C. Vann[3], T. H. Welsh, Jr.[1], and R. D. Randel[2], *[1]Texas AgriLife Research, College Station, [2]Texas AgriLife Research, Overton, TX, [3]MAFES, Mississippi State University, Raymond.*

Brahman (n = 771) and F_1 Brahman × Hereford (n = 56) calves born over 9 years (2002 to 2010) from 33 sires and 355 dams at the Texas AgriLife Research Center in Overton were utilized to evaluate the genetic and non-genetic factors influencing calf temperament. Calves were evaluated for pen score (PS), exit velocity (EV) and temperament score (TS) 28 d before weaning, at weaning, 28 d post-weaning, 56 d post-weaning, and as yearlings. Mixed models were used to determine non-genetic factors influencing PS, EV and TS at each sampling day and also as repeated records analyses. Contemporary group (calves of the same sex and weaned together) and dam age group were fixed effects, calf age at weaning and proportion Brahman were linear covariates, and sire and calf nested within sire were random effects. Exit velocity, PS and TS differed across contemporary groups ($P < 0.05$) and by day ($P < 0.0001$) but not by proportion Brahman ($P = 0.63$). Dam age group was significant for PS ($P < 0.03$) but not for TS ($P = 0.07$) or EV ($P = 0.17$). Solutions for calf age at weaning were 0.0048, 0.0033 and 0.0040 for PS, EV and TS, respectively ($P < 0.02$; average SE = 0.001). Table 1 presents means for temperament traits by day. Animal models were subsequently used to estimate heritability of PS, EV and TS at weaning: 0.48, 0.29 and 0.43, respectively (average SE = 0.08). From repeated records analyses, the proportion of phenotypic variance due to permanent environmental effects were 0.31, 0.43 and 0.25 (average SE = 0.02) and heritability estimates were 0.44, 0.28 and 0.41 (average SE = 0.07) for PS, EV and TS, respectively. These results suggest temperament is moderately to highly heritable and is influenced by contemporary group, dam age, calf age at weaning, and permanent environmental effects.

Table 1. Means for temperament traits by day[1]

Day	Records, n	PS	EV	TS
28 d pre-wean	519	2.53 ± 0.09[a]	2.18 ± 0.08[abd]	2.35 ± 0.07[a]
Wean	824	2.59 ± 0.08[a]	2.28 ± 0.08[bc]	2.43 ± 0.07[b]
28 d post-wean	520	2.79 ± 0.09[b]	2.33 ± 0.08[c]	2.56 ± 0.07[c]
56 d post-wean	485	2.79 ± 0.09[b]	2.13 ± 0.08[d]	2.45 ± 0.07[b]
Yearling	79	2.43 ± 0.12[a]	1.99 ± 0.12[a]	2.20 ± 0.09[a]

[a,b,c,d]Means within a column lacking a common superscript differ ($P < 0.05$).

[1]PS = pen score; EV = exit velocity; TS = temperament score.

Key words: cattle, heritability, temperament

538 Effects of transportation and lipopolysaccharide (LPS) challenge on vaginal temperature in crossbred heifer calves. A. N. Loyd*[1,4], R. C. Vann[2], J. P. Banta[3], T. H. Welsh, Jr.[1], J. A. Carroll[4], and R. D. Randel[5], *[1]Texas AgriLife Research, College Station, [2]MAFES, Mississippi State University, Raymond, [3]Texas AgriLife Extension, Overton, [4]Livestock Issues Research Unit, USDA-ARS, Lubbock, TX, [5]Texas AgriLife Research, Overton.*

This study evaluated the effects of transportation and subsequent LPS challenge on heifer vaginal temperature (T_{vag}). Brahman × British heifers (n = 44) from Raymond, MS were weaned and acclimated to a high roughage diet fed in GrowSafe bunks for 25 d. Heifers were blocked by BW and breed and randomly assigned to a transportation treatment group: transport (Trans; n = 14); no transport with access to feed and water (Feed; n = 15); and no transport without access to feed and water (NoFeed; n = 15). Hobo loggers were fitted onto blank CIDR devices and inserted to monitor T_{vag}. Trans heifers were loaded onto a livestock trailer, Feed heifers were returned to the GrowSafe bunks, and NoFeed heifers were placed in a dry-lot. Transport ensued for 12 h before Trans heifers were unloaded in Overton, TX. Trans and NoFeed heifers were then allowed access to hay and water for 6.5 h. Trans heifers were transported 12 h back to MS. NoFeed heifers were restricted from feed and water during this time. Feed heifers had access to feed and water throughout the study. Following transport, all heifers had ad libitum access to water and feed in GrowSafe bunks for 12 h. Heifers were then injected subcutaneously with LPS (0.5 µg/kg BW; n = 22) or saline (4.5 µL/kg BW; n = 22). T_{vag} data were analyzed using mixed models specific for repeated measures. Fixed effects for transport T_{vag} included transport, time and their interaction. Fixed effects for post-LPS T_{vag} included transport, LPS, time and all interactions. Trans T_{vag} was maximal (39.7°C) at the onset of transport and declined through 5 h below that of Feed and NoFeed (transport x time; $P < 0.01$). Trans T_{vag} remained lower than Feed and NoFeed for the remainder of both transports. No transport x LPS interaction was observed ($P = 0.92$) post-LPS. LPS-treated heifers had elevated ($P = 0.01$) T_{vag} above that of saline-treated heifers from 1 h to 7 h, with peak T_{vag} (39.6°C) occurring 4 h post-LPS. At 7 h, T_{vag} of LPS- and saline-treated heifers were similar. These results indicate that handling and loading of calves before transport induced a transient febrile response that subsided once transportation began.

Key words: cattle, LPS, transport

539 Chromium supplementation enhances the metabolic response of steers to lipopolysaccharide (LPS) challenge. N. C. Burdick*[1], B. C. Bernhard[2], J. A. Carroll[1], A. N. Loyd[1], D. N. Finck[2], R. J. Rathmann[2], and B. J. Johnson[2], *[1]Livestock Issues Research Unit, USDA-ARS, Lubbock, TX, [2]Department of Animal and Food Sciences, Texas Tech University, Lubbock.*

The effect of chromium (Cr; KemTRACE Chromium Proprionate 0.04%, Kemin Industries) supplementation on the metabolic response to LPS challenge was examined. Steers (n = 20; 235 ± 4 kg BW) received a premix that added 0 (Con) or 0.2 mg/kg Cr to the total diet (DM basis) for 55d. Jugular catheters were placed before challenge. Blood samples were collected every 30min from −2 to 8, and at 24h relative to LPS challenge (0.5 µg/kg BW). Individual BW were recorded at cannulation, and 24h and 7d post-LPS. Concentrations of glucose, insulin, and nonesterified fatty acid (NEFA) were measured. Data were analyzed using the Mixed procedure of SAS specific for repeated measures with fixed effects of treatment (trt), time, and their interaction. Initial BW did not differ ($P = 0.37$) for Cr (314 ± 8 kg) and Con (324 ± 8 kg). Twenty-four hours post-LPS, Cr steers had lost less weight ($P = 0.03$; −7 ± 2 kg) than Con steers (−14 ± 2 kg). Overall, Con steers tended to lose weight (initial compared with 7d post-LPS BW; −2.4 ± 3.6 kg) and Cr steers tended to gain weight (6.4 ± 3.6 kg; trt $P = 0.09$). Pre-LPS glucose did not differ for Con and Cr steers ($P = 0.97$). Post-LPS there was a time x trt interaction ($P < 0.01$) in that glucose peaked within 0.5h in Cr (153 ± 4 mg/dL) but not Con (111 ± 4 mg/dL)

steers. Glucose then decreased in Cr steers and also decreased in Con steers at 2h compared with baseline ($P < 0.01$). Insulin concentrations were not different between trt pre-LPS ($P = 0.63$). Post-LPS insulin increased ($P < 0.01$), peaking at 2h before returning to baseline. There was a trend for insulin to be greater in Con (1.1 ± 0.1 ng/mL) than Cr (0.9 ± 0.1 ng/mL) steers ($P = 0.13$). Concentrations of NEFA did not differ pre-LPS ($P = 0.54$). Post-LPS NEFA increased ($P < 0.01$), with Cr steers producing greater peak NEFA (0.21 ± 0.02 nmol/L) at 0.5h than Con steers (0.16 ± 0.02 nmol/L; $P < 0.04$). Following peak values, NEFA decreased before increasing again at 3.5h in Cr ($P = 0.04$) and 4h in Con ($P < 0.01$), and remained elevated 24h post-LPS. These data suggest supplementation of Cr enhanced the availability of energy resources, attenuated weight loss, and allowed for a quicker recovery following LPS challenge.

Key words: chromium, LPS, metabolism

540 Effects of transportation and lipopolysaccharide (LPS) challenge on body weight and feed intake of crossbred heifers. A. N. Loyd*[1,4], R. C. Vann[2], J. P. Banta[3], T. H. Welsh Jr.[1], J. A. Carroll[4], and R. D. Randel[5], *[1]Texas AgriLife Research, College Station, [2]MAFES, Mississippi State University, Raymond, [3]Texas AgriLife Extension, Overton, [4]Livestock Issues Research Unit, USDA-ARS, Lubbock, TX, [5]Texas AgriLife Research, Overton.*

An experiment was conducted to examine the effects of transportation and LPS challenge on feed intake (FI) and BW of calves. Brahman x British heifers (n = 44) from Raymond, MS were acclimated to a high roughage diet fed in GrowSafe bunks. Heifers were blocked by BW and breed and randomly assigned to a transportation treatment group: transport (Trans; n = 14); no transport with access to feed and water (Feed; n = 15); and no transport without access to feed and water (NoFeed; n = 15). Trans heifers were loaded onto a livestock trailer, Feed heifers were returned to the GrowSafe bunks, and NoFeed heifers were placed in a dry-lot. Transport ensued for 12 h before Trans heifers were unloaded in Overton, TX. Trans and NoFeed heifers were then allowed access to hay and water for 6.5 h. Trans heifers were loaded onto the trailer and transported for 12 h to Raymond, MS. During this time, NoFeed heifers were restricted from feed and water. Feed heifers had continual access to feed and water throughout the study. After transport, all heifers had ad libitum access to feed and water for 12 h. Heifers were then injected subcutaneously with LPS (n = 22) or saline (n = 22). BW was recorded before transport, after the second transport, before LPS challenge, and 24 and 48 h post-LPS. Daily FI was monitored when heifers had access to GrowSafe bunks. Mixed models were used to analyze FI and BW with transport, LPS, day and all interactions as fixed effects. During the 12-h post-transport period, NoFeed heifers had greater ($P < 0.01$) FI than Trans heifers, which had greater ($P < 0.01$) FI than Feed heifers (8.5, 5.9 and 2.4 kg). Post-LPS FI did not differ among treatments ($P > 0.10$). During the transport period Trans and NoFeed heifers lost more BW ($P < 0.01$; −34.4 and −25.9 kg) than Feed heifers (1.21 kg); BW change was not different ($P > 0.20$) between NoFeed and Trans heifers. Change in BW from pre- to 24 h or 48 h post-LPS was not different ($P > 0.20$). These results suggest that shrink observed in transported calves is likely the result of feed and water withdrawal. However, stress associated with transport may hinder FI immediately following transport.

Key words: cattle, feed intake, transport

541 Microbial diversity in bovine papillomatous digital dermatitis in Holstein dairy cows from upstate New York. T. Santos and R. Bicalho*, *Cornell University, Ithaca, NY.*

Papillomatous digital dermatitis (PDD) is one of the most contagious diseases of cattle adversely affecting the dairy industry by its negative effect on milk production and reproductive performance. Despite this, all the precise factors that predispose to its occurrence are not well understood and, although it is suspected that bacteria play a critical role in the pathogenesis of the lesion, the main agents involved in the etiology remains unclear. The purpose of this study was to use culture-independent methods to determine the microbial diversity in 3 strata of Holstein dairy cows PDD lesions, analyzing whether major differences exist comparing to foot skin of non-infected cows. Both group-specific 16S rDNA PCR-DGGE and clone library sequence of broad-range 16S rDNA showed differences between the microbial composition of healthy dairy cows and the different strata of the lesion. The predominant bacterial community in the lesion, regardless the stratum, consisted of 166 specific phylotypes that fell into 7 bacterial phyla; Firmicutes, Proteobacteria, Spirochaetes, Bacteroidetes, Tenericutes, Synergistetes, and Actinobacteria. Firmicutes and Spirochaetas (particularly, treponemes) were the most prominent group detected. Additionally, one phylotype phylogenetically affiliated with uncultured Archaea was detected in 2 strata of the lesion. Sequences from healthy foot skin samples revealed 86 specific phylotypes that were affiliated with Firmicutes and Proteobacteria, with the latter being the most diverse and frequent. Our study showed a previously unrecognized complexity of the microbial composition in bovine PDD infections from dairy cows. It corroborated the theory that treponemes are involved in PDD disease etiology and it suggested, for the first time, the presence of archaeal members in this particular infection.

Key words: digital dermatitis, microbial diversity, *Treponema*

542 Non-steroidal anti-inflammatory drug administration and repeated muscle biopsies affect the phosphorylation of translation initiation factors. A. L. Wagner*, R. B. Ennis, and K. L. Urschel, *University of Kentucky, Lexington.*

Protocols for measuring protein synthesis (PS) or phosphorylation (P) of translation initiation factors (eIF) require the collection of repeated biopsies (RB) for 48 h post anabolic stimuli. The effect of local inflammation (I) due to RB on the P of eIF has yet to be determined after 48 h. Non-steroidal anti-I drugs (NSAID) have been reported to blunt or not affect muscle PS in response to exercise when administered oral or local in humans, respectively. However, this has not been examined in the horse. The objective of this study was to determine if 5 d of RB in muscle with (+; n = 6) or without (–; n = 6) oral NSAID (phenylbutazone 2g/d) administration would affect the P of eIF in the gluteal muscle of mature horses in response to a feeding stimulus (3g/kg BW of 32.5 ± 0.04% CP as fed). The effects of treatment (treat; + or – NSAID), side, sampling day (day) and treat*day interaction were tested on P of eIF using repeated measures in the MIXED models procedure of SAS. Muscle biopsies were taken 60 min post-feeding from both the left and right gluteal muscles to measure the P of eIF (Akt at Ser^{473}, 4EBP1 at $Thr^{37/46}$, rpS6 at $Ser^{235/236;240/244}$, and p70 S6 Kinase at Thr^{389}) using Western blotting. Within each day, the P of all eIF studied was the same in both the left and right gluteal muscles ($P > 0.05$). For p70 S6 Kinase, rpS6, and 4EBP1 there was a treat*day interaction ($P < 0.05$); where there were increases in the P forms over time in horses not receiving NSAID, and no change in the NSAID group. There was no treat*day interaction for Akt; however, there was

a decrease with day ($P < 0.05$), regardless of treat. Total abundance of rpS6 and 4EBP1 were affected by time ($P < 0.05$), increasing and decreasing, respectively. These results show potential increases in local I due to RB elevates P of eIF after a meal; however, oral NSAID administration eliminates this response. Additional research is needed to determine if increased P of eIF after a meal due to RB in horses not receiving NSAIDs results in elevated PS. Further research is necessary to determine if RB cause locally elevated I cytokines.

Key words: horse, inflammation, mTOR

543 Infusion of interferon-τ into the uterine vein protects the corpus luteum from prostaglandin F2α induced down-regulation of cell survival genes. A. Q. Antoniazzi* and T. R. Hansen, *Animal Reproduction and Biotechnology Laboratory, Department of Biomedical Sciences, Colorado State University, Fort Collins.*

The ovine conceptus secretes interferon-T (IFNT), acts in a paracrine manner to silence upregulation of endometrial estrogen receptor and as a result, the oxytocin receptor; thus preventing luteolytic pulses of prostaglandin F2α (PGF). IFNT also is released into the uterine vein (UV) and has endocrine action on the corpus luteum (CL) through activating IFN stimulated genes (ISGs) such as ISG15. Recently, we described protection of the CL from a 5 mg injection of PGF through 12h pre-exposure to infusion of 200 μg roIFNT/day into the UV on Day 10 of the estrous cycle. It was hypothesized herein that an endocrine role of IFNT during early pregnancy is to stabilize cell survival genes in the CL. Osmotic pumps delivering 200 μg BSA or roIFNT over 24h were surgically installed on Day 10 of the estrous cycle with catheters entering the UV in 20 ewes (n = 10/group). One half (n = 5) of the ewes in each group received a single injection of PGF (5 mg) 12h after pump installation. CL collected 24h following insertion of pumps were examined for ISG15, AKT, BCL-XL, and XIAP mRNA concentration with semiquantitative RT-PCR. All differences described are significant at $P < 0.05$. Infusion of roIFNT into the UV increased ISG15 mRNA concentrations in CL confirming endocrine delivery of roIFNT to the CL. AKT mRNA concentrations were similar in CL from BSA, roIFNT and roIFNT+PGF groups, but were downregulated in the BSA+PGF group. XIAP mRNA concentrations increased in CL from roIFNT-infused ewes and decreased in CL from BSA+PGF infused ewes compared with BSA-infused ewes and IFN-infused ewes injected with PGF. Infusion of roIFNT resulted in BCL-XL mRNA concentrations that were similar to BSA-infused ewes, and following injection with PGF to levels that were lower than IFN-infusion alone, but greater than IFNT-infused and PGF injected ewes. It is concluded that AKT, BCL-XL and XIAP mRNAs are downregulated within 12h in response to PGF. Endocrine action of IFNT on the CL stabilizes these cell-life genes, which may contribute to luteal resistance to luteolysis during pregnancy. USDA AFRI 2011–67015–20067.

Key words: interferon, pregnancy, corpus luteum

544 The influence of the addition of heparin binding protein and tissue inhibitors of metalloproteinases-2 to sexed bovine semen on conception rate and pregnancy rate. B. J. Agado*[1,2], D. A. Neuendorff[2], G. L. Shafer[1,2], M. E. Kjelland[4], J. Moreno[4], M. A. Lammoglia[5], S. Romo[6], A. W. Lewis[2], T. H. Welsh Jr.[1,3], and R. D. Randel[2], *[1]Texas A&M University, College Station, [2]Texas AgriLife Research-Overton, Overton, [3]Texas AgriLife Research, College Station, College Station, [4]Sexing Technologies, Navasota, TX, [5]Universidad Autonoma de Veracruz, Tuxpan, Veracruz, Mexico, [6]Universidad Nacional Autonoma de Mexico, Cuautitlan, Estado de Mexico, Mexico.*

The addition of heparin binding protein (HBP) and tissue inhibitors of metalloproteinases-2 (TIMP-2) to enhance fertility of bovine semen sexed by flow cytometry was evaluated. Hereford bulls (n = 2) were transported to Sexing Technologies (Navasota, TX) for semen collection and isolation of X chromosome bearing sperm. Addition of exogenous HBP and TIMP-2 to semen samples was verified by immuno-fluorescence. Brahman heifers (n = 26) and cows (n = 86) were randomly and equally assigned to one of 2 treatment groups, HBP/TIMP-2 (HBP) addition or no HBP/TIMP-2 (C) addition. The females were artificially inseminated (AI) by 2 technicians. Thirty-seven cows were AIed with conventional Brahman bull semen to determine a baseline herd fertility. Females were AIed 12 h after the onset of standing estrus. The straw concentrations were 2.1×10^6 cells/straw for sexed semen and $25*10^6$ cells/straw for the conventional semen. Post thaw motilities of sexed sperm cells are: Sire 1 C = 55%, HBP = 60%; Sire 2 C = 50%, HBP = 50%. Pregnancy was determined via rectal palpation 45 d after the end of the breeding season (15 May to 22 June 2010). Two criteria were contrasted: 1st service conception rate (FSCR) and pregnancy rate (PR). Data were analyzed by Pearson Chi-Square test. The addition of HBP did not influence FSCR (HBP: 28.1% vs. C: 38.2%; $P = 0.2554$) or PR (HBP: 45.6% vs. C: 52.7%; $P = 0.4616$). Sire influenced FSCR (Sire 1: 41.7% vs. Sire 2: 23.1%; $P = 0.0370$) and PR (Sire 1: 65.0% vs. Sire 2: 30.8%; $P = 0.0003$). Parity did not influence FSCR (cow: 30.2% vs. heifer: 42.3%; $P = 0.2513$) but tended to influence PR (cow: 44.2% vs. heifer: 65.4%; $P = 0.0581$). Conventional Brahman semen had a 56.8% FSCR compared with 33.0% for sexed semen ($P = 0.0103$) and PR of 75.7% with conventional semen compared with 49.1% for sexed semen ($P = 0.0048$). The addition of HBP/TIMP-2 did not improve fertility in female Brahman bred using AI. Sire was a major source of variation in fertility of sexed semen. Conventional frozen semen had greater fertility than sexed frozen bull semen.

Key words: sexed semen, heparin binding protein, bovine

545 Effects of acclimation to handling on performance, reproductive, and physiological responses of *Bos taurus* beef heifers. B. I. Cappellozza*, R. F. Cooke, F. N. T. Cooke, and D. W. Bohnert, *Oregon State University–Eastern Oregon Agricultural Research Center, Burns.*

Thirty-eight Angus × Hereford heifers were initially evaluated, within 45 d after weaning, for body weight (BW) and puberty status (d 0 and 10), and temperament by measurements of chute score and exit velocity (d 10 only). On d 11, heifers were stratified by puberty status, temperament, BW and age, and randomly assigned to receive or not (control) an acclimation treatment. Acclimated heifers were exposed to a handling process 3 times weekly (Mondays, Wednesdays, and Fridays) for 4 weeks (d 11 to 39 of the experiment). The acclimation treatment was applied individually to heifers by processing them through a handling facility, whereas control heifers remained undisturbed on pasture. Heifer puberty status, evaluated via plasma progesterone concentrations, and BW were assessed again on d 40 and 50, d 70 and 80, d 110 and 120, d 140 and 150, d 170 and 180, and d 210 and 220 of the study. Blood samples collected before (d 10) and at the end of the acclimation period (d 40) were also analyzed for plasma concentrations of cortisol, haptoglobin, and ceruloplasmin. Heifer temperament was assessed again on d 40 and d 220. No treatment effects were detected for BW gain ($P = 0.88$). Acclimated heifers tended ($P = 0.08$) to have greater

exit velocity after the acclimation process, but reduced ($P = 0.02$) exit velocity on d 220 compared with control cohorts. Acclimated heifers had reduced plasma concentrations of cortisol ($P = 0.04$) and haptoglobin ($P = 0.01$) compared with control heifers after the acclimation period (25.7 vs. 34.1 ng/mL for cortisol and 5.3 vs. 5.9 absorbance at 450 nm × 100 for haptoglobin, respectively). Puberty attainment was hastened in acclimated heifers compared with control ($P = 0.01$). At the end of the study (d 220), a greater ($P = 0.02$) number of acclimated heifers were pubertal compared with control cohorts (63.1 vs. 31.6% of pubertal heifers, respectively). Results from this study indicated that acclimation to human handling after weaning reduced circulating concentrations of substances associated with behavioral stress and hastened puberty attainment in *Bos taurus* beef heifers.

Key words: *Bos taurus* heifers, acclimation to handling, puberty

546 Effects of temperament on reproductive and physiological responses of beef cows. R. F. Cooke*[1], D. W. Bohnert[1], F. N. T. Cooke[1], C. Mueller[2], and T. DelCurto[2], *[1]Oregon State University–Eastern Oregon Agricultural Research Center, Burns, [2]Oregon State University–Eastern Oregon Agricultural Research Center, Union.*

A total of 435 multiparous lactating Angus × Hereford cows, located at 2 different research stations (Burns, n = 243; Union, n = 192) were sampled for blood and evaluated for BCS and temperament before the beginning of the breeding season. Temperament was assessed by chute score and chute exit velocity score, which were combined into a final temperament score (1 to 5 scale; 1 = calm temperament, 5 – excitable temperament). Cows were classified according to the final temperament score (≤3 = adequate temperament, > 3 = excitable temperament). Blood samples were analyzed for plasma concentrations of cortisol, haptoglobin, and ceruloplasmin. During the breeding season, cows were exposed to mature Angus bulls for a 50-d breeding season (1:18 bull to cow ratio). However, cows located at the Union station were also assigned to an estrus synchronization + timed-AI protocol before bull exposure. Pregnancy status was verified by detecting a fetus with rectal palpation approximately 180 d after the end of the breeding season. Plasma cortisol concentrations were greater ($P < 0.01$) in cows with excitable temperament compared with cohorts with adequate temperament (19.7 vs. 15.1 ng/mL, respectively). No effects were detected ($P > 0.26$) for BCS and plasma concentrations of haptoglobin and ceruloplasmin. Pregnancy rates tended to be reduced ($P = 0.10$) in cows with excitable temperament compared with cohorts with adequate temperament (89.3 vs. 94.0% pregnant cows/total exposed cows, respectively). Further, the probability of cows to become pregnant during the breeding season was affected quadratically ($P = 0.05$) by temperament score (91.4, 95.0, 94.3, 87.6, and 59.3% of pregnancy probability for temperament scores of 1 through 5, respectively). Results from this study indicate that excitable temperament is detrimental to reproductive performance of *Bos taurus* beef cows, independently of BCS and breeding system.

Key words: beef cows, temperament, reproduction

Production, Management and the Environment: Beef Production I

547 Relationships between feedlot morbidity, performance, and carcass quality in Angus steers. M. L. Hands[1], L. R. Corah[2], T. T. Marston[3], D. W. Moser[1], and C. D. Reinhardt*[1], *[1]Kansas State University, Manhattan, [2]Certified Angus Beef, Manhattan, KS, [3]University of Nebraska, Norfolk.*

Performance data from Angus steers (n = 17,919) fed at a single feedlot in southwestern Kansas between 1997 and 2007 were used to evaluate the interrelationships between various demographic and phenotypic characteristics (season of arrival, geographic origin, health status, rate of gain, quality grade, and yield grade) on feedlot health, performance, and carcass traits. Cattle were not commingled before or following arrival at the feedlot and were predominantly preconditioned and backgrounded before shipment to the feedlot. Data were analyzed using a mixed model with the main and interactive effects of number of times treated per animal (0, 1, 2, ≥ 3) and arrival BW as fixed effects and year of arrival as a random effect. Morbidity was associated with reduced ADG (1.64 vs. 1.48 kg/d for healthy [0 times treated] vs. morbid steers [treated ≥3 times]; $P < 0.01$). Quality grade and initial BW decreased linearly with increasing number of treatments ($P < 0.01$). In steers not treated for disease, there was little association between arrival BW and percentage Choice (68.3 vs. 70.2% for steers with arrival BW <295 vs. > 409 kg; linear $P = 0.02$). Morbid steers had a lower percentage Choice vs. healthy steers (69 vs. 57% Choice for healthy vs. morbid steers; $P < 0.01$); however, in steers marketed at yield grade 3, the difference in percentage Choice narrowed (73.1 vs. 64.0% Choice for healthy vs. morbid steers; $P < 0.01$). Also, in yield grade 3 steers, there was no difference in ADG (1.65, 1.69, and 1.64 kg/d; SEM = 0.051) or HCW (375, 377, and 375 kg; SEM = 4.8) between Prime, Choice, or Select carcasses; although compared with Choice-grading cattle, ungraded cattle had lower ADG (1.49 vs. 1.69 kg/d; $P < 0.01$) and HCW (368 vs. 377 kg; $P < 0.01$). Morbidity dramatically reduced feedlot performance and quality grade, but the reduction in quality grade and HCW was less severe by marketing morbid cattle at yield grade 3.

Key words: morbidity, quality grade, feedlot

548 Impact of beef heifer development systems on ADG, reproduction, and feed efficiency. S. P. Weber*, A. F. Summers, T. L. Meyer, and R. N. Funston, *University of Nebraska, West Central Research and Extension Center, North Platte.*

Two experiments were conducted to evaluate the effect of winter management strategies during heifer development on growth and reproductive performance. In Exp. 1, 299 weaned crossbred Angus heifers, from a 3 year study, were randomly assigned to one of 2 treatments: (1) to graze winter range then be fed in a dry lot (DL; 248 ± 4 kg)or (2) placed on corn residue (CR; 247 ± 4 kg). In Exp. 2, 118 AI pregnant heifers from each year of Exp. 1 (yr 1 = 40; yr 2 = 38, yr 3 = 40) were stratified by weight and winter development system into pens and individually fed during late gestation. In year 1 of Exp. 2, diets contained 90% grass hay (11% CP; DM basis) and 10% supplement (21.8% CP; DM basis). In years 2 and 3 of Exp. 2 heifers received one of 3 dietary supplements: no supplement; a distillers grain based supplement; or a dried corn gluten feed supplement. Supplements in yr 2 and 3 were designed to be isonitrogenous (29% CP), isocaloric, but differed in RUP. In Exp. 1 heifer BW and ADG did not differ ($P = 0.48$) during winter treatment. After winter treatment, DL tended to have increased ADG ($P = 0.057$) and differences in BW were greater ($P = \leq 0.01$) for DL compared with CR heifers. Pre-breeding BW and breeding BW were also greater ($P = 0.02$; $P = 0.03$, respectively) for DL compared with CR (350 vs. 313 ± 9 kg; 374 vs. 350 ± 12 kg). Percent of heifers cycling pre-breeding, AI conception, AI pregnancy, and overall pregnancy rates were similar ($P \geq 0.41$) between treatments. DMI, ADG, and G:F in Exp. 2 were not different ($P = 0.32$) for heifers developed on CR or DL, although final weight of CR (493 ± 3 kg) was lower ($P = 0.03$) than DL (503 ± 3 kg) approximately one month before calving. These data indicate that although heifers developed on CR have decreased ADG and BW through breeding, there is no difference in reproductive performance compared with DL developed heifers. These findings also provide evidence for reducing input costs for developing heifers without sacrificing reproductive performance.

Key words: beef cattle, heifer development, pre-breeding weight

549 Late gestation supplementation impacts primiparous beef heifers and progeny. A. F. Summers*, S. P. Weber, T. L. Meyer, and R. N. Funston, *University of Nebraska, West Central Research and Extension Center, North Platte.*

A 2-yr study utilizing primiparous crossbred beef heifers (yr 1 = 38; yr 2 = 40) was conducted to determine the effects of protein supplement during late gestation on cow and progeny performance. Pregnant heifers were stratified by heifer development system, initial BW, and service sire. Heifers were individually fed meadow hay (11.3% CP) from early November to mid February and provided no supplement (CON; yr 1 = 12; yr 2 = 13), 0.91 kg/d of a dried distillers grain based supplement (HIGH; yr 1 = 13; yr 2 = 14) or 0.91 kg/d of a dried corn gluten feed based supplement (LOW; yr 1 = 13; yr 2 = 13). Supplements were designed to be isonitrogenous (29% CP), isocaloric, but differ in RUP with HIGH (59% RUP) having greater levels of RUP than LOW (34% RUP). After the individual feeding period, heifers were placed in a dry lot for calving. All heifers were bred using a fixed-timed AI protocol and pairs moved to a commercial ranch in the Nebraska Sandhills for summer grazing. Approximately 10 d after AI, a bull was placed with the cows for 60 d. Pregnancy rates were determined via rectal palpation at weaning and calves placed in a feedlot. Feeding period initial age, initial BW and midterm BW did not differ ($P \geq 0.57$) among groups. Final off test BW was greater ($P = 0.05$) for supplemented heifers compared with CON heifers (509 vs. 434 kg ± 4 kg). Supplemented heifers had greater ($P \leq 0.06$) ADG, NE DMI, and G:F during the individual feeding period compared with CON heifers. The following calf data are only for the first year. Calving date and calf birth BW did not differ ($P \geq 0.24$) among groups. Weaning calf BW and BW at feedlot entry were greater ($P \leq 0.07$) for LOW compared with CON calves (261 vs. 239 kg ± 7 kg; 275 vs. 255 ± 7 kg) and feedlot entry BW tended ($P = 0.13$) to be greater for HIGH (273 ± 7 kg) compared with CON (255 ± 7 kg) calves. Re-implant interim feedlot BW and ADG did not differ ($P > 0.30$) among groups. Protein supplementation improved heifer ADG and G:F and calves from heifers fed lower levels of RUP had greater weaning BW and feedlot entry BW compared with calves from non supplemented dams.

Key words: beef cattle, maternal nutrition, protein supplementation

550 Cattle performance comparison in three feedlot facility designs in South Dakota. B. P. Holland*, E. R. Loe, and R. H.

Pritchard, *Department of Animal and Range Sciences, South Dakota State University, Brookings.*

The Opportunities Farm, located in southeastern South Dakota, contains 3 feedlot facility designs. Each facility design contains 4, 80 head pens. The open (OPN) design has concrete bunk aprons and mounded earthen pen floors and provides 25.5 m^2/head. The partially covered (PTL) design has a monoslope building over the feed alley and 6 m of pen, and the remainder of the pen is mounded earthen surface (20.0 m^2/head). The Confined (CON) pens are completely roofed in a monoslope building (11 m deep) with concrete floors (4.3 m^2/head) and are managed with deep pack bedding. All pens contain 24.3 m of bunk space. Beginning in 2004, cattle were sourced by lot (204 to 252 cattle/lot; 6,615 total) and randomly allotted at arrival to one pen in each housing facility. Yearling or backgrounded cattle (28 lots; BW = 215 ± 93; range = 285 to 455 kg) were managed similarly as to diet, health and implant protocols, and days on feed (117 to 226 d) across facilities within lot. Lots were closed during quarter 1 (Jan-Mar; n = 8), 2 (Apr-Jun; n = 8), 3 (July–Sep; n = 6), and 4 (Oct-Dec; n = 6). Closeout data were analyzed using mixed models with main effects of facility design, quarter closed, and their interaction. Lot was included as a random effect. Facility design × quarter closed interactions were significant ($P < 0.01$) for final BW, ADG, and G:F. Quarter 1 final BW and ADG were lowest ($P < 0.01$) for OPN compared with PTL and CON (600, 616, 617 kg and 1.45, 1.54, and 1.56 kg, respectively), and G:F was lowest for OPN (0.125), intermediate for PTL (0.134) and greatest for CON (0.138). Similarly, quarter 2 ADG and G:F were lowest for OPN compared with PTL and CON (1.66, 1.71, and 1.72 kg and 0.152, 0.159, 0.158, respectively). Performance was similar across facilities during quarters 3 and 4. Overall performance for OPN, PTL, and CON, respectively were: ADG 1.61^b, 1.66^a, 1.64^a ± 0.03 kg ($P = 0.003$); DMI 11.1, 11.1, 11.0 ± 0.17 kg ($P = 0.18$); and G:F 0.145^b, 0.150^a, 0.149^a ± 0.002 ($P < 0.001$). Averaged over the year, cattle gained faster and were more efficient when finished with protection of a building, but advantages in performance are dependent on quarter closed.

Key words: beef cattle, feedlot, housing

551 Season of arrival affects feedlot performance, health, and carcass traits of Angus steers. M. L. Hands[1], T. T. Marston[2], L. R. Corah[3], D. W. Moser[1], and C. D. Reinhardt*[1], *[1]Kansas State University, Manhattan, [2]University of Nebraska, Norfolk, [3]Certified Angus Beef, Manhattan, KS.*

Performance data from Angus steers (n = 17,919) fed at a single feedlot in southwestern Kansas between 1997 and 2007 were used to evaluate the interrelationships between various demographic and phenotypic characteristics (season of arrival, geographic origin, health status, rate of gain, quality grade, and yield grade) on feedlot health, performance, and carcass traits. Cattle were not commingled before or following arrival at the feedlot and were predominantly preconditioned and backgrounded before shipment to the feedlot. Season of arrival was categorized as winter (December, January, and February), spring (March, April, and May), summer (June, July, and August), or fall (September, October, and November). Data were analyzed using a mixed model with the main and interactive effects of season and arrival BW as fixed effects and year of arrival as a random effect. Steers which arrived during fall had the lowest ADG and those which arrived during the summer had the greatest morbidity ($P < 0.01$), but there were also interactions between the effects of season and arrival BW ($P < 0.01$) on quality grade and ADG. There was a range of 20 percentage units from the greatest to lowest percent Choice by season of arrival in the light steers (295–330 kg; 62 vs. 82% for spring and summer, respectively), an 11 unit range in the medium steers (331–375 kg; 68 vs. 79% for spring and summer, respectively) and only a 3 unit range in the heavy steers (>375 kg; 74 vs. 77% for winter vs. fall, respectively). A similar interaction was noted for ADG; there was a 0.23 kg/d range in the light steers (1.51 vs. 1.74 kg/d for fall vs. spring, respectively) and a 0.11 kg/d range in heavy steers (1.63 vs. 1.74 kg/d for fall vs. winter, respectively). Season of arrival was associated with differences in performance and carcass quality, but the degree of the seasonal impact diminished with increasing arrival BW.

Key words: feedlot, season, morbidity

552 Relationships between feedlot performance, yield grade, and quality grade in Angus steers. M. L. Hands[1], T. T. Marston[2], L. R. Corah[3], D. W. Moser[1], and C. D. Reinhardt*[1], *[1]Kansas State University, Manhattan, [2]University of Nebraska, Norfolk, [3]Certified Angus Beef LLC, Manhattan, KS.*

Performance data from Angus steers (n = 17,919) fed at a single feedlot in southwestern Kansas between 1997 and 2007 were used to evaluate the interrelationships between various demographic and phenotypic characteristics (season of arrival, geographic origin, health status, rate of gain, quality grade, and yield grade) on feedlot health, performance, and carcass traits. Cattle were not commingled before or following arrival at the feedlot and were predominantly preconditioned and backgrounded before shipment to the feedlot. Data were analyzed using a mixed model with the main effects of quality grade (Prime, Choice, Select, or Ungraded), yield grade group (yield grade 1 and 2, yield grade 3, and yield grade 4 and 5), daily gain (<1.36, 1.36 to 1.55, 1.56 to 1.81, and > 1.81 kg/d), and arrival BW group (295–330, 331–375, > 375 kg) and the interactions between quality grade, yield grade, and daily gain with arrival BW as fixed effects and year of arrival as a random effect. Increasing yield grade from 1 and 2 to yield grade 3 increased percentage Choice by 12.1 points ($P < 0.01$); there was no additional gain in quality grade moving to yield grade 4 and 5 (quadratic $P < 0.01$). More rapidly gaining steers had greater final BW, HCW, and yield grade at marketing ($P < 0.01$) and had greater quality grade ($P < 0.01$) in all but steers with initial BW >375 kg. Average daily gain did not differ greatly among cattle which graded Prime, Choice, and Select (1.61, 1.68, and 1.63 kg/d, respectively; SEM = 0.025), although ADG was lower for cattle which were ungraded (1.50 kg/d; $P < 0.01$). These data suggest that producers do not need to choose between performance and quality grade; instead, much of the difference in quality grade can be explained by differences in yield grade.

Key words: feedlot, performance, quality grade

553 Relationship of feed efficiency of replacement beef heifers to subsequent feed efficiency as 3-year old suckled beef cows. T. E. Black*[1], K. M. Bischoff[1], V. R. G. Mercadante[1], G. H. L. Marquezini[1], C. C. Chase Jr.[2], S. W. Coleman[2], and G. C. Lamb[1], *[1]North Florida Research and Education Center, University of Florida, Marianna, [2]USDA-ARS, SubTropical Agricultural Research Station, Brooksville, FL.*

We determined the correlation between Residual Feed Intake (RFI) measured as post-weaned growing heifers (phase 1) and RFI measured as lactating beef cows (phase 2) in the same cohort. Individual performance and daily DMI were evaluated in 74 yearling heifers, and

were subsequently reevaluated upon the birth of their second calf. For both phases, a 14-d acclimation period preceded a 70 d test using the GrowSafe System (GrowSafe Systems Ltd., Alberta, Canada) to record individual feed intakes. Forage-based diets fed in both phases were formulated to support 1 kg/d in phase 1 and lactation maintenance requirements in phase 2. Cattle were weighed every 14 d and for phase 2 cows were milked on d 14 (lactation d 28 ± 7) and d 70 (lactation d 84 ± 7) to determine energy corrected milk (ECM) production. Fat thickness over the 13th rib (BF) and ribeye area (REA) were determined by ultrasound. Heifers were ranked by RFI and placed into Low (<0.5 SD; n = 24), Med (<0.5 SD > ; n = 24), and High (>0.5 SD; n = 26) RFI groups. Daily DMI differed for all groups ($P < 0.0001$) and was greatest (10.82 ± 0.23 kg/d) for High; intermediate (9.63 ± 0.24 kg/d) for Med; and lowest (8.47 ± 0.24 kg/d) for Low RFI heifers. Phase 2 RFI model included d 28, d84 ECM and d 84 BF which explained 36%, 11%, and 3%, respectively, of the variation in DMI not explained by ADG and MBW. Cows which were most efficient as heifers (Low) had lower ($P < 0.05$) daily DMI and RFI values (13.6 ± 0.6; −1.17 ± 0.5 kg/d, respectively) than cows ranked as Med (15.5 ± 0.6; 0.8 ± 0.5 kg/d) or High (15.7 ± 0.6; 0.24 ± 0.46) as heifers. In addition, cows which were least efficient as heifers (High) had the greatest d28 and d84 ECM (6.27 ± 0.36 ; 5.4 ± 0.31 kg/d) compared with cows that were more efficient heifers (4.66 ± 0.38 and 4.58 ± 0.33 kg/d Low; 4.66 ± 0.38 and 4.0 ± 0.33 kg/d Med). Pearson rank correlation between heifer and cow RFI was r = 0.19 ($P = 0.12$). We conclude that ECM and BF are important sources of variation affecting evaluation of RFI in lactating beef cows and heifers ranked as more efficient subsequently consumed less as cows.

Key words: residual feed intake, beef cows, dry matter intake

554 Effect of injectable trace minerals on the humoral immune response to multivalent vaccine administration in beef calves. J. D. Arthington*[1] and L. J. Havenga[2], *[1]University of Florida, Range Cattle Research and Education Center, Ona, [2]Multimin USA Inc., Fort Collins, CO.*

The objective of this experiment was to investigate the effects of injectable trace minerals (ITM) on humoral responses of calves receiving a viral vaccination. Steer calves (n = 99; average BW = 302 ± 4.2 kg), seronegative for bovine herpesvirus-1 (BHV-1) and bovine viral diarrhea virus, genotypes 1 and 2 (BVDV-1 and BVDV-2) were sourced from 2 locations. All calves, except 15 non-vaccinated (sentinel) calves, received a single dose of a multivalent modified live vaccine (Titanium 5; AgriLabs, St. Joseph, MO) containing BHV-1, BVDV-1, BVDV-2, bovine parainfluenza virus type 3, and bovine respiratory syncytial virus. Among the vaccinated calves, 2 treatments were concurrently and randomly applied; including, 1) ITM (n = 42; 7 mL s.c.; MultiMin, Fort Collins, CO) containing 15, 40, 10 and 5 mg/mL of Cu, Zn, Mn (all as disodium EDTA salts) and Se (as Na selenite), or 2) saline-injected control (Control; n = 41). Neutralizing antibody titers were measured on d 0, 14, 30, 60 and 90 relative to vaccine and treatment administration. All calves were seronegative for each of the 3 viruses on d 0 and sentinel calves remained seronegative throughout the study. Serum mineral concentrations were evaluated on d 0 and 14. No differences ($P \geq 0.30$) in serum Cu, Zn, Mn, or Se were observed between treatments on d 0. Control steers had a decrease ($P < 0.001$) in serum Zn and Se and ITM steers had an increase ($P = 0.007$) in serum Cu on d 14 relative to d 0 values. On d 14, serum Zn and Se concentrations were greater ($P < 0.01$) in ITM compared with Control steers. All vaccinated calves experienced increases in neutralizing antibody titers by d 30 following vaccine administration. Calves receiving ITM at the time of vaccination had greater ($P \leq 0.003$) neutralizing antibody titers to BHV-1 on d 14, 30, and 60 compared with Control. These results demonstrate that the ITM formulation evaluated in this study does not impair humoral immune responses in beef calves. Further, concurrent administration of ITM and BHV-1 vaccine may enhance the production of neutralizing antibodies to BHV-1 in previously naïve beef calves.

Key words: trace mineral, vaccine, calves

555 The effect of beta-agonists on feedlot performance and carcass merit in yearling steers. 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.*

Yearling steers (n = 864; BW = 347 kg) were used to study the effects of β-agonist (BA) treatment on feedlot performance and carcass merit. Steers arrived at the feedlot in 2 groups and were ranked by BW within each group and divided into 4 BW blocks. Within each BW block, each successive set of 12 ranked steers were randomly assigned to 1 of 12 pens of 9 head. After an average of 111 d on feed, steers were weighed and all 96 pens were ranked by BW and each pen was assigned to 1 of 8 BW blocks (12 pens/BW block). Within each BW block, pens were randomly assigned to 3 BA treatments (32 pens/treatment). Treatments included: 1. Control (no BA), 2. Optaflexx (OPT, 200 mg/hd/d for 28 d), and 3. Zilmax (ZIL, 8.33 mg/kg diet DM about 75 mg/hd/d for 20 d). A 3 d withdrawal from ZIL was used. All steers were fed steam-flaked corn based finishing diets 2X daily. Cattle were started on their respective BA treatments and slaughtered in 3 groups by BW block. Average final BW and ADG the final 28 d for steers treated with BA were greater ($P < 0.01$) than no BA supplemented steers. Treatment had no effect on DMI and gain-to-feed ratio was improved ($P < 0.001$) during the final 28 d by 35% for steers fed BA compared with no BA. There was no difference in final BW for OPT versus ZIL. Least squares means for HCW, adjusted for BW at the initiation of the BA feeding, were heavier ($P < 0.01$) for ZIL compared with no BA and heavier ($P < 0.05$) for ZIL than OPT. Dressing percentage (DP) was higher ($P < 0.001$) for steers fed ZIL compared with OPT and no BA (64.4, 63.2, and 63.4%, respectively). Yield grades (YG) were similar for OPT and ZIL steers and both were reduced ($P < 0.05$) compared with no BA. Average marbling score for no BA carcasses was greater ($P < 0.01$) than BA carcasses but was similar for OPT and ZIL. Carcasses from steers receiving no BA had a greater likelihood ($P < 0.01$) of grading low choice or higher than steers fed BA. The effect of OPT and ZIL on BW appears similar; however, an increase in DP for ZIL as compared with OPT or no BA resulted in a 5.8 and 9.2 kg heavier HCW for ZIL as compared with OPT and no BA, respectively.

Key words: beta-agonists, ractopamine, zilpaterol

556 Moderate exercise alters blood constituents, growth performance, and carcass characteristics in finishing heifers. A. D. Stickel[1], L. N. Edwards[1], T. A. Houser[1], J. R. Jaeger[2], T. G. Rozell[1], L. D. Hollis[1], S. Uwituze[1], C. L. Van Bibber[1], K. A. Miller[1], J. J. Higgins[1], and J. S. Drouillard*[1], *[1]Kansas State University, Manhattan, [2]Kansas State University, Hays.*

Crossbred heifers (n = 30; 448 ± 27 kg initial BW) were used in an randomized complete block experiment to assess impact of exercise regimen on serum IGF-1 and insulin, plasma glucose and lactate, feedlot performance, and carcass characteristics. Heifers were stratified by initial BW and body condition and assigned randomly, within strata,

to Sedentary and Exercised groups. Cattle were housed in individual pens (1.5 m X 6.5 m) and fed a finishing diet consisting of 93% concentrate and 7% roughage. Each Mon, Wed, and Fri, Exercised cattle were removed from their pens and moved by a caretaker at a pace of 5 to 6 km/h (20 min/d for the first 2 wk, 30 min/d for the next 2 wk, and 40 min/d thereafter). Blood samples were collected via jugular puncture before exercise on d 0, 28, and 60; ultrasound measures of LM depth, 12th rib fat thickness, and marbling were collected on d 0 and 60; and heifers were harvested on d 62. Data were analyzed using Proc Mixed of SAS, with fixed effect of exercise regimen and random effects of strata and exercise regimen x strata. Study day and the interaction between study day and exercise regimen were included as fixed effects for repeated measures. Exercise decreased insulin (exercise x d interaction, $P = 0.06$; exercise effect, $P = 0.01$), but had no effects ($P \geq 0.10$) on IGF-1, glucose, or lactate, or ultrasound measures of LM depth and marbling. Exercised cattle had poorer ADG (0.79 vs 1.14 kg/d), DMI (8.98 vs 10.06 kg/d), and gain:feed (0.083 vs 0.111) compared with Sedentary cattle ($P \leq 0.05$), but yielded similar HCW (312 vs 321 kg; $P \geq 0.10$), marbling (Slight^{74} vs Small^{01} ; $P \geq 0.10$), LM area ($P \geq 0.15$), and KPH ($P \geq 0.80$), and had less 12th rib fat (1.09 vs 1.45 cm; $P \leq 0.01$) and lower yield grades (2.22 vs 2.86; $P \leq 0.01$). Feed intakes were not different between days of exercise and rest ($P \geq 0.10$). Response to exercise was highly variable, and decreased performance was largely attributable to 2 heifers that gained no BW during the 62-d trial. Moderate physical activity in feedlot cattle alters insulin concentrations, feed intake, gain, efficiency, and carcass fatness.

Key words: exercise, cattle, feedlot

557 Acidosis challenge effects on ruminal pH and temperature in beef cattle. D. L. Christensen*, J. L. Wahrmund, A. K. Sexten, C. L. Goad, C. R. Krehbiel, and C. J. Richards, *Oklahoma State University, Stillwater.*

Twelve ruminally cannulated steers with ruminal pH and temperature monitoring devices were used to determine the effects of an acidosis challenge on ruminal pH and temperature. Steers were offered the control diet at 2% BW/d before the challenge and starting 24 h after the challenge. Challenges were ruminal dosing of 2% BW of 62% concentrate diet (CON), mixture of 50:50 dry rolled corn:wet distillers grains (MIX), or 100% dry rolled corn (DRC) at 0 h. Bolus readings for pH and temperature were recorded every minute for 72 h after dosing and compiled in 3 h increments for repeated measures analysis. Ruminal fluid samples were obtained every 3 h for 72 h after dosing and analyzed with a repeated measures analysis. For ruminal fluid samples, pH of MIX was lower ($P < 0.05$) than CON for h 3 to 27, 57 and 63. DRC pH was lower ($P < 0.05$) than CON for h 3 to 27 and 57. MIX pH was lower ($P < 0.05$) than DRC for h 3 to 15. All ruminal temperatures less than 37.8°C were considered to be associated with water consumption and were removed before analysis. Continuous ruminal pH measures resulted in significant treatment and sampling time effects ($P < 0.01$) with CON > DRC > MIX. Continuous ruminal temperatures resulted in a sampling time ($P < 0.08$) trend and significant treatment ($P < 0.01$) effect with DRC greater ($P < 0.01$) than CON or MIX. These results indicate that increased availability of highly fermentable substrates in the rumen that result in decreases in rumen pH also result in increases in ruminal temperatures. However, the type of fermentable substrate may change the relationship between ruminal temperature and pH, particularly when substrates such as distillers grains that have a low pH are included in the diet.

Key words: acidosis, beef cattle, body temperature

558 Fatty acid profile of muscle and subcutaneous fat of Red Norte bulls fed ionophores and lipids sources. M. M. Ladeira, L. C. Santarosa, O. R. Machado Neto, M. L. Chizzotti*, T. M. Gonçalves, E. M. Ramos, L. S. Lopes, J. S. F. Hostalácio, D. M. Oliveira, and M. C. L. Alves, *Federal University of Lavras, Lavras, MG, Brazil.*

The objective was to determine the fatty acids (FA) profile of muscle and subcutaneous fat of Red Norte bulls fed ground soybean grain (GSG) or rumen protected fat (RPF), with or without the inclusion of the sodic monensin. Forty animals, with initial LW of 359 kg, were allotted in a completely randomized design using a 2x2 factorial arrangement. The diets had 12.7% CP, 29.0% NDF and 7.2% EE. When the ionophore was supplemented, the dosage used was 230 ppm/day. The concentrate:forage ratio was 60:40 and it was used corn silage as roughage. The diets was fed ad libitum, and presented 17.2% of GSG or 4.2% of RPF, as DM basis. The duration of the experiment was 112 d, and the animals were slaughtered with on average 497 kg. The determination of FA was performed using GC. The data were analyzed using PROC GLM of SAS 9.1. There was no effect of monensin on FA profile ($P > 0.05$). The diets do not affected the C14:0 (2.3%) and C16:0 (22.7%) contents ($P > 0.05$). The meat of animals that received RPF had higher C18:1 content in muscle (38.1% vs. 34.5%, ($P < 0.01$), which can be explained by partial protection to rumen biohydrogenation. The CLA (cis-9, trans-11 C18:2) content was higher in muscle from animals fed soybean (0.72% vs. 0.60%, ($P < 0.01$), which can be justified by the higher exposure of FA from soybean to biohydrogenation. The GSG diet promoted greater concentration of linoleic acid in the muscle, than RPF (10.1% vs. 7.51%, ($P < 0.01$). However, linolenic acid was found in higher concentration in muscle of animals feeding RPF (0.48% vs. 0.31%, ($P < 0.01$), despite the higher concentration of this FA in soybean, which can be also justified by the partial protection of this ingredient. Subcutaneous fat from animals fed GSG presented lesser C12:0 and C14:0 content ($P < 0.01$), and had a greater C18:0 content (21.1% vs. 18.3%, ($P < 0.05$). The inclusion of RPF increased levels of C18:1 (41.3% vs. 38.3%, ($P < 0.01$) and CLA (0.84% vs. 0.37%, ($P < 0.01$) in subcutaneous fat. The concentrations of C18:2 and C18:3 were increased with the use of GSG, compared with RPF. The monensin did not affect the FA profile of meat. Funded by Fapemig, CNPq, CAPES and INCT-CA

Key words: cla, monensin, soybean

559 Effects of energetic supplementation strategies on performance of growing cattle grazing tropical forage and on animal performance during the feedlot finishing phase. L. R. D. Agostinho Neto, J. R. R. Dorea, V. N. Gouvea, A. L. Marra, and F. A. P. Santos*, *University of Sao Paulo/ESALQ, Piracicaba, São Paulo, Brazil.*

The objective of this study was to evaluate the effect of strategies of energetic supplementation to growing cattle grazing well managed tropical pastures during the summer and fall season on animal ADG, pasture stocking rate and on animal performance during the feedlot finishing phase. Seventy 6 crossbred bull calves, averaging 208 kg initial BW and 8 mo of age, were used in a randomized block design trial to compare 3 energetic supplementation strategies: T1) Control: grazing animals fed only a mineral mixture; T2) Constant level: constant daily feeding of energetic supplement at 0.6% of BW; T3) Increased level: daily feeding of energetic supplement at increasing levels of 0.3, 0.6, and 0.9% BW, according to the experimental period. Animals were allocated in a 8.5 ha area of *Brachiaria brizantha* 'Marandu' pasture under a rotational grazing system with a variable defoliation interval. Supplemented animals had greater ADG ($P < 0.05$) than animals not supplemented (0.535, 0.787, and 0.867 kg/animal per d), respectively for the control, constant, and increasing treatment levels. Furthermore, animals in the increasing supplementation group presented a higher ADG when compared with the constant supplementation, although animals from both treatments have consumed similar amounts of supplement. Supplementation also increased ($P < 0.05$) the pasture stocking rate, which averaged 5.94, 7.13, and 6.90 AU/ha, respectively for the control, constant, and increasing treatment levels. Supplementation strategies during the grazing period had no effect ($P > 0.05$) on animal DMI, ADG and feed efficiency during the feedlot finishing phase.

Table 1. Animal performance, pasture stocking rate, dry matter intake, ADG:DMI

	Pasture Phase				
	Control	Constant level	Increased level	*P*-value	SEM
ADG (kg/d)	0.535c	0.787b	0.867a	*	0.016
Stocking rate (AU/ha)	5.94b	7.13a	6.90a	*	0.01
	Feedlot Phase				
	Control	Constant level	Increased level		
ADG (kg/d)	1.07	1.02	1.08	ns	0.05
DMI (kg/d)	7.89	8.04	8.34	ns	0.32
ADG/DMI (g/kg)	0.136	0.127	0.130	ns	0,005

*$P < 0.05$; ns = not significant.

Key words: supplementation, beef cattle, tropical grasses

560 Effect of rate of gain on fat deposition during grazing and final carcass characteristics in growing beef cattle. E. D. Sharman*, P. A. Lancaster, C. P. McMurphy, G. G. Hilton, C. R. Krehbiel, and G. W. Horn, *Oklahoma Agricultural Experiment Station, Stillwater.*

Recent evidence suggests that a moderate rate of gain is required throughout an animal′s life to achieve desirable quality grades in beef cattle. The objective of this study was to determine the effect of rate of gain to similar initial finishing BW on fat deposition during grazing and final carcass characteristics in growing beef cattle. Angus steers (n = 72; 259 ± 28 kg) were allotted on Dec. Four in a completely randomized design with 4 grazing treatments: (1) grazing dormant native range (NR) plus a protein supplement (1.0 kg•hd^{-1}•d^{-1}) followed by season-long grazing NR (CON); (2) grazing dormant NR plus a corn-based supplement (1% of BW) followed by short-season grazing NR (CORN); (3) grazing wheat pasture (WP) at a high stocking rate (3.0 steers/ha) for a moderate ADG (LGWP); and (4) grazing WP at a low stocking rate (1.0 steers/ha) for a high ADG (HGWP). Supplements met DIP requirements and were individually fed 5 d/wk during the first 130 d of grazing. When steers in each treatment reached an estimated carcass weight of 200 kg, 4 steers were randomly selected for intermediate harvest (Table 1). The remaining steers were transitioned to the finishing phase and fed to a backfat endpoint of 1.27 cm. At final harvest, steers had similar ($P > 0.14$) HCW, backfat, and marbling scores (456, 404, 421, and 426 ± 17.04; treatments 1–4, respectively). These data indicate that rate of gain during grazing does not significantly impact final marbling score suggesting that wintering beef steers at low rates of gain will not negatively affect final quality grade when cattle are fed to a similar backfat endpoint.

Table 1. Grazing performance and intermediate carcass characteristics

Item	CON	CORN	LGWP	HGWP
Grazing ADG, kg/d	0.49^{a}	0.63^{b}	0.84^{c}	1.41^{d}
HCW, kg	207^{ab}	201^{a}	226^{b}	204^{a}
Dressing %	52.08^{a}	52.29^{a}	59.23^{c}	54.98^{b}
Backfat, cm	0.38^{bc}	0.14^{a}	0.21^{ab}	0.51^{c}
KPH, %	0.65^{a}	0.58^{a}	0.98^{b}	1.42^{c}
LM area, cm^2	53.06^{a}	57.74^{ab}	60.64^{b}	55.16^{ab}
Marbling score[1]	158^{a}	143^{a}	315^{c}	228^{b}

^{a,b,c,d}Means within a row lacking a common superscript letter differ ($P < 0.05$).

[1]Marbling grid: 100 = Practically Devoid; 200 = Traces; 300 = Slight.

Key words: growing beef cattle, marbling deposition, winter grazing

561 Nutrient mass balance and performance of feedlot cattle fed barley based diets with and without dried distillers grains plus solubles. E. M. Hussey*[1], G. E. Erickson[1], R. E. Peterson[3], and L. O. Burciaga-Robles[2], *[1]University of Nebraska-Lincoln, Lincoln, [2]Feedlot Health Management Services Ltd., Okotoks, AB, Canada, [3]Western Feedlots Ltd., High River, AB, Canada.*

Crossbred yearling heifers (n = 9,538, 32 pens, 492 ± 50 kg initial BW, days on feed = 81) were assigned randomly at reimplant to a 2 × 2 factorial arrangement of treatments. Main effects included LOW or HIGH starch:NDF barley and 0 or 20% inclusion of dried distillers grains plus solubles (DDGS). Barley was determined to be HIGH (starch:NDF >3.25) or LOW (starch:NDF <3.25) at feedlot arrival based on values determined by Near Infrared Spectroscopy. The objective was to evaluate the impact of HIGH or LOW barley and 0% or 20% DDGS on feedlot performance, carcass characteristics and N and P mass balance. Data were analyzed using Proc Mixed, with fixed effects of treatments and the random effect of replicate. No barley x DDGS interactions were observed. Intake, ADG, and HCW were greater ($P < 0.02$) and carcass adjusted G:F tended to be greater ($P = 0.10$) for LOW starch:NDF barley. Barley treatment did not affect yield or quality grade ($P \geq 0.18$). Intake, retention, and excretion of N and P were greater ($P \leq 0.01$) and removal of N and DM from the pen tended to be greater ($P = 0.09$) for LOW. Loss and excretion of N on a kg per heifer basis was greater ($P = 0.05$) for LOW, but was not different when expressed as a % of N excretion, averaging 85%. Intake and G:F based on live ADG were greater ($P < 0.01$), and G:F tended to be greater on a carcass basis ($P = 0.07$) for 20% compared with 0% DDGS. Fat depth and the percentage of Yield grade 4 carcasses were greater ($P \leq 0.05$) for 20% DDGS compared with 0%, but no differences in quality grade were observed ($P \geq 0.25$). Intake and excretion of N and P were greater ($P < 0.01$) for 20% DDGS. Removal of N, P, and DM were not different ($P \geq 0.17$) between 0 and 20% DDGS. Losses of N (82% vs. 87%) and P were greater ($P \leq 0.01$) for 20% compared with 0%. Feeding low starch:NDF barley improved feedlot performance, increased DM removed from the pen, and increased N loss. Feeding 20% DDGS increased DMI, had a slight negative impact on G:F, and increased N and P losses.

Key words: barley, distillers grains plus solubles, mass balance

562 Effects of levels of energetic supplementation on forage intake and ruminal fermentation in beef cattle grazing tropical pastures. J. R. R. Dórea[1], L. R. D. Agostinho Neto[1], V. N. Gouvêa[1], M. A. C. Danés[1], L. G. R. Pereira[2], J. A. G. Azevêdo[3], and F. A. P. Santos*[1], *[1]University of Sao Paulo/ESALQ, Piracicaba, São Paulo, Brazil, [2]Embrapa Dairy Cattle, Juiz de Fora, Minas Gerais, Brazil, [3]State University of Santa Cruz, Ilhéus, Bahia, Brazil.*

The objective of this trial was to evaluate the effects of increasing levels of energetic supplementation on forage intake, ruminal parameters, microbial synthesis and N retention in beef steers grazing tropical pastures (12 to 15% CP), during the rainy season in the southeast region of Brazil. Treatments were: 0, 0.3, 0.6 and 0.9% BW of an energetic supplement containing fine ground corn plus monensin fed once a day. Eight Nellore steers (410 kg) with cannulas in the rumen were used in a replicated 4 × 4 Latin-square experiment. One hectare of pasture of *Brachiaria brizantha* ‘Marandu’ was used for the experiment. Chromium oxide was used as a digesta marker. Increasing levels

of supplementation decreased linearly ($P < 0.05$) forage DMI and increased total DMI. There was a dramatic decrease in forage intake with the low level of energetic supplementation (0.3% of BW) with subsequent smaller decreases with 0.6 and 0.9% BW levels. Because of the dramatic decrease in forage DMI the low level of supplementation (0.3% BW) had negligible effect on total DMI. However the 0.6 and 0.9% supplementation levels were very effective to increase total DMI of grazing steers. Ruminal pH and total VFA concentration were not affected by treatments ($P > 0.05$). Increasing levels of energetic supplementation increased linearly ruminal propionate ($P < 0.05$). The concentrations of rumen ammonia were decreased linearly ($P < 0.05$) and microbial synthesis and N retention were increased ($P < 0.05$) with energetic supplementation. The decrease on forage DMI caused by the energetic supplementation was not associated to inadequate ruminal pH or impairment of fiber degradation (in vitro gas production method).

Table 1. Forage and total intake, ruminal parameters, microbial synthesis and nitrogen retention

	Levels of supplement (%BW)				*P*-value	Contrast	
	0	0.3	0.6	0.9	trat	Linear	SE
Forage intake, %BW	1.90	1.64	1.55	1.50	*	*	0.11
Total intake, %BW	1.90	1.94	2.10	2.35	*	*	0.12
pH	6.51	6.42	6.38	6.37	ns	ns	0.03
NH_3,mg/dL	7.88	6.58	5.55	5.46	*	*	0.69
Propionate, mmol/mL	18.32	19.57	20.08	20.72	*	*	0.58
Microbial synthesis, g/d	448.58	591.12	593.14	981.84	*	*	114.6
Nitrogen retention, %N intake	20.07	19.10	33.32	47.09	*	*	5.85

*= significant, Ns=not significant, SE=standard error.

Key words: beef cattle, grazing cattle, supplementation

563 The relationship between rumen acidosis resistance and expression of genes involved in regulation of intracellular pH in rumen epithelial cells in steers. N. Schlau*, L. L. Guan, and M. Oba, *University of Alberta, Edmonton, AB Canada.*

The objective of this study was to compare the expression of genes involved in regulating intracellular pH in rumen epithelial cells between acidosis-resistant (AR) and acidosis-susceptible (AS) steers. Acidosis indexes (area under pH 5.8 divided by DMI) were measured for 17 steers, and the 3 steers with the lowest (1.4 ± 1.2) and the 3 with the highest (23.9 ± 7.4) values were classified as AR and AS, respectively, and used for the subsequent study. The steers were force-fed a meal consisting of a diet containing 85% grain at 60% of expected DMI (5.8 ± 0.8 and 5.6 ± 0.6 kg for AR and AS, respectively). Rumen papillae were biopsied at 0, 2, 4, and 6-h after feeding, and RNA was extracted and quantified using quantitative real time reverse transcriptase PCR. Mean rumen pH over the 6-h period was higher for AR compared with AS steers (6.02 vs. 5.55; $P < 0.01$). Relative mRNA abundance of monocarboxylate cotransporter isoform 1, sodium hydrogen exchanger isoform 2, and downregulated in adenoma (an anion exchanger) did not differ between AR and AS groups or among time points relative to feeding. However, an hour by group interaction ($P < 0.05$) was detected for relative mRNA abundance of sodium hydrogen exchanger isoforms 1 and 3 (NHE1 and NHE3), both of which import Na^+ to the cell and export H^+ to the rumen. Relative expression of NHE1 and NHE3 did not differ between AR and AS group at 0 and 6-h after feeding, but that of NHE1 was 56% ($P = 0.05$) and 72% ($P = 0.04$) greater, and that of NHE3 was 17% ($P < 0.001$) and 235% ($P < 0.001$) greater in AR compared with AS group at 2 and 4-h after feeding, respectively. Additionally, relative mRNA abundance of putative anion transporter isoform 1 (PAT1), which imports dissociated VFA to the cell and exports HCO_3^- to the rumen, and that of NHE1 increased linearly ($P < 0.001$) for the 6-h period. These results suggest that genes coding for transport proteins involved in intracellular pH regulation can be upregulated by supply of fermentation substrates, and the extent can differ between AR and AS steers.

Key words: acidosis resistance, gene expression, ruminal acidosis

564 Evaluation of diet net energy calculations on intake and gain compared to prediction equations for finishing steers. M. F. Wilken*, L. L. Berger, G. E. Erickson, and K. J. Hanford, *University of Nebraska-Lincoln, Lincoln.*

Four years of data collected at the University of Illinios-Urbana were utilized to evaluate 3 intake prediction equations (NRC, 1996; Galyean et al., 2009; Owens et al., 2002) calculated one of 2 ways: diet energy determined by hand (HAND = feedstuff inclusion*feedstuff NE (NRC, 1996)) or by a quadratic equation (QUAD; Zinn et al., 2003). Individual DMI and ADG were analyzed for 1,794 individually fed calf-fed steers. Thirteen treatments were utilized containing corn, dry and modified wet distillers grains plus solubles, dry and wet corn gluten feed, soybean hulls, corn silage, and/or brome hay. Observed DMI (ObsDMI) was compared with the 6 intake prediction equations (PredDMI). Observed ADG (ObsADG) was also compared with a predicted ADG (PredADG) calculated using HAND or QUAD from ObsDMI. Analysis of ObsDMI vs PredDMI showed that all 3 equations overestimated intake ($P < 0.01$), regardless of energy value calculation for all treatments. The NRC QUAD PredDMI was not different from ObsDMI within 5 treatments ($P > 0.05$) and was closest to the ObsDMI for 12 of the 13 diets consumed. The Galyean QUAD PredDMI was statistically similar to the NRC QUAD PredDMI for steers consuming byproduct containing diets ($P > 0.05$). The Owens PredDMI was the most overestimated and was statistically different ($P < 0.05$) for all treatments regardless of HAND or QUAD. For steers fed diets containing corn, there was no difference ($P > 0.05$) in ObsADG vs PredADG and energy value calculation was not significant ($P > 0.15$). However steers consuming diets containing byproducts, PredADG was overestimated compared with ObsADG ($P < 0.05$) for both HAND and QUAD. These findings suggest that the NRC equation is the most accurate but overestimation from calculations containing HAND energy values could be from inaccurate byproduct energy values in the NRC. Additionally, QUAD energy values are more accurate but vary with animal response and does not allow for a defined diet energy value.

Key words: dry matter intake, feedlot cattle, prediction equation

565 Effect of finishing system (feedlot or pasture) on energy requirements of Zebu cattle. M. L. Chizzotti*[1], M. I. Marcondes[2], S. C. Valadares Filho[2], M. P. Gionbelli[2], P. V. R. Paulino[2], and M. F. Paulino[2], *[1]Universidade Federal de Lavras, Lavras, MG, Brazil, [2]Universidade Federal de Viçosa, Viçosa, MG, Brazil.*

The aim of the present study is to evaluate the effect of the finishing system, pasture or feedlot, in the energy requirements of Zebu cattle. A database of 20 feedlot finishing studies (n = 626) and 5 pasture finishing studies (n = 127) with Zebu cattle using the comparative slaughter technique was used in a meta-analysis using PROC MIXED of SAS 9.1 to evaluate the fixed effect of finishing system on net energy requirements for maintenance and growth, assuming random effect of studies. Breed (Nelore purebred or Nellore crossbred with Bos Taurus) and gender (bulls, steers and heifers) effects were also tested and included as fixed effect if they are significant at $P < 0.10$. The coefficients AIC and BIC were used to choose the best structure of the variance-(co)variance matrix. Net energy requirements for maintenance (NEm) was obtained by the regression of heat production (HP) on metabolizable energy intake (MEI), on Mcal/kg $EBW^{0.75}$/d basis: $HP = NEm \times e^{B \times MEI}$. The metabolizable energy requirement for maintenance (MEm) was calculated by iteration to equals MEI to HP. The net energy for gain (NEg) was obtained by a multiple regression on equivalent $EBW^{0.75}$ ($eqEBW^{0.75}$) and empty body gain (EBG), according to: $NEg = C \times eqEBW^{0.75} \times EBG^{D}$. There was effect ($P < 0.05$) of finishing system in the relation empty body weight/ shrunk body weight, which was of 0.895 for feedlot and 0.863 for pasture finishing system. The relation of MEI and HP for feedlot and pasture were $HP = 0.0742 \times e^{3.703 \times MEI}$ and $HP = 0.0717 \times e^{4.439 \times MEI}$, respectively. There was no difference ($P > 0.05$) for NEm between finishing system but there was a difference ($P < 0.05$) for MEm which was of 112 and 125 kcal/$EBW^{0.75}$/d for feedlot and pasture finishing systems, respectively. There was gender effect for C coefficient of NEg for feedlot, which was of 0.053, 0.064 and 0.072 for bulls, steers and heifers, respectively. There was effect of finishing system on D coefficient of NEg, which was of 1.095 and 1.062 for feedlot and pasture, respectively. Pasture finishing Zebu cattle presented MEm 11% greater than feedlot and lower energy concentration in the gain. Funded by INCT-CA CNPq, CAPES, FAPEMIG.

Key words: growth, maintenance, Nellore

566 A chemical evaluation of the chemical composition of four corn milling co-products with focus on fatty acids. C. S. Dose*[1], P. J. Kononoff[1], T. C. Jenkins[2], L. O. Tedeschi[3], and K. Karges[4], *[1]Department of Animal Science, University of Nebraska-Lincoln, Lincoln, [2]Department of Animal and Veterinary Sciences, Clemson University, Clemson, SC, [3]Department of Animal Science, Texas A&M University, College Station, [4]Dakota Gold Research Association, Sioux Falls, SD.*

Technological advancements in ethanol production have resulted in corn milling co-products that, when compared with those most commonly produced, may differ in chemical composition. The objectives of this study were to further characterize major nutrient fractions and evaluate differences in fatty acid profile of a range of corn milling co-products. The 4 corn milling co-products evaluated in this study were: corn bran (BRAN), dehydrated germ (GERM), high protein dried distillers grains (HP), and dried distillers grains and soluble (BPX) which were produced without exposure to heat before fermentation. Over the course of 4 mo, samples of each feedstuff were collected weekly until a total of 30 replicate samples of each feedstuff were collected. Data was analyzed as a completely randomized design with treatment (feedstuff) considered as a fixed effect. The average CP was significantly different ($P < 0.01$) among the co-products and was highest for HP (44.06 ± 0.227) followed by BPX (31.17 ± 0.227), GERM (15.74 ± 0.227), and BRAN (14.45 ± 0.227). The average NDF content, with sodium sulfite, of the co-products were similar ($P < 0.01$) between HP (29.42 ± 0.5195) and BPX (29.27 ± 0.5195), with BRAN (25.70 ± 0.5195) and GERM (24.36 ± 0.5195) to follow. The average ether extract (EE) of GERM was the highest value (19.48 ± 0.1607) and HP had the lowest (4.67 ± 0.1607), with BPX (11.63 ± 0.1607) and BRAN (10.27 ± 0.1607) being similar ($P < 0.01$). Similarly, the mean concentration of total fatty acids (TFA) was also different ($P < 0.01$) and observed to be 15.7, 6.00, 9.84 and 8.3 ± 0.125% DM for GERM, HP, BPX and BRAN respectively. The proportions of C16:0, C18:0, C18:1, C18:2 and C18:3 were also different ($P < 0.01$) and averaged as follows (% TFA): GERM = 11.9, 1.65, 26.3, 55.4, and 1.11; HP = 16.2, 2.47, 22.8, 52.9, and 2.00; BPX = 13.7, 2.06, 25.0, 54.8, and 1.44; BRAN = 14.1, 2.21, 24.7, 53.3, and 1.62., respectively. Our analyses defined differences of CP, NDF, TFA, and the profile of TFA.

Key words: chemical composition, co-products, fatty acid

567 Evaluation of polyclonal antibodies in cattle adapted or not to highly fermentable carbohydrates diets. T. Barros[1], C. Marino*[1], R. Pacheco[2], F. Ferreira[1], F. Perna Jr.[1], E. Cassiano[1], M. Martins[1], M. Arrigoni[2], and P. Rodrigues[1], *[1]University of Sao Paulo, FMVZ-USP, Pirassununga, Sao Paulo, Brazil, [2]University of Sao Paulo State, FMVZ-UNESP, Botucatu, Sao Paulo, Brazil.*

The objective of this work was to evaluate the effect of polyclonal antibodies (PAP) against specific rumen bacteria *Streptococcus bovis*, *Fusobacterium necrophorum* and *Lactobacillus* on rumen fermentation parameters (pH, total volatile fatty acids (tVFA) and ratio acetate:proprionate Ac:Pr) in ruminally cannulated cows adapted or not to highly fermentable carbohydrates diets (HFC). The experimental design was 2 Latin squares 3 × 3 in a factorial arrangement of treatments 3 × 2 regarding 2 feed additives (PAP in powder presentation (PAPP) and PAP in liquid presentation (PAPL)) plus control group (CON) and 2 managements of diets adaptation resulting in 6 treatments. The first Latin square had a step-up adaptation diet: from D0 to D4 – 100% forage; D5 to D9 – 30% HFC and D10 to D14 – 60% HFC. The second Latin square received 100% forage from D0 to D14 (no adaptation). Each experimental period had 15 d, where rumen fluid samples for pH and volatile fatty acids analysis were collected from D0 to D14 at 3 h postfeeding. Data were analyzed by MIXED procedure with a significance level of 0.05. It was observed an interaction between time and adaptation ($P < 0.0001$) for rumen pH in the d 2 and 4–14, where the non-adapted group had higher values compared with adapted (6.80 vs. 6.34, respectively). It was observed an interaction between time and adaptation ($P < 0.0001$) for total VFA at D1 to 14, where the group adapted had higher values when compared with non-adapted animals (99.72 vs. 74.96 mM, respectively). It was also observed an interaction between time and adaptation ($P < 0.0001$) to ratio Ac:Pr, in D2, 5 to 7 and 12 to14, where the adapted group had lower values than non-adapted group until D7 (1.96 vs. 2.29) and after D12 (2.69 vs. 2.33) the position reversed and the adapted group had greater values. From these results, it was concluded that step-up adaptation reduced rumen pH and increased total VFA as expected by the total highly fermentable carbohydrate available. This effect was dependent on time and independent from feed additive used.

Key words: acidosis, feed additive, passive immunization

568 Evaluation of polyclonal antibodies in cattle adapted or not to highly fermentable carbohydrates diets after an acidosis challenge. T. Barros[1], C. Marino*[1], R. Pacheco[2], F. Ferreira[1], F. Perna Jr.[1], E. Cassiano[1], M. Martins[1], M. Arrigoni[2], and P. Rodrigues[1], *[1]University of Sao Paulo, FMVZ-USP, Pirassununga, Sao Paulo, Brazil,*

[2]*University of Sao Paulo State, FMVZ-UNESP, Botucatu, Sao Paulo, Brazil.*

The objective of this work was to evaluate the effect of polyclonal antibodies (PAP) against specific rumen bacteria Streptococcus bovis, Fusobacterium necrophorum and Lactobacillus on rumen fermentation parameters (pH, volatile fatty acids (VFA)) in ruminally cannulated cows adapted or not to highly fermentable carbohydrates diets (HFC) after an acidosis challenge. The experimental design was 2 Latin squares 3 × 3 in factorial arrangement of treatments 3 × 2 regarding 2 feed additives (PAP in powder presentation (PAPP) and PAP in liquid presentation (PAPL)) plus control group (CON) and 2 managements of diets adaptation resulting in 6 treatments. The first Latin square had a step-up diet adaptation: from D0 to D4 – 100% forage; D5 to D9 – 30% HFC and D10 to D14 – 60% HFC. The second Latin square received 100% forage from D0 to D14. For pH and total concentration of VFA analysis, samples of rumen fluid were collected at 0 and every 3 h postfeeding totalizing 36 h (D15 and D16) of challenge with a diet of 80% of HFC. Data were analyzed by MIXED procedure with a significance level of 0.05. It was observed an interaction between time and adaptation for pH ($P < 0.0001$). The adapted group had lower values of pH than non-adapted until 24 h and at 36 h after the start of challenge (6.18 vs. 6.55 and 5.92 vs. 6.08, respectively). For VFA total concentration, it was also observed an interaction between time and adaptation ($P < 0.0001$), where from 0 to 9 h (109.38 vs. 82.26 mM) and at 36 h (121.11 vs. 107.62 mM) after the start of challenge the adapted group had greater values compared with non-adapted group. At 24h and 27h, the non-adapted group had greater values compared with adapted (114.75 vs. 127.4 mM). From these data, it is concluded that step up adaptation was not efficient in preventing the drop of rumen pH in conditions of great availability of highly fermentable carbohydrates. High total VFA concentration was expected in adapted group due to the adaptation of rumen microbial population to the substrate, increasing their fermentative capacity.

Key words: feed additive, passive immunization

569 Optimizing barley grain feeding and processing for post-modern dairy cows. A. Nikkhah*, *University of Zanjan, Zanjan, Iran.*

Optimum dietary barley grain (BG) use and processing leads our efforts in improving starch utilization. Grinding is considered a risk to diet palatability and healthy rumen while is steam-processing rationalized to reduce BG fermentation rate and the risk of subacute rumen acidosis. The main objective of the first study was to determine effects of feeding either (1) finely ground, (2) steam-rolled, (3) finely dry-rolled, or (4) coarsely dry-rolled BG on rumen fermentation, digestibility and milk production. Eight multiparous Holsteins (85 ± 15 d in milk) were used in a replicated 4 × 4 Latin square design with 4 periods of 21-d. Diets contained 256 g BG/kg DM. Processing did not affect milk yield (28 kg/d) and composition, DMI (23.5 kg/d), rumen pH and volatile fatty acids (VFA), fecal and urine pH, and nutrient digestibility. Results established that finely ground BG was no different than dry-rolled and steam-rolled BG in stimulating DMI and productivity. The objective of another study was to compare grinding vs. steam-rolling of BG at 30% vs. 35% of diet DM on DMI, chewing time, rumen fermentation, and milk production. Eight multiparous Holstein cows (85 ± 9 d in milk) were used in a replicated 4 × 4 Latin square design with 4 21-d periods. Treatments included ground (GB) or steam-rolled (SB) BG fed at either 35% or 30% of diet DM. Diets were prepared as a mixed ration and fed twice daily at 0730 and 1600 h. Neither processing method nor dietary BG% affected DMI, daily eating, ruminating and chewing times, rumen pH and major VFA molar %, or milk % and yields of fat and protein. Energy-corrected milk yield increased for SB compared with GB at 35% (37.5 vs. 35 kg/d, $P < 0.05$) but not at 30% BG (37.8 vs. 37.3 kg/d). Feed efficiency was increased by SB vs. GB (1.54 vs. 1.46, $P < 0.01$), but was unaffected by dietary BG %. Therefore, at 30% grain, GB resulted in similar productivity as SB, and that SB did not affect productivity when BG rose from 30% to 35%. Regardless of BG level, GB vs. SB effectively maintained DMI (24.9 vs. 24.4 kg/d) and rumen pH (5.71 vs. 5.72) at 4 h post-feeding. Increasing dietary BG starch did not improve DMI and productivity.

Key words: barley, inclusion rate, processing

570 Potassium reduces the accumulation of trans-10, cis-12 conjugated linoleic acid and trans-18:1 in continuous cultures of mixed ruminal microorganisms regardless of dietary fat level. T. C. Jenkins*[1], E. Block[2], and P. H. Morris[1], *[1]Clemson University, Clemson, SC, [2]Arm & Hammer Animal Nutrition, Princeton, NJ.*

Previous studies demonstrated that K addition to continuous cultures of ruminal microorganisms caused shifts in conjugated linoleic acid (CLA) production that based on the biohydrogenation theory of milk fat depression, explained reports of increased fat percentages in milk of lactating dairy cattle fed potassium carbonate. This study was done to determine if level of dietary fat affected K effects on biohydrogenation pathways. Six dual-flow continuous fermenters were fed 60 g/d of 1:1 forage (10% alfalfa hay and 90% corn silage) to concentrate mix in 2 equal portions at 0800 and 1600 h. The study was done as a randomized block design consisting of 4 blocks (4 10 d periods) and 6 treatments arranged in a 2 × 3 factorial to examine 2 levels of soybean oil (0 and 4%, designated 0F and 4F) and 3 levels of added K (0, 1.5, and 3%). Culture pH was adjusted daily to maintain pH values above 6. Potassium was injected just before each feeding using a 10% (w/w) stock potassium carbonate solution to provide the equivalent of 0.9 (K1.5), and 1.8 (K3) g added K/d. Culture pH over the last 5 d of each period was held between 6.0 and 6.3 for all treatments. Addition of K to the cultures decreased ($P < 0.05$) propionate and increased ($P < 0.05$) acetate and acetate/propionate for 0F but K had no effect on volatile fatty acids for 4F. Adding K to the cultures had no effect on daily losses of unsaturated fatty acids from the cultures. Addition of K increased ($P < 0.05$) stearic acid and cis-9, trans-11 CLA but decreased ($P < 0.05$) daily production of trans-C18:1 and trans-10, cis-12 CLA biohydrogenation intermediates. This study showed that K addition to cultures of mixed ruminal microorganisms, regardless of dietary fat level, decreased production of trans-C18:1 and trans-10, cis-12 CLA that have been linked to milk fat depression.

Key words: potassium, conjugated linoleic acid, continuous culture

571 Metabolic effects of feeding supplemental tallow to lactating Nili-Ravi buffalo. H. Nawaz[1], M. Yaqoob*[2], J. I. Sultan[1], M. Sarwar[1], and M. Younas[2], *[1]Institute of Animal Nutrition and Feed Technology, University of Agriculture, Faisalabad, Pakistan, Faisalabad, Punjab, Pakistan, [2]Faculty of Animal Husbandry, Dept. Livestock Management, University of Agriculture, Faisalabad, Pakistan, Faisalabad, Punjab, Pakistan.*

Four early lactating Nili-Ravi buffaloes were fed 4 experimental diets containing 0, 2, 4 and 6% tallow in an experiment conducted in a 4 × 4 Latin Square design to study the effect of feeding different levels of tallow on nutrient intake, digestibility, rumen fermentation and blood metabolites. The intakes of DM, OM, CP, ADF and NDF decreased ($P < 0.01$) but intakes of EE ($P < 0.01$) increased with increasing level of tallow in the diets. The intakes of NEL and DE did not decrease with the reduction of DM intake. Digestibility of DM, OM, ADF and NDF improved in buffaloes fed diets containing 2 and 4% tallow but beyond 4% it tended to decline significantly. Digestion coefficients of CP did not differ, while that of EE improved ($P < 0.01$) from 68.2 to 74.5%. Rumen pH did not differ significantly ($P > 0.05$) but acetate content decreased significantly ($P < 0.01$) as the level of dietary tallow increased, whereas, propionate molar percentages increased ($P < 0.01$) with increasing level of tallow in the diets. However, butyrate contents were not statistically different among different treatment groups. Acetate to propionate ratio decreased linearly ($P < 0.05$) with increasing level of tallow in the diets. Blood pH and concentration of glucose did not vary significantly but cholesterol, triglycerides and total lipids increased ($P < 0.01$) as the level of tallow increased in the diets. These results suggest that tallow up to 4% of diet dry matter is a suitable fat supplement as an energy source for lactating Pakistani Nili-Ravi buffaloes.

Key words: tallow levels, nutrient intake, digestibility, rumen fermentation, blood metabolites

572 Use of a mechanistic, dynamic model of metabolism to investigate the biological basis for variation in genetics of feed conversion efficiency in lactating dairy cattle. J. Onken[1], G. Hobgood[2], S. L. Sheilds*[1], and J. P. McNamara[1], *[1]Washington State University, Pullman, [2]North Carolina State University, Raleigh.*

In dairy cattle, efficiency of feed use must take into account metabolic flux in body tissues, primarily in visceral, muscle, and adipose tissues. These processes are affected by genotype, phenotype, and intake, and are under control of hormonal and neural systems. In continued work

with the objective of identifying the patterns of metabolic flux in the most efficient dairy cattle, an existing mechanistic metabolic model (Molly, UC Davis) was used, which explicitly includes elements of genetics, including metabolic interactions in the viscera and body. Data were collected from 2nd to 4th parity cows (n = 80) in the first 3 to 4 mo postpartum, from studies that measured nutrient intake, milk component output, changes in adipose tissue lipid, visceral and body protein and lipid, and metabolism rates and gene expression in adipose tissue. Explicit inputs into the model included nutrient intake, initial body fat and protein, milk production, fat, and protein output. Body fat, body protein and visceral protein all varied ($P < 0.05$) in daily flux and overall change in direct relation to their milk productive efficiency. Intake energy ranged from 89 to 139 Mcal/d; maintenance energy ranged from 20 to 42 Mcal/d and milk energy secretion ranged from 19 to 34 Mcal/d. Efficiency of milk synthesis varied in a narrow range (81 to 84%), while visceral energy use averaged 37% of intake energy (range 33 to 46%) and 68% of maintenance energy (range 63 to 73%). The variation in maintenance energy accounted for 37.6% of the variation in milk energy efficiency (milk energy/absorbed energy). Expression of several genes coding for metabolic enzymes in adipose tissue were also related to efficiency of milk production. The model identified visceral energy and body energy (muscle protein turnover) ($P < 0.05$) as the 2 major contributors to variation in milk production efficiency. Using a systems model at the metabolic level will increase understanding of the reasons for inefficiency and speed improvement of milk productive efficiency.

Key words: lactation, feed efficiency, systems model

573 Ruminal Mg transport and assessment of Mg intake in dairy cows: Two sides of one coin. H. Martens* and F. Stumpff, *Dept. of Veterinary Physiology/Freie Universitaet Berlin, Berlin-Germany.*

The objective of this compilation of published data was to combine knowledge about Mg transport mechanisms in the rumen with a recent meta-analysis about Mg absorption for a better understanding of Mg absorption in vivo and prediction of Mg intake in lactating cows for the daily requirement. Ruminal Mg absorption is mediated by 2 apical uptake mechanisms: A potential-dependent or K-sensitive (K-s) and a potential-independent or K-insensitive (K-ins) mechanism. The K-s mechanism is suggested to work at low and the K-ins one at high Mg concentrations. The negative effect of K on Mg absorption should be high at low Mg (uptake via K-s) and low at high Mg intake (uptake via K-ins). This suggestion was confirmed in a model study with sheep (Ram et al., J. Dairy Sci. 1997 [81]: 2485–2492). In a recent meta-analysis of Mg absorption in dairy cows Schonewille et al. (J. Dairy Sci. 2008 [91]: 271–278) demonstrated that the true Mg absorption depends on Mg intake and K concentration: True Mg absorption (g/d) = 3.6(g/d) + 0.2 x Mg intake(g/d) – 0.08(kg/d) x K(g/kg DM)[1]. An endogenous Mg secretion of 2.8 g/d has to be subtracted to yield the apparent Mg absorption (g/d) = 3.6(g/d) - 2.8(g/d) + 0.2 x Mg intake (g/d) – 0.08(kg/d) x K (g/kg DM)[2]. This equation clearly shows that the effect of K on Mg digestibility is high at low Mg intake and vice versa: Apparent Mg absorption and digestibility is 3 g/d and 20% at Mg intake of 15 g/d and a K content of 10/kg. An increase of K content to 40 g/kg reduces apparent Mg absorption and digestibility to 0.6 g/d and 4%, respectively. At Mg intake of 60 g/d the effect of K (40/kg) is much less pronounced and reduces apparent Mg absorption and digestibility from 12 g/d and 20% to 9.6 g/d and 16%, respectively. In lactating cows, apparent Mg absorption has to cover both the secretion in milk (M l/d x 0.12 g/l) and endogenous secretion (2.8 g/d). Entry of these values into equation [2] yields Mg intake (g/d) = M (l/d) x 0.6 (g/l) + 0.4(kg/d) x K (g/kg DM) + 10 (g/d)[3]. Equation [3] permits the quantitative calculation of Mg intake according requirement and dietary K concentration.

Key words: magnesium, dairy cow, rumen

574 Effects of direct-fed microbes and their combinations with yeast culture on in vitro rumen fermentation characteristics. S. P. Doto* and J. X. Liu, *Institute of Dairy Science, College of Animal Sciences, Zhejiang University, Hangzhou, P.R. China.*

This experiment was conducted to determine the effects of different doses of *Bacillus licheniformis* (Bl) and *Clostridium butyricum* (Cb) (Zhejiang Future, Hangzhou, China) and their combinations with yeast culture, Diamond V Mills, Inc., Iowa, USA) on in vitro rumen fermentation characteristics. A 2-way factorial design was employed involving Bl or Cb at 0, 0.5, 1, 5 and 10 mg and yeast culture at 0, 18, 27, 36 and 60 mg per 200 mg substrate, respectively. The in vitro gas test based on syringes was conducted and gas volume was recorded at 2, 4, 6, 9, 12, 24, 36, 48 and 72 h incubation. The 24 h gas value was used to estimate the in vitro organic matter digestibility (IVOMD). Effects on pH, VFA, ammonia-N, microbial crude protein and populations of solid- and liquid-associated microbes were investigated after 24 h of incubation. The IVOMD was not influenced ($P > 0.05$) by addition with Bl or Cb alone, but was improved ($P < 0.05$) in the 60 mg yeast culture treatment, with the highest ($P < 0.05$) IVOMD observed when Bl or Cb was combined with a high dose of yeast culture, implying that Bl and Cb may have a synergistic effect with yeast culture. Potential gas production or gas production from the insoluble fraction was not influenced significantly ($P > 0.05$) by Bl or Cb alone, but increased ($P < 0.05$) by 60 mg of yeast culture. The rate constant of gas production was not influenced by Bl or Cb, but increased ($P < 0.05$) with inclusion of yeast culture. The pH was influenced by Bl and yeast culture ($P < 0.01$), but not by Cb ($P > 0.05$). However, all the pH values were in normal range. Significant interaction effect ($P < 0.05$) was observed on ammonia-N between Bl or Cb and yeast culture. Total VFA was affected by Bl and yeast culture ($P < 0.01$), but not by Cb ($P > 0.05$). Treatment did not have significant influence ($P > 0.05$) on microbial crude protein yield. Solid-associated microbes were not affected by any treatments, but liquid-associated *R. flavefaciens* populations were significantly influenced ($P < 0.05$) by combination treatment.

Key words: direct-fed microbes, rumen fermentation, yeast culture

575 Effects of grain, fructose and histidine on ruminal pH, fermentation products and histamine in an induced subacute acidosis protocol. H. M. Golder[1,2], P. Celi[1], A. R. Rabiee[1,2], C. Heuer[3], E. Bramley[4], D. W. Miller[4], R. King[5], and I. J. Lean*[1,2], *[1]University of Sydney, Faculty of Veterinary Science, Camden, New South Wales, Australia, [2]SBScibus, Camden, New South Wales, Australia, [3]Massey University, Epicentre, Institute of Veterinary, Animal and Biomedical Sciences, Palmerston North, New Zealand, [4]Murdoch University, School of Veterinary and Biomedical Sciences, Murdoch, Western Australia, Australia, [5]Dairy Australia, Southbank, Victoria, Australia.*

We investigated the effects of grain, fructose and histidine on ruminal pH and fermentation products. Holstein heifers (n = 30) were randomly allocated to 5 treatments; 1. Control (no grain), 2. Grain (1.2% liveweight (LW) rolled triticale)(GR), 3. Grain (0.8% LW) + fructose (0.4% LW)(FR), 4. GR + histidine (6g/head) (HIS) and 5. FR + HIS in an incomplete factorial design. Heifers were fed 1kg of grain daily with ad libitum access to mixed silage and alfalfa hay for 10 d. Feed

was withheld for 14 h before challenge day, on which heifers were fed 200g alfalfa hay, and immediately after their treatment diet. Rumen samples were collected 5 min after diet ingestion, 60 min later and at 3 further 50 min intervals. Samples were analyzed for ruminal pH immediately. Ruminal histamine, volatile fatty acids, ammonia and D- and L-lactate measures were made after storage at −20°C. The main effects and interactions of grain, fructose, histidine and time were examined using a PROC MIXED repeated measures model. Grain significantly reduced ruminal pH (6.70 ± 0.04), compared with control (7.14 ± 0.87) and increased ammonia, acetate, butyrate, propionate and valerate concentrations. The addition of grain had no effect on log-transformed ruminal D- and L-lactate concentrations. Fructose markedly decreased ruminal pH (6.49 ± 0.06), compared with the no fructose groups (6.92 ± 0.06) and markedly increased log-transformed D- and L-lactate concentrations (0.97 ± 0.35 and 0.23 ± 0.43 mM) compared with diets not containing fructose (−2.14 ± 0.35 mM and −2.87 ± 0.43 mM). Fructose increased butyrate and decreased valerate concentrations. While histidine did not have a marked effect on ruminal fermentation or histamine concentrations, the interactions between histidine, grain and fructose was significant ($P < 0.001$). The interactions between grain, fructose and histidine were significant for all ruminal parameters with the exception of log-transformed D- and L-lactate and caproate. This study demonstrates that the substitution of grain for fructose results in decreased ruminal pH and increased lactate concentrations.

Key words: fructose, histidine, subacute acidosis

576 Dry matter intake, ruminal pH and fermentation capacity of rumen fluid in heifers fed temperate pasture, total mixed rations or both. A. Santana*[1], J. Ubilla[1], M. Berrutti[1], T. Konrath[1], M. Aguerre[1], A. Britos[2], C. Cajarville[2], and J. L. Repetto[1], *[1]Facultad de Veterinaria, UdelaR, Depto. Bovinos, Montevideo, Uruguay, [2]Facultad de Veterinaria, UdelaR, Depto. Nutricion, Montevideo, Uruguay.*

The aim of this work was to evaluate dry matter intake, ruminal pH and fermentation capacity of rumen fluid in heifers fed total mixed rations (TMR), pasture as sole fed or a mix of both. Nine individually housed cross-breed heifers (214 ± 18kg BW) provided with permanent ruminal cannulas were fed total mixed rations (TMR), a temperate pasture ad libitum (*Trifolium repens* and *Lolium multiflorum*) (Pa) or TMR for 18h plus 6h of pasture (P6h) in a triplicated 3 × 3 latin-square design. Each experimental period consisted in 10 d of adaptation and 8 d for sampling and DMI when measured. On d 5, ruminal pH was determined hourly during 24 h. Fermentation capacity of ruminal microbiota was estimated through the in vitro gas production of at 12 h, using the inocula of each heifer and 3 different forages as substrates (*Digitaria sanguinalis*, *Medicago sativa*, and a mixture of *Trifolium repens*, and *Lolium multiflorum*). All data were analyzed with Proc Mixed of SAS. DMI of P6h was higher than TMR treatment (7.74 vs 6.37 kg DM/day; $P < 0.05$) and only pasture (7.74 vs 5.45 kg DM/day; $P < 0.01$). Ruminal pH for Pa group was higher than TMR and P6h group ($P < 0.01$). Mean daily pH values for pasture, TMR and P6h were 6.87, 6.51 and 6.46 respectively (SEM = 0.04). No differences on in vitro gas production were observed among groups for any substrate. The combination of pasture with TMR resulted in increased DMI, but not affected fermentation capacity of rumen microbiota.

Key words: feeding management, pasture, total-mixed ration

577 Protein and fertility in lactating dairy cattle: A meta-analysis and meta-regression. I. J. Lean*[1,2], P. Celi[1], J. McNamara[3], H. Raadsma[1], and A. Rabiee[1], *[1]Faculty of Veterinary Science, The University of Sydney, Camden, New South Wales, Australia, [2]SBScibus, Camden, New South Wales, Australia, [3]Department of Animal Sciences, Washington State University, Pullman.*

Treatment designs used to evaluate the effects of dietary intervention on fertility are subject to confounding, because modification of one nutritional input requires a change in at least one other input. Meta-analytical modeling allows an examination of a main intervention for a series of studies, but also an examination of a series of related effects through use of meta-regression. We examined the effects of dietary protein on fertility using this approach. Literature searches and contact with workers in the field produced 23 studies containing 36 comparisons that had fertility data and met the eligibility criteria for meta-analysis of randomized controlled trials providing information on diets used. The search strategy was to identify papers that contained data on prospective, examining the effects of dietary protein, either concentrations or degradability, or the effects of a specific feed ingredient intervention (e.g., fishmeal) on fertility. Data recorded included pregnancy or conception rates (n = 36 trials); milk production (n = 23 trials) and blood urea nitrogen (n = 24 trials). The most commonly reported fertility indicator was conception rate (CR) was used as the measurement of fertility. Details on dietary formulation and diet intake were extracted from papers, as were measures of urea in blood (BUN). Estimated fixed and random effects relative risks showed that risk of conception was lower in cows fed higher protein or more degradable protein diets (Fixed effect (M-H Relative Risk) = 0.91 (95% CI 0.84 to 0.98); $P = 0.040$). This effect was homogenous ($I^2 = 0\%$) and not influenced by difference in BUN, duration of intervention, breed, parity, milk production or type of diets (TMR vs. PMR). Significant associations among protein components of the diet and carbohydrate fractions supported the hypothesized potential for confounding. However, multivariate meta-regression to evaluate the effects of differences in dietary components between the treatment and control groups found that soluble protein eaten (kg) was a significant covariate. This work supports the concept that soluble protein eaten (kg) is a significant contributor to the biological action of protein on fertility.

578 Effect of increasing proportions of energy concentrates on in vitro gas production estimates. A. Britos*[1], J. L. Repetto[2], and C. Cajarville[1], *[1]Departmento de Nutrición Animal, Facultad de Veterinaria, UdelaR, Montevideo, Uruguay, [2]Departmento de Bovinos, Facultad de Veterinaria, UdelaR, Montevideo, Uruguay.*

The aim of the study was to evaluate the effect of energy supplementation of pasture silage on in vitro gas production. Mixtures of pasture silage with soyhulls (SH), corn (C) or barley (B) from 0 to 100% (by 10% steps) were used as substrates. 0.5g of each substrate (n = 31) was weighed in triplicate into 125mL fermentation flasks and 38.5mL of N-free media was added before inoculum addition (10mL). Inoculum was collected from a lactating cow after 15d eating pasture silage. Gas measures were made at 2, 4, 6, 8, 10, 12, 18, 24, 48, 72 and 96h. Data were fitted to a simple exponential model with lag time. Linear (L) and quadratic (Q) regression analysis were performed according to level of each concentrate included and linear equations were compared between concentrates by making dummy variables that combine concentrate*level. Potential gas production (a) of SH (L: $P < 0.001$, $R^2 = 0.953$; Q: $P < 0.001$, $R^2 = 0.873$), C (L: $P < 0.001$, $R^2 = 0.973$; Q: $P < 0.001$, $R^2 = 0.656$) and B (L: $P < 0.001$, $R^2 = 0.965$; Q: $P < 0.001$, $R^2 = 0.714$) increased; while fractional rate of gas production (kd) of SH (L: $P < 0.001$, $R^2 = 0.920$; Q: $P < 0.001$, $R^2 = 0.658$), C (L: $P < 0.001$, $R^2 = 0.980$; Q: $P < 0.001$, $R^2 = 0.902$) and B (L: $P < 0.001$, R^2

= 0.944; Q: $P < 0.001$, $R^2 = 0.521$) decreased as inclusion level raised. Lag time (l) was extended as inclusion levels of C (L: $P < 0.001$, $R^2 = 0.708$; Q: $P < 0.001$, $R^2 = 0.621$) and B (L: $P < 0.001$, $R^2 = 0.$ 0.628; Q: $P < 0.001$, $R^2 = 0.762$) increased, when SH only had Q effect ($P = 0.022$, $R^2 = 0.336$). Responses to concentrate level increases differed between concentrates for 'a', 'kd' and 'l'. Regression coefficients for 'a' differed among concentrates ($P = 0.007$), slopes decreased as SH > C > B. Slopes of the curves for 'kd' were different ($P < 0.001$), B showed the lowest regression coefficient, followed by SH and finally C. Regression coefficient of B tended to be lower than that of C ($P = 0.052$) for 'l'. Effects on 'kd' and 'l' as concentrate inclusion increased could be due to use a donor fed only forage, with a microbiota adapted to fiber degradation. Reduction of 'kd' as SH proportion raised suggests that its fiber is degraded by microbiota in a different manner than forage fiber. Funded by PEDECIBA and ANII.

Key words: carbohydrates, silage, fermentation

579 Hypophagic effects of propionate are greater for cows with elevated hepatic acetyl CoA concentration. S. E. Stocks* and M. S. Allen, *Michigan State University, East Lansing.*

We previously showed that propionate (PR) was more hypophagic than acetate (AC) when infused intraruminally in cows in the postpartum period and that the degree of hypophagia from short-term infusion (18 h) was related to hepatic acetyl CoA concentration. The objective of this experiment was to evaluate adaptation to treatment with longer-term (3 d) infusions. Twelve multiparous cows (2–13 d postpartum) were blocked by calving date and randomly assigned to treatment sequence in a crossover design experiment with a covariate period. Treatments were 1.0 M propionic acid or 1.0 M acetic acid, infused intraruminally at 0.5 mol VFA/h beginning 6 h before feeding and continuing for 78 h with 3 d between infusions. PR decreased DMI relative to AC (15.9 vs. 17.0 kg/d; $P < 0.05$) by decreasing DM consumed in the first 4 h after feeding (DMI-4h; 6.95 vs. 7.87 kg; $P = 0.004$). No interactions were detected between day within period and treatment for DMI and DMI-4h indicating a sustained effect of treatment across the 3-d infusion periods. PR decreased hepatic acetyl CoA concentration (2.74 vs. 5.78 nm/g; $P < 0.01$) and plasma concentrations of NEFA (640 vs. 800 μEq/L; $P = 0.08$) and BHBA (5.6 vs. 15.8 mg/dl; $P < 0.001$) and increased plasma concentration of glucose (53.2 vs. 48.7 mg/dl; $P < 0.01$) relative to AC. However, a period by treatment interaction was detected for DMI ($P = 0.07$). During period 1, PR decreased DMI relative to AC (14.3 vs. 17.5 kg/d; $P < 0.01$) because of a reduction in meal size (1.30 vs. 1.65 kg; $P < 0.05$) with no effect on intermeal interval ($P = 0.72$). PR decreased DMI-4h (5.82 vs. 8.15 kg; $P < 0.01$) but did not affect DMI 4 h to 24 h after feeding ($P = 0.25$). The depression in DMI in period 1 was positively related to covariate hepatic acetyl CoA concentration. PR was increasingly more hypophagic than AC when hepatic acetyl CoA concentration was high (interaction $P = 0.07$ for daily DMI and $P < 0.01$ for DMI-4h). These results suggest that propionate is more hypophagic when hepatic acetyl CoA concentrations are elevated such as when cows are in a lipolytic state.

Key words: propionic acid, feeding behavior, lipolytic state

580 Effects of added direct-fed microbials on rumen microbial fermentation in continuous culture. W. L. Braman* and I. Knap, *Chr. Hansen Animal Health and Nutrition, Milwaukee, WI, and Horsholm, Denmark.*

The purpose of this trial was to determine the benefits of *Enterococcus faecium* bacteria (EF) and live cell yeast *Saccharomyces cerevisiae* (Y) on in vitro ruminal fermentation when added to a lactating dairy TMR diet. The experiment using continuous culture of rumen contents (Hoover et al., 1976) compared a control (C), the control with a commercial product Probios TC (TC), and the control with a product containing 2 proprietary strains of EF (CH212 and CH273) and Y (EF+Y). Direct-fed microbial additions were based on a predicted intake of 24.5 kg cow/day and microbials were added at the rate of 2.0g/head/day. All diets were incubated in 1164 mL fermenters in triplicate for 8 d in continuous cultures, with effluent samples for analysis composited over the last 3 d. Experimental diet (DM basis) consisted of 22% alfalfa hay, 34% corn silage, 23% ground corn, 17% soybean meal, and 6% concentrate mix. Major diet components measured 18.2% crude protein, 29.7% NDF, 20.8% ADF, 34.9% NSC, 30.4% starch and 42.6% NFC. Results were analyzed using ANOVA with treatment sum of squares partitioned into orthogonal comparisons. The addition of EF+Y resulted in increases ($P < 0.05$) in NDF digestion (69.2 vs. 56.4%), and decreases ($P < 0.05$) in rumen ammonia (8.68 vs.14.26 mg/dl) and D-lactic acid production (0.67 vs 1.09 mmoles/day) compared with C. The addition of EF+Y resulted in significant increases ($P < 0.05$) in NDF digestion (69.2 vs. 54.8%) compared with TC. Except for reduced ($P < 0.05$) ammonia (mg/dl) and increased ($P < 0.05$) calculated by-pass N (g/day), there were no differences between TC and C. There was a tendency ($P < 0.10$) for TC and EF+Y to increase L-lactic acid production (mmoles/day). These data indicate that EF CH212 and CH273 +Y increased fiber digestibility, increased L-lactic acid and decreased D-lactic acid accumulation in this in vitro model suggesting this combination could improve rumen health in lactating dairy cows fed high starch and high NSC diets which requires further research.

Key words: direct fed microbials, yeast, rumen

581 Evaluation of weaning hair sheep lambs at 63 or 120 d of age in an accelerated lambing system in the tropics. R. W. Godfrey* and A. M. Hogg, *University of the Virgin Islands, Agricultural Experiment Station, St. Croix, VI.*

This study was designed to evaluate the impact of weaning age on lamb and ewe productivity in an accelerated lambing system. St. Croix White ewes (STX; n = 25) and lambs (n = 43), and Dorper x St. Croix White ewes (DRPX; n = 33) and lambs (n = 44) were used. Lambs were weaned at 63 (CTRL; n = 44) or 120 d of age (LATE; n = 43) based on breed, sex and litter size. 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. Pregnancy was determined after a 35-d breeding season using transrectal ultrasonography. Ewe weight at breeding before the first lambing was the same ($P > 0.10$) as at the subsequent breeding (41.9 ± 1.1 vs. 41.6 ± 1.1 kg, respectively). At the start of the subsequent breeding 100% of LATE and 0% of CTRL ewes were nursing lambs ($P < 0.0001$). There was no difference ($P > 0.10$) in days to first heat in the breeding season between LATE and CTRL ewes (16.2 ± 1.3 vs. 14.0 ± 1.5 d, respectively). Lambing rate after the subsequent breeding was not different ($P > 0.10$) between LATE and CTRL ewes (72.4 vs. 75.9%, respectively). At weaning LATE lambs were heavier ($P < 0.0001$) than CTRL lambs (20.5 ± 0.6 vs. 11.9 ± 0.5 kg, respectively) and DRPX were heavier ($P < 0.0001$) than STX lambs (18.7 ± 0.5 vs. 13.7 ± 0.6 kg, respectively). At 63 d LATE and CTRL DRPX lambs were heavier ($P < 0.0001$) than LATE and CTRL STX lambs (15.4 ± 0.7 and 13.7 ± 0.6 kg vs. 11.5 ± 0.7 and 10.2 ± 0.7 kg, respectively). At 120 d LATE DRPX were heavier ($P < 0.006$) than CTRL DRPX lambs (23.6 ± 0.9 vs. 20.2 ± 0.8 kg, respectively) and LATE STX were heavier ($P = 0.09$) than CTRL STX (17.3 ± 0.9 vs. 15.1 ± 0.9 kg, respectively). Weaning lambs at 120 d of age in an accelerated lambing system resulted in heavier lambs at weaning with no negative impact on ewe productivity. Late weaning led to a decrease in the amount of time that lambs received high cost, imported feed resulting in a savings of $10 per lamb.

Key words: hair sheep, weaning, lambs

582 Comparison of two forage systems for performance of lactating doe and kid meat goats in Kentucky. K. Andries* and E. Sherrow, *Kentucky State University, Frankfort.*

Meat goat producers are looking at forage based systems of production as possible ways to reduce cost of production and access higher value markets. To be successful, research is needed to evaluate different forages during critical production periods, especially around lactation. Many producers in the upper southeast region have difficulty finding forages to meet the needs of lactating animals in spring. This study was designed to evaluate differences in doe and kid performance on tall Fescue (*Festuca arundinacea*) and cereal rye (*Secale cereale* L.) during early lactation in spring kidding meat goats. Sixty-six crossbred meat goat does with 106 Boer sired kids were available for use in this project. Two 0.88 ha pastures were available for this project. One was seeded in the fall of 2009 to cereal rye and the other had an established stand of tall fescue. Does were evenly divided between the 2 treatments with consideration for the number of kids and age. Grazing started April 20 and continued for 28 d. Data collected included starting and ending weights for both kids and does, doe body condition score, and color score of the mucous membranes of the eye. Average daily gain was calculated for each kid and doe on the project. The data was analyzed using Proc GLM in SAS. Both kids and does on the rye pasture had significantly ($P < 0.01$) higher average daily gains. Kids on the rye pastures gained 5.36 kg while those on the fescue pastures only gained 2.60 kg in the 28 d period. The does in both groups lost weight but the ones on the rye group lost 1.68 kg and the fescue group lost 3.57 kg over the 28 d. In the kid data birth type was not significant for average daily gain or total weight gain of the kids, number of kids nursing was not significant for any trait on the doe data set. There was a significant ($P < 0.01$) change in eye membrane color score with does in the rye group having improved scores while the fescue group had poorer scores. This research indicates that there is potential for forage based goat production in the upper southeast if the proper forages are utilized to ensure adequate nutrition for the doe during lactation.

Key words: meat goat, forage

583 Effect of synchronization protocols (Ovsynch vs 2PG) and GnRH on reproductive performance in goats. N. Ahmad*, H. Riaz, and M. Abdullah, *University of Veterinary and Animal Sciences, Lahore, Punjab, Pakistan.*

The objective of the experiment 1 was to determine if the estrus response and pregnancy rate are similar between the 2 synchronization protocols Ovsynch vs 2PG(2 PGF2α injections 10 d apart) in Pakistani goats. Ovsynch goats (n = 14) received an intramuscular injection of GnRH analog (12.5 µg lecirelin, Dalmaralin, Fatro, Italy) on Day 0 and treated with injection of PGF2α analog (37.5µg d-cloprostenol, Dalmazin, Fatro, Italy) on Day 7 followed by second injection of GnRH analog after 48 h (Day 9). 2PG goats (n = 14) received 2 intramuscular injection of PGF2α analog 10 d apart. Onset of estrus and its duration were assessed by aproned male while follicular development, ovulation rate and pregnancy rate were determined by transrectal ultrasonography. All does were bred naturally 12 h after standing heat. Estrus response was non-significant ($P > 0.05$) between regimens (Ovsynch 71%, 2PG 100%). Interval from standing heat to ovulation (24 ± 3.7 h and 30 ± 2.7 h), ovulatory diameter (7.1 ± 0.2 mm, 7.0 ± 0.2 mm), pregnancy rate (43% (6/14) and 78% (11/14) and fecundity (1.6 ± 0.5, 1.6 ± 0.7) did not differ ($P > 0.05$) between Ovsynch and 2PG groups respectively. The objective of experiment 2 was to determine if administration of GnRH at the time of natural breeding enhances the pregnancy rate in goats. Goats were randomly allocated into 2 groups (GnRH, n = 11 and Control, n = 14). GnRH does received 0.63µg lecirelin on the day of natural breeding (12 h after standing heat) while control does did not receive any treatment. Interval from standing heat to ovulation (31.2 ± 2.9 h, 36 ± 5.3 h ($P > 0.05$), ovulatory diameter (6.7 ± 0.1mm, 7.2 ± 0.5 mm ($P < 0.05$), pregnancy rate (54% (6/11) and 64% (9/14), ($P > 0.05$) and fecundity (1.5 ± 0.5, 1.7 ± 0.5, ($P > 0.05$) were evaluated between GnRH and control does respectively. It is concluded that Ovsynch appears to be similar to 2PG protocol in terms of the reproductive performance; however, this needs to be tested on larger sample size. Furthermore, use of GnRH at the time of breeding does not improve reproductive parameters in goats.

Key words: synchronization, estrus response, pregnancy rate

584 Carcass fat and muscle measurements in terminally sired F1 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, US 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.

Science-based data for growth and carcass traits of terminal-sire breeds of sheep can be used to improve the value of market lambs, but information for modern terminal-sire breeds in the United States is limited. Thus, the effects of terminal-sire breed on live weight, chilled carcass weight, loin muscle area, and 3 measures of fat were determined in F1 wether lambs. Over a 3-yr period, Columbia, USMARC Composite, Suffolk, and Texel rams were mated with mature Rambouillet ewes. From weaning until harvest each year, the F1 lambs (n = 518) were fed a step-up finishing diet and harvested in 3 groups at a targeted mean BW of 54.5, 61.4, or 68.2 kg. Lamb BW was measured before transport to the abattoir. The following traits were measured on each carcass: kidney pelvic fat (KPF), chilled carcass weight (CCW), 12th and 13th rib loin muscle area (LMA), backfat thickness (BF), and body wall thickness (BWT; approximately 12.7 cm ventral to the dorsal midline). All traits were analyzed with mixed models that included fixed effects of sire breed, year of harvest (YR), harvest group (HG), weight-on-test deviation from the breed mean, and random effects of sire and maternal grandsire. The YR and HG were significant ($P < 0.03$) in all models. Sire breed was significant ($P < 0.03$) for all traits except BF ($P > 0.09$) and BWT ($P > 0.06$). Suffolk-sired lambs had the largest BW and CCW, 65.66 and 32.56 kg, respectively, and Texel-sired lambs had the smallest, 59.43 and 29.06 kg, respectively. Suffolk-sired lambs had the most KPF, 1.29 kg, and Columbia-sired lambs had the least, 1.13 kg. Texel- and Suffolk-sired lambs tended to have the greatest BF and BWT, while Columbia-sired lambs tended to have the least. The LMA for Suffolk- and Texel-sired lambs was greater than that for Columbia- and Composite-sired lambs, 17.05, 16.79, 15.47, and 16.049 cm^2, respectively. Producers can use data such as these to select a terminal-sire breed of sheep that will match their production system and improve the value of their market lambs.

Key words: lamb, terminal sire, carcass

585 Compositions of volatile compounds in fat tissues from male and female Hu sheep. Y. J. Peng*, J. Lin, and J. X. Liu, *Institute of Dairy Science, College of Animal Sciences, Zhejiang University, Hangzhou [310029], P. R. China.*

Fat tissue is rich in the volatile compounds that determine the flavor of meat. Hu sheep is widely distributed breed in Southern China. In this study, the compositions of volatile compounds in fat tissue from male and female Hu sheep were analyzed to investigate the characterization of Hu sheep meat. Twenty-four Hu sheep,12 male and 12 female, were slaughtered as 2 year-olds. The perirenal and caudal subcutaneous fat tissues were sampled and vacuum-packed from all the sheep. After aging at 4°C for 24 h, the samples were stored at −80°C to avoid oxidation, and then were moved to −20°C before analysis. Solid-phase microextraction technique was used to extract the volatile compounds from 1 g of sample with 50/30 μm divinylbenzene-carboxen-polydimethylsiloxane fiber at 120°C. The volatile compounds were then analyzed by gas chromatography-mass spectrometry technique. All data were analyzed using the GLM procedure of SAS software system. Fifty-seven volatile compounds were detected in the fat tissue samples. Forty compounds were found to distinguish ($P < 0.05$) between male and female sheep, among which 17 compounds were aldehydes, including hexanal, heptanal, octanal, nonanal, undecanal and dodecanal. Fat tissues in female sheep contained more aldehydes than those from male sheep. Since these compounds were mainly derived from lipid oxidation, it is suggested that different anti-oxidation level caused the varying contents of aldehydes, which accounted for the difference in contents of volatile compounds between male and female sheep. A principal component analysis showed that nonanal, triacetin, butylated hydroxytoluene were the main compounds played the most important role in the first principal component. Contrast to the sexual factor, location of fat tissue caused less difference, and only 23 compounds were found to be different between 2 kinds of fat tissues ($P < 0.05$). These results suggested that sexual factor mainly contribute to the characterization of volatile compounds composition.

Key words: fat tissue, volatile compounds, sheep

586 Chemical composition of milk of West African Dwarf (WAD) ewe fed Mexican sunflower leaf meal based diets during early and late lactation. A. H. Ekeocha*, *University of Ibadan, Ibadan, Oyo, Nigeria.*

Milk composition of major and minor components is affected by feeding regimens, ration components and forage: grain ratios. In view of this a study was conducted to determine the chemical composition of milk of WAD ewe fed MSLM based diets during late lactation. Sixteen lactating WAD ewes weighing between 22.80 and 26.03 kg on a basal diet of *Panicum maximum* were allotted into four treatment groups of four replicates each. The experiment was conducted using completely randomized design with four replicates. The Mexican sunflower leaf (MSL) replaced wheat bran (WB) gravimetrically at 0,15,30,45% . The control treatment (treatment A) had no MSL but treatments B, C and D had 15, 30 and 45% MSL as graded replacement for WB. The experiment lasted 6 weeks . Feed and water were provided ad libitum and routine vaccination and medication administered. Parameters measured include milk total solids, butter fat, crude protein, lactose, casein, energy, calcium and phosphorus. Apart from milk ash, observed variation were not significant ($P > 0.05$) during early and late lactation, although values of milk composition were higher during late lactation for milk total solids, fat, protein, ash, casein, energy, calcium and phosphorus while lactose values were reduced during late lactation. Inclusion of up to 45% MSLM based diets enhanced the milk composition of ewe and can be used successfully in place wheat bran without any adverse effect.

Key words: milk composition, West African dwarf ewe, Mexican sunflower leaf

Wednesday, July 13, 2011

POSTER PRESENTATIONS

Animal Health III

W1 Effects of low doses lipopolysaccharide infusion on plasma proteome in lactating cows using comparative proteomics. T. J. Yuan, J. Q. Wang*, Y. X. Yang, D. P. Bu, S. S. Li, and P. Sun, *State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China.*

Subacute ruminal acidosis (SARA) increases the concentration of lipopolysaccharide (LPS) in the rumen. Previous studies have indicated that LPS could translocate into the peripheral blood and increase acute phase proteins, such as serum amyloid A, haptoglobin. The objective of this study was to investigate the effects of infusing low dose LPS into external pudic artery on plasma proteome in lactating dairy cows using comparative proteomics, and to explore the mechanism of host response to LPS challenge. All cows (n = 6) were infused LPS (0.01μg/kg body weight) via external pudic artery. Milk and blood samples were collected at different times after infusing LPS. Two-dimensional electrophoresis gel coupled with MALDI-TOF-TOF spectrometry was used. Plasma proteins at 0, 6, 12 and 24 h after LPS infusion were separated by 2-dimensional electrophoresis. After visualization proteins with Coomassie Brilliant Blue G250 solution, protein spots were detected by PDQuest 8.0.1 software and differential proteins were identified by MALDI-TOF-TOF spectrometry. Milk SCS started to increase after infusing LPS and peaked at 6 h, and then gradually decreased to the level before infusing LPS at 24 h. Eight protein spots were upregulated at 6, 12 and 24 h in cows after infusing LPS, but there was not significantly different among 6 to 24 h, and were identified to be 4 proteins including vitamin D-binding protein precursor, serpin A3–6, α-1 antitrypsin and serpin A3–1 precursor. These results suggests that vitamin D-binding protein precursor, serpin A3–6, α-1 antitrypsin and serpin A3–1 precursor may play an important role in response to LPS challenge, and further study was needed.

Key words: lipopolysaccharide, dairy cow, plasma proteome

W2 Evaluation of endotoxin (LPS) activity in bovine blood using neutrophil dependent chemiluminescence. S. Kahl*[1], T. H. Elsasser[1], and C. V. Obiezu-Forster[2], *[1]USDA, Agricultural Research Service, Beltsville, MD, [2]Spectral Diagnostic Inc., Toronto, ON, Canada.*

The purpose of this study was to evaluate the applicability of a neutrophil chemiluminescence-based assay for the measurement of LPS stimulatory activity in bovine whole blood. The assay is based on the capacity for LPS to trigger the respiratory oxidative burst activity (RBA) of autologous neutrophils. This RBA is then detected as photons released from oxidized added luminol in a chemiluminometer. In the protocol, chemiluminescence (CL) of blood samples without (CL_{BL}) and with an added reference quantity of LPS (100 ng/ml, CL_{BL+LPS}) was measured in luminol/zymosan solution and the relative LPS blood activity (EA_R) was expressed as a CL_{BL}/CL_{BL+LPS} ratio. EDTA-stabilized whole blood was collected from 16 healthy steers, 9 cows diagnosed with advanced mastitis of gram(-) bacterial etiology, and 4 steers given an i.v. bolus of low (0.25 μg/kg BW) or high (2.0 μg/kg BW) LPS. In the in vitro recovery studies a linear relationship was observed between added LPS (up to 100 ng/ml) and EA_R ($R^2 = 0.99$, $P < 0.01$). Estimated mean (±SE) blood EA_R in healthy cows was 0.058 ± 0.010 and increased to 0.353 ± 0.062 ($P < 0.01$) in cows with mastitis. Individual EA_R values exceeded a calculated clinical cut-off value of 0.137 (upper limit of 95% confidence interval of observed EA_R in healthy group) in 78% of infected cows. After the in vivo injection of high LPS dose, estimated blood EA_R values exceeded clinical cut-off value at 2 min (0.317 ± 0.057; n = 2) and 5 min (0.163 ± 0.018), but returned to baseline at 10 min (0.084 ± 0.027). Within 10 min after low LPS dose injection, estimated EA_R values remained below cut-off value, although animals showed clinical symptoms of initial proinflammatory response. Results indicate that bovine neutrophil chemiluminescence assay has the potential to detect LPS stimulation of neutrophil respiratory burst activity in bovine blood and to discriminate between healthy cows and cows infected with gram(-) bacteria displaying clinical mastitis. Additional studies are needed to evaluate the specificity of the assay while further modifications to this protocol may result in increased sensitivity.

Key words: bovine, chemiluminescence, endotoxin assay

W3 Evaluation of yeast nucleotides on intestinal barrier function in vitro. A. Ganner*, M. Werner, S. Henikl, and G. Schatzmayr, *BIOMIN Research Center, Tulln, Lower Austria, Austria.*

Yeast contains between 3 and 18% of ribonucleic acid. During manufacturing process and autolysis, the RNA breaks down in its monomers. Nucleotides have been considered nutritionally as semi-essential, they are synthesized de novo using amino acids as precursors, or by salvage of dietary amino acids and nucleotide breakdown. Under field conditions, challenge and stress, the endogenous synthesis may not be capable of supplying the animal's actual nucleotide needs. Nucleotides are involved in various essential biochemical processes; in animal studies they have been shown to have positive effects on performance, growth, gut health and the immune system. Target of the present study was to evaluate the effect of purified nucleotides (adenosine monophosphate (AMP), adenine, adenosine, guanosine monophosphate (GMP), guanine, guanosine, inosine monophosphate (IMP), inosine, uridine, uracil, cytidine and cytosine) and commercially available yeast nucleotide products on intestinal barrier function using a porcine intestinal epithelial cell line (IPEC-J2). IPEC-J2 cells were incubated in 24-well plates with Transwell inserts in the presence of the respective test substance at 41 °C and 5% CO2 for a maximum of 15 days. Transepithelial electrical resistance (TER) was measured daily by a volt-ohm meter. Results were expressed as increase in TER compared to untreated cells (0%). TER was increased up to 200% by AMP. Adenine and adenosine increased TER up to 80% and 140%, respectively. GMP, guanine and guanosine showed an increase in TER over the first 2 days. IMP and inosine showed an increase in TER up to 100% and 60%, respectively. Uridine and uracil, cytidine and cytosine increased TER between 30% and 70%. Five commercially available yeast nucleotide or yeast extract samples with analyzed nucleotide profile were tested in different dos-

ages. Increase in resistance was noticed between 80 and 170%. Our results indicate that nucleotides improve the intestinal barrier function by increasing the TER in a dose-dependent manner. Thus, yeast nucleotides may have protective effects to the intestine and as a result to exert beneficial effects on animal's health.

Key words: yeast nucleotides, gut epithelial cell line, TER

W4 Oral treatment of pregnant cows with lipopolysaccharide and lipoteichoic acid modulated selected plasma metabolites and innate immunity in newborn calves. S. Iqbal*, Q. Zebeli, D. A. Mansmann, S. M. Dunn, and B. N. Ametaj, *University of Alberta, Edmonton, AB, Canada.*

Immunization of pregnant dams is commonly used to enhance the newborn immune status. The aim of this study was to orally challenge prepartum dairy cows with repeated doses of lipopolysaccharide (LPS) and lipoteichoic acid (LTA) and evaluate clinical disease, and metabolic and immune status of their newborn calves. Thirty pregnant Holstein dairy cows were blocked by parity and the anticipated day of calving, and were randomly allocated to 2 groups, 28 d before the expected day of parturition. Cows were orally administered 2 mL of saline solution (CTR), or 2 mL of saline solution containing 3 increasing doses of LPS from *Escherichia coli* 0111:B4 as follows: 1) 0.01 μg/kg BW on d −28 and −24, 2) 0.05 μg/kg BW on d −21 and −18, and 0.1 μg/kg BW on d −14 along with a flat dose of LTA from *Bacillus subtilis* (i.e., 120 μg/animal). Ten calves per group were randomly selected to determine the disease incidence and evaluate their health and metabolic and immune status collecting blood samples at wk 1 to 4 after birth and analyzing for glucose, lactate, β-hydroxybutyric acid (BHBA), nonesterified fatty acids (NEFA), cholesterol, and haptoglobin. Results demonstrated that the group of calves from treated cows had greater plasma cholesterol (140 vs.120 mg/dL; $P = 0.02$), and a numerical increase of BHBA in the plasma (152 vs. 133 mmol/L; $P < 0.10$). Furthermore, this group of calves showed better energy status with greater plasma lactate (107 vs. 81 mmol/L; $P < 0.01$), although treatment did not affect concentration of plasma glucose and NEFA ($P > 0.05$). Interestingly, the calves from the treated cows had greater plasma haptoglobin (234 vs. 119 mg/dL; $P = 0.04$). No effect of treatment was observed on calf diarrhea, number of medications given to calves, and their mortality rate. In conclusion, oral treatment of dams with LPS and LTA modulated selected plasma metabolites and markers of innate immunity in their newborns suggesting that treatment of pregnant cows with bacterial immunogens might improve the immunity and wellbeing of newborn dairy calves.

Key words: lipopolysaccharide, lipoteichoic acid, newborn calves

W5 Repeated oral administration of lipopolysaccharide and lipoteichoic acid modulated post-treatment plasma metabolites and innate immunity of prepartal dairy cows. S. Iqbal*, Q. Zebeli, D. A. Mansmann, 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 high incidence of metabolic diseases. The objective of this study was to investigate metabolic, immune, and clinical responses to repeated oral administration of lipopolysaccharide (LPS) and lipoteichoic acid (LTA) in prepartal dairy cows. Thirty pregnant Holstein dairy cows were blocked by parity and the anticipated day of calving, and were randomly allocated to 2 groups 28 d before the expected day of parturition. Cows were orally administered 2 mL of 0.85% saline solution (CTR), or 2 mL of saline solution containing 3 increasing doses of LPS from *Escherichia coli* 0111:B4 as follows: 1) 0.01 μg/kg BW on d −28 and −24, 2) 0.05 μg/kg BW on d −21 and −18, and 0.1 μg/kg BW on d −14 along with a flat dose of LTA from *Bacillus subtilis* (120 μg/animal). Clinical responses including rectal temperature, respiration and rumen contraction rates were evaluated during the 5 h post-treatment and blood samples were collected from the tail vein before and after administration of each dose at 1, 3, and 5 h post-treatment. Blood samples were analyzed for plasma glucose, lactate, NEFA, BHBA, cholesterol, and haptoglobin (Hp). Results demonstrated that treatment did not affect rectal temperature and respiration rate; however, it numerically lowered rumen contraction rate ($P < 0.10$). Moreover, treatment increased plasma glucose (76 vs. 62 mg/dL; $P < 0.01$) and lactate (78 vs. 63 mmol/L; $P < 0.01$) especially at 1 h post-injection for lactate ($P = 0.02$) and 3 and 5 h for glucose ($P < 0.01$). In addition, treated cows tended to have greater concentration of circulating NEFA (102 vs. 92 mmol/L; $P = 0.06$) and lower plasma cholesterol (130 vs.167 mg/dL; $P = 0.01$), and plasma Hp (554 vs. 753 mg/dL; $P = 0.04$). There was no effect of treatment on plasma BHBA ($P > 0.05$). Overall, repeated oral administration of LPS and LTA modulated post-treatment patterns of selected plasma metabolites, clinical responses, and markers of innate immunity in transition dairy cows.

Key words: lipopolysaccharide, lipoteichoic acid, metabolic and clinical response

W6 Diets enriched in barley grain treated with lactic acid and heat lowered rumen endotoxin and improved innate immunity in dairy cows. S. Iqbal*, Q. Zebeli, A. Mazzolari, S. M. Dunn, and B. N. Ametaj, *University of Alberta, Edmonton, AB, Canada.*

Feeding early lactation dairy cows high grain based diets is associated with an inflammatory state and high incidence of various metabolic diseases. The aim of the present study was to investigate the effects of feeding barley grain steeped in lactic acid (LA) and heat on ruminal endotoxin and plasma biomarkers of innate immunity. Eight mid-lactation (170 DIM) rumen-fistulated Holstein cows were used in a 2 × 2 crossover design with 2 21-d periods, with the first 11 d used for diet adaptation and the last 10 d for measurements. Cows were fed once daily a total mixed ration containing barley silage and rolled barley grain (31.5% DM basis) steeped for 48 h in equal quantity of tap water (CTR), or in 1.0% LA and heat at 55°C (LAH). The rumen fluid and blood samples were collected on d 11, 15, and 21 shortly before the morning feeding of each experimental period. Postprandial patterns of rumen endotoxin and plasma haptoglobin (Hp) were evaluated collecting rumen fluid and blood samples every 2 h starting at 0800 to 2000 on the last day of each experimental period. The principal component analysis revealed that each of the 2 diets fed could be distinguished on the basis of the measured rumen and plasma variables. Data revealed that cows fed LAH diet had lower concentration of preprandial rumen endotoxin (472 vs. 793 ng/mL; $P < 0.01$), however, treatment had no effect on plasma Hp ($P > 0.05$). Results of postprandial responses showed that LAH diet had numerically lower concentration of plasma Hp (586 vs. 679; $P < 0.10$) and a treatment by time interaction for rumen endotoxin ($P < 0.01$), suggesting a role for both the treatment and the time of sampling on this variable. Interestingly, cluster analysis showed a cluster between rumen endotoxin and plasma Hp indicating strong interrelationship between these 2 variables. Overall, results of this study indicated that feeding barley grain steeped in LAH lowered concentration of rumen endotoxin and modulated postprandial innate responses in mid-lactation dairy cows.

Key words: barley grain, lactic acid and heat, innate immunity

W7 Oral administration of bacterial lipopolysaccharide and lipoteichoic acid modulated milk composition and efficiency in transition dairy cows. S. Iqbal*, Q. Zebeli, D. A. Mansmann, S. M. Dunn, and B. N. Ametaj, *University of Alberta, Edmonton, AB, Canada.*

The transition period is characterized by high incidence of metabolic disorders, which influence subsequent milk production and composition of dairy cows. The objective of this study was to evaluate the production response of postpartal dairy cows to repeated oral administration of lipopolysaccharide (LPS) and lipoteichoic acid (LTA). Thirty pregnant Holstein dairy cows were blocked by parity and the anticipated day of calving, and were randomly allocated to 2 groups, 28 d before the expected day of parturition. Cows were orally administered 2 mL of 0.85% saline solution (CTR), or 2 mL of saline solution containing 3 increasing doses of LPS from *Escherichia coli* 0111:B4 as follows: 1) 0.01 μg/kg BW on d −28 and −24, 2) 0.05 μg/kg BW on d −21 and −18, and 0.1 μg/kg BW on d −14 along with a flat dose of LTA from *Bacillus subtilis* (i.e., 120 μg/animal) prepartum. Feed intake was obtained during the 4 wk before and 4 wk after parturition, whereas milk data were collected during 4 wk after calving to determine milk production and composition. The data showed that treatment tended to increase milk energy efficiency (1.30 vs. 1.06; $P = 0.06$) and was associated with a trend for lower feed intake (31 vs. 34 kg/d; $P = 0.10$). Furthermore, the overall variance analysis demonstrated that treatment group had greater fat to protein ratio (1.37 vs. 1.25; $P = 0.04$), and fat-corrected milk to feed intake ratio (milk fat efficiency; 0.82 vs. 0.68; $P = 0.01$). Milk lactose yield was higher only in primiparous cows in the treatment group (1.41 vs. 1.19 kg/d; $P = 0.01$). In addition, primiparous cows in this group, showed a tendency for greater fat yield and 4% fat corrected milk ($P < 0.10$). Treatment increased milk urea nitrogen in treated multiparous cows ($P < 0.01$) and lowered protein yield ($P = 0.04$). No effect of treatment was observed on other milk components and on the overall milk production ($P > 0.05$). In conclusion, the results indicated that repeated oral administration of LPS and LTA modulated milk production and composition in dairy cows postpartum.

Key words: oral lipopolysaccharide, lipoteichoic acid, milk production and composition

W8 Oronasal exposure to lipopolysaccharide differentially affected blood metabolites in multiparous dairy cows. A. Hosseini*, D. A. Mansmann, Q. Zebeli, S. Iqbal, S. M. Dunn, and B. N. Ametaj, *University of Alberta, Edmonton, Alberta, Canada.*

Translocation of endotoxin into blood circulation causes alterations in blood metabolites and immunity. In this study, we evaluated the hypothesis that repeated oronasal application of lipopolysaccharide (LPS) prepartum might improve the metabolic and immune status of periparturient dairy cows. One hundred primiparous (PP) and multiparous (MP) Holstein dairy cows (PP and MP with ~BW 620 and 720 kg, respectively) were randomly assigned into control (CTR; PP = 18; MP = 32) and treatment (TRT; PP = 19; MP = 31) groups. Either carrier alone (3 mL of 0.85% saline) or 3 increasing doses (0.01, 0.05, and 0.1 μg/kg BW) of LPS from *E. coli* 0111:B4 were applied oronasally (1 mL nasally and 2 mL orally) twice a week on wk −4, −3, and −2. Several blood variables including β-hydroxybutyric acid (BHBA), cholesterol, glucose, lactate, nonesterified fatty acids (NEFA) and haptoglobin (Hp) were measured during d −28, −25, −21, −14, −7, 2, 14, 21, and 28; however, HP was measured only in MP cows. All data were processed statistically by the MIXED procedure of SAS. Overall results indicated that TRT increased concentrations of cholesterol ($P = 0.06$) and lactate in the serum ($P < 0.01$) of all cows. Data also showed that parity affected ($P < 0.01$) concentrations of cholesterol, NEFA and lactate. Interestingly, concentration of NEFA in serum was greater in PP cows ($P < 0.01$). Furthermore, an effect of day ($P < 0.01$), and interactions of day × parity ($P = 0.03$) and TRT × parity ($P = 0.04$) were obtained for serum glucose with a decreased concentration postpartum in all cows. The results showed that serum BHBA was increased ($P < 0.01$) on d 14 in PP cows. Additionally, concentrations of glucose, cholesterol, and lactate were influenced by TRT × parity interactions ($P < 0.10$), while TRT × day interaction influenced ($P < 0.10$) serum Hp. In conclusion results of this investigation indicated potential involvement of LPS in alteration of blood metabolites in dairy cows. Moreover, the oronasal treatment with LPS might be used to improve the metabolic status and immunity of transition dairy cows.

Key words: oronasal lipopolysaccharide, blood metabolites, innate immunity

W9 Oral administration of lipopolysaccharide and lipoteichoic acid modulated plasma metabolites and decreased the risk of metabolic diseases in periparturient dairy cows. S. Iqbal*, Q. Zebeli, D. A. Mansmann, S. M. Dunn, and B. N. Ametaj, *University of Alberta, Edmonton, AB, Canada.*

The transition period imposes enormous stress on the dairy cow and may impair long-term herd health. The aim of this study was to investigate metabolic and health status of periparturient dairy cows repeatedly administered orally with lipopolysaccharide (LPS) and lipoteichoic acid (LTA). Thirty pregnant Holstein dairy cows were randomly assigned to one of the 2 treatment groups starting at 28 d before the expected day of parturition. Cows received orally either 2 mL of 0.85% saline solution (CTR), or 2 mL of saline solution containing 3 increasing doses of LPS from *Escherichia coli* 0111:B4 as follows: 1) 0.01 μg/kg BW on d −28 and −24, 2) 0.05 μg/kg BW on d −21 and −18, and 0.1 μg/kg BW on d −14 along with flat dose of LTA from *Bacillus subtilis* (i.e., 120 μg/animal). Blood samples were collected on d 1 and 3 of wk −4, and then once on wk −3, −2, −1, +1, +2, +3, and +4 around parturition and analyzed for glucose, BHBA, NEFA, lactate, and cholesterol. Cows were monitored for metabolic and infectious disease incidence, body condition score (BCS), manure score, and urine pH throughout the experimental period. Results showed that oral administration of LPS and LTA lowered plasma lactate in the treated cows (2.58 vs. 3.67 mmol/L; $P < 0.01$) and had a tendency to increase plasma cholesterol (152 vs. 137 mg/d; $P < 0.10$). Treatment did not affect concentrations of BHBA, NEFA, and glucose in the plasma ($P > 0.05$). Interestingly, repeated oral LPS and LTA showed a tendency for lower incidence of metritis, laminitis, retained placenta, and uterine discharges ($P < 0.10$). Furthermore, the incidence of uterine horn fluctuations was lower in the treated group ($P = 0.01$). No effect of oral treatment was obtained for BCS, manure score, and urine pH ($P > 0.05$). In conclusion, oral administration of LPS and LTA modulated selected plasma metabolites related to carbohydrate and lipid metabolism and lowered the incidence of multiple metabolic diseases in periparturient dairy cows.

Key words: lipopolysaccharide, lipoteichoic acid, blood metabolites and metabolic diseases

W10 Bovine acute-phase response following different doses of corticotrophin-releasing hormone (CRH) challenge. R. F. Cooke*[1], J. A. Carroll[2], F. N. T. Cooke[1], B. I. Cappellozza[1], C. Trevisanuto[1], V. D. Tabacow[1], J. Dailey[2], and D. W. Bohnert[1], *[1]Oregon State University–Eastern Oregon Agricultural Research Center, Burns, [2]USDA–ARS Livestock Issues Research Unit, Lubbock, TX.*

Fourteen weaned, halter-trained Angus steers (BW = 191 ± 2.1 kg) were fitted with indwelling jugular catheter and rectal temperature monitoring device on d −1 of the study. On d 0, steers were ranked by BW and randomly assigned to receive 1 of 3 infusion treatments (i.v.): 1) 0.1 μg of bovine CRH/kg of BW (CRH1), 2) 0.5 μg of bovine CRH/kg of BW (CRH5), and 3) 10 mL of saline. Blood samples were collected via catheters, relative to treatment infusion (0 h), hourly from –2 to 0 h and 4 to 8 h, and every 30 min from 0 to 4 h. Rectal temperatures were recorded every 30 min from −2 to 8 h relative to infusion. Blood samples were collected via jugular venipuncture and rectal temperatures were assessed using a digital thermometer every 6 h from 12 to 72 h, and every 24 h from 96 to 168 h. Samples collected from −2 to 8 h relative to CRH infusion were analyzed for plasma concentrations of cortisol, ceruloplasmin, and haptoglobin, whereas samples collected from 12 to 168 h were analyzed for plasma concentrations of ceruloplasmin and haptoglobin only. Plasma cortisol peaked at 0.5 h for CRH1 steers (58.9 ng/mL) but returned to baseline levels at 1 h relative to infusion (time effect; $P < 0.01$). Within CRH5 steers, plasma cortisol peaked at 0.5 h (51.3 ng/mL) and returned to baseline levels 3 h relative infusion (time effect; $P < 0.01$). Plasma cortisol concentrations did not change after infusion for saline steers (time effect; $P = 0.42$). Rectal temperatures were greater ($P < 0.05$) for CRH1 steers compared with CRH5 and saline steers at 36 and 42 h relative to challenge. Plasma haptoglobin concentrations in CRH1 steers increased significantly and were greater ($P < 0.02$) compared with CRH5 and saline steers from 48 to 96 h relative to challenge (time effect; $P < 0.01$). Conversely, plasma haptoglobin concentrations were similar ($P > 0.23$) and did not change across time for CRH5 and saline steers (time effect; $P > 0.48$). No treatment effects were detected on plasma ceruloplasmin concentrations. In conclusion, both CRH5 and CRH1 increased plasma cortisol concentrations, but only CRH1 elicited an acute-phase protein response in beef steers.

Key words: acute-phase, bovine, CRH

W11 Feasibility of high immune response technology as a health management tool to characterize immune response profiles of dairy cattle. L. C. Wagter*, S. Cartwright, and B. A. Mallard, *Ontario Veterinary College, University of Guelph, Guelph, Ontario, Canada.*

High immune response (HIR) is a patented evaluation technology that has the potential to improve the health and food quality of dairy cattle through the reduction of antibiotics and enhanced resistance to economically important diseases such as mastitis. The test includes a blood sample to evaluate antibody-mediated immune response (AMIR) and a skin thickness measurement to evaluate cell-mediated immune response (CMIR) together. Dairy cattle with high immune response following immunization with specified test antigens are at a lower risk for developing disease compared with average and low responding animals. To determine if HIR technology would be utilized by the dairy industry, 2 focus groups were conducted within 2 important Ontario dairy regions. Qualitative market information gathered from those focus groups indicated a significant interest in using HIR to test calves or cows for HIR (75% of producers), and that they would use this information for culling decisions, grouping, breeding and/or treating animals. Pre-commercialization research is currently underway to test the transferability of HIR to the dairy marketplace and includes: 1) a quantitative market assessment of interest in HIR throughout Ontario (n = 400 producers; 10% of Ontario herds) to build on previous qualitative focus group data; 2) a validation study of previous research to rank cattle based on antibody from milk in lieu of blood (n = 26 cows); 3) β-testing the application of HIR on one to 2 Ontario dairy herds to demonstrate the economic value of HIR (n = 2; 350–450 animals per herd); 4) HIR testing of Gencor AI cull-sires to demonstrate the ability of the sire immune system to respond to test antigens without adverse reactions and to confirm no cross-reactivity to governmental health testing. In 10 cull-sires tested to-date no cross-reactivity was noted for the tuberculosis DTH test and other serological tests thus indicating that HIR should benefit all sires including young sires before entering a bull-test facility. All research including analysis should be completed by June 2011.

Key words: high immune response, health management, breeding for health

W12 Influence of blood sample storage temperature and latency until analyzed on various ex vivo innate immune response assays in Holstein heifers. M. A. Ballou*[1] and L. E. Hulbert[1,2], *[1]Department of Animal and Food Sciences, Texas Tech University, Lubbock, [2]Department of Animal Science, University of California at Davis, Davis.*

Objectives were to determine the influence of peripheral blood sample storage temperature and how quickly the blood samples needed to be processed for ex vivo innate immune responses. Eight Holstein heifers, approximately 1 yr old, were briefly restrained in self-locking stanchions and 2, 10 mL heparinized vacutainers were collected via jugular venipuncture. One sample from each heifer was placed immediately on ice (ICE; 0.18 ± 0.39°C) while the other was placed in an ice chest with no–ice (NI; 21.88 ± 0.51°C). Samples were serially analyzed for ex vivo innate immune parameters at 2 (baseline), 4, 6, 8, 10, and 24 h after collection. Data were analyzed by ANOVA with the fixed effects of heifer, storage temperature (ST), time, and the interactions of heifer x ST and ST x time. The ICE samples had more leukocytes than NI samples (ST, $P < 0.001$). All samples had decreased total leukocyte counts (time, $P < 0.05$) from baseline measurements at 10 and 24 h for ICE and NI samples, respectively (ST x Time $P < 0.01$). Neutrophil proportions in ICE samples did not change with time, but NI samples were lower at 2 h and increased over time (ST x time, $P < 0.03$). The NI samples had greater neutrophil proportions at 8 h compared with 2 h (time $P < 0.01$). Hematocrits were lower (ST, $P < 0.01$) in ICE samples and were above baseline (ST x time $P < 0.01$) at 24 h after collection. More (ST, $P < 0.01$) TNF-α was secreted after NI whole blood samples were stimulated with LPS than ICE samples. NI samples had lower neutrophil L–selectin expression expression compared with ICE samples, except at 24 h (ST x time, $P < 0.03$). At 2 h, samples stored on ice had a greater neutrophil oxidative burst response than NI samples (ST x time, $P < 0.01$). There were no differences ($P < 0.10$) in neutrophil oxidative burst response between ICE or NI samples from 4 to 10 h, but at 24 h, samples stored on ice had less intense oxidative burst (ST x time, $P < 0.01$). These data indicate that ST and latency until analyzed influences ex vivo innate immune response measurements and should be controlled for when designing experiments.

Key words: immune, time, temperature

W13 Caprylic acid fractionation of serum followed by refractometry to predict serum IgG in preweaned calves. C. Rodríguez[1], N. Saborido[1], L. Castillejos[2], M. Rodríguez[2], A. Lago*[3], J. Campbell[3], J. Quigley[3], and J. Polo[1], *[1]APC Europe, S.A., Granollers, Spain, [2]Animal Nutrition and Welfare Service, Autonomous University of Barcelona, Barcelona, Spain, [3]APC Inc., Ankeny, IA.*

We evaluated the use of caprylic acid (CA) fractionation of IgG from serum followed by refractometry of supernatant as a rapid method to predict IgG concentration in young calves. Jugular blood samples were collected from calves (n = 100) between 2 and 60 d of age from 4 farms in Girona, Spain. Calves were managed according to standard management practices on each farm. Serum was separated by centrifugation and total protein (TP; automatic analyzer Mira Plus, ABX Diagnostics), IgG (radial immunodiffusion) and refractive index (nD; Refracto 30PX Refractometer, Mettler Toledo) were measured. Serum (1 mL) was placed in a 1.5 mL tube and 0.06 mL of CA was added. The tube was left at room temperature for 15 min and stirred vigorously every 5 min; thereafter, it was centrifuged and nD of the supernatant was measured. Mean nD of CA supernatant was 1.338 ± 0.0002 and ranged from 1.333 to 1.343. Mean serum IgG was 17.74 ± 0.60 mg/mL and ranged from 4.01 to 33.21. Mean serum TP was 4.73 ± 0.12 g/dL and ranged from 2.81 to 7.60. Mean serum nD was 1.345 ± 0.0001 and ranged from 1.343 to 1.349. The nD of the CA supernatant was highly correlated with serum IgG (r = 0.86; IgG = 3591.3 x nD - 4787.3) and serum TP (r = 0.87; TP = 446.1 x nD - 591.53). Similarly, nD of whole serum was highly correlated with serum IgG (r = 0.90; IgG = 4405 x nD - 5908.3). Finally, serum TP was less well correlated with serum IgG (r = 0.74; 3.877 x TP - 0.699). The CA fractionation method was useful for rapidly measuring IgG level in serum of young calves and was highly correlated with serum IgG and TP. Direct measurement of nD to predict serum IgG was also precise. Serum TP, currently the most common on-farm test to estimate serum IgG, was a less precise method to estimate serum IgG than both nD of whole serum and nD of the CA supernatant.

Key words: calves, immunoglobulin, caprylic acid

W14 Development of a rapid method to estimate IgG in bovine colostrum. K. M. Morrill*[1], J. D. Quigley[2], A. Lago[2], and H. D. Tyler[1], *[1]Iowa State University, Ames, [2]APC Inc., Ankeny, IA.*

Caprylic acid (CA) has been utilized to fractionate colostral IgG for further laboratory purification and analysis. The objective of this study was to develop a rapid, cow-side test for determining colostrum IgG concentration using CA fractionation followed by refractometry of the IgG-rich supernatant. Frozen colostrum samples (n = 85) obtained from Holstein cattle, were warmed to room temperature in a water bath and treated with varying concentrations of CA and acetic acid (AA). Samples were then centrifuged or allowed to sit for an allotted time to precipitate non-IgG proteins. Supernatant liquid was then analyzed with a digital refractometer (SPER Scientific, model 300034) to determine refractive index (nD). The nD of Ig-rich fraction was compared with total colostral IgG concentration determined by radial immunodiffusion (Triple J Farms; Bellingham, WA). The nD of supernatant was positively correlated (r = 0.96) to RID when 1 mL of colostrum was added to a tube containing 75 µL CA and 1 mL 0.06 M AA, shaken for 10 s and not centrifuged. Refractive index was measured within 1 min of addition of CA. Decreasing AA to 1 mL or increasing AA to 2 mL decreased the correlation (r = 0.73 and r = 0.63, respectively) between nD and IgG. For centrifuged samples, altering the sitting time before centrifugation from 30 min to 0, 10 or 20 min numerically increased correlation (r = 0.82 to 0.87, 0.85 and 0.87, respectively), but these were not statistically different. When the centrifuge step was removed, nD after samples sat for 1 min was highly correlated (r = 0.96) with IgG; however visible separation of supernatant and precipitate did not occur in samples with IgG concentrations >20 mg/ml until after 10 min. Total protein (TP) was measured on a subset of 45 samples and weakly correlated (r = 0.41) with IgG; this suggests that TP is a poor method to determine colostral IgG concentration. These results indicate that a simple procedure requiring only CA, AA and a refractometer may rapidly and effectively estimate colostral IgG concentration in bovine colostrum.

Key words: colostrum, refractometer, IgG

W15 The effect of treatment with long-acting antibiotic upon arrival at a custom heifer rearing facility on non-specific fever, otitis media, neonatal calf diarrhea complex and growth. A. L. Stanton*[1], S. J. LeBlanc[1], L. K. Fox[2], J. Wormuth[3], D. F. Kelton[1], and K. E. Leslie[1], *[1]University of Guelph, Guelph, Ontario, Canada, [2]Washington State University, Pullman, [3]CY Heifer Farm, Elba, NY.*

The primary objective of the study was to evaluate a single subcutaneous injection of tulathromcyin (TUL) in the early postnatal period, administered upon arrival at a commercial heifer rearing facility, on the incidence of disease in young dairy calves. A second objective was to describe the risk factors for morbidity and the impact of disease on growth of these calves. The third objective was to investigate the role of *Mycoplasma bovis* in the incidence of otitis media in this population of calves. Calves (n = 788) were randomly assigned to study treatment with TUL or a placebo (CONTROL) upon arrival at the heifer raising facility and were observed for disease daily for 8 weeks by farm staff. Microbiological culture and speciation of *M.bovis* was performed on nasal swabs collected from a subset of (n = 66) calves at 0, 2 and 4 weeks of age. All analyses were conducted using SAS v9.1 and controlled for source farm and group as random effects. Linear mixed models were used to analyze ADG. Generalized linear mixed models with a logit-transformation were used to analyze morbidity. CONTROL calves were 1.7 (CI: 1.2–2.6;$P < 0.01$), 3.7(CI: 1.6–9.1; $P < 0.005$), and 1.7 (CI: 1.2–2.5; $P < 0.005$) times more likely than TUL calves to be treated for neonatal calf diarrhea complex, unilateral ear droop and bilateral ear droop, respectively. The ADG of TUL calves was 0.03 ± 0.01 kg greater than CONTROL calves ($P < 0.01$). Failure of passive transfer (FPT), non-specific fever, bovine respiratory disease complex and neonatal calf diarrhea complex decreased ADG. The largest decrease in ADG (0.14 ± 0.04 kg) associated with disease was seen in calves with non-specific fever ($P < 0.05$). Of animals sampled for *M. bovis*, 26% tested positive, and 4 different strains were identified. In summary, TUL was associated with decreased the incidence of several common calfhood diseases in the early post-natal period. *M. bovis* was present in this population but not clearly associated with otitis media.

Key words: tulathromycin, otitis media, calfhood disease

W16 Immune status of calves that naturally suckle their dams in dairy farms of Costa Rica. J. A. Elizondo-Salazar*[1], J. Sánchez-Salas[1], J. Rodríguez-Zamora[1], and A. J. Heinrichs[2], *[1]Estación Experimental Alfredo Volio Mata, Facultad de Ciencias Agroalimentarias, Universidad de Costa Rica, [2]The Pennsylvania State University, University Park.*

The measurement of serum total protein (STP) in dairy calves by refractometer as an estimate of serum immunoglobulin concentration is the simplest test to give an indication of adequate passive transfer of immunity. A value of 5.0 g/dL has been established as the cutoff point for assessment of passive transfer status. Since there is no data on the immune status of dairy calves in Costa Rica, the objective of this study was to determine STP concentration in neonatal dairy calves that naturally suckle their dams. Blood samples were collected between d 1 and 7 of age from 417 heifer and 105 bull calves from more than 40 farms in different regions of Costa Rica. All blood samples were collected into serum (red top) Vacutainer tubes, refrigerated overnight, centrifuged, and the serum separated from clot within 24 h of collection. A hand-held refractometer (Atago Master-Sur/Nα, Bellevue, WA) was used to measure STP. GLM procedure was used to establish differences between parity and breed of the dams, and sex of the calf. Descriptive statistics were generated to define percentage of failure of passive transfer by sex of the calf and parity of the dam. Calves coming from dams of first and second parity had statistically ($P < 0.05$) higher STP concentration (6.40 ± 0.14 and 6.21 ± 0.14 g/dL) than those coming from cows with 3 or ≥4 calvings (6.01 ± 0.15 and 5.91 ± 0.12 g/dL). There was no significant difference between sex of the calves (heifers 6.13 g/dL, bulls 6.14 g/dL). Jersey calves had higher STP concentrations than Holstein, Holstein-Jersey cross, or other breeds (6.43 ± 0.11 vs. 6.18 ± 0.11, 6.01 ± 0.21 and 6.01 ± 0.16, respectively). Overall, 21.5% of calves had failure of passive transfer (heifers 22.5%, bulls 17.1%).

Table 1. Failure of passive transfer (%) by parity of dam and sex of neonates

Parity	Heifers	Bulls	Both
1	7.6	10.3	8.3
2	21.0	22.2	21.1
3	28.6	18.2	26.3
≥4	28.2	19.4	26.6

Key words: calves, passive transfer of immunity, serum total protein

W17 Determining the heritable component of dairy cattle foot lesions. A. M. Oberbauer*, S. L. Berry, J. M. Belanger, and T. R. Famula, *Department of Animal Science, University of California, Davis.*

Lameness and hoof health impacts dairy producers both as an animal welfare issue as well as being implicated in lowered milk production. Further, it is one of the top 3 reasons dairy cattle are culled prematurely, following infertility and mastitis, thus contributing to the overall carbon footprint of the dairy industry due to the environmental costs associated with raising replacement dairy heifers. Selection schemes for dairy cattle focus on sire contribution to milk production with little consideration to the cow′s physical structure. On a commercial California Holstein dairy, 2 binary hoof phenotypic traits, hoof lesions (sole lesion/upper limb lameness) and lameness due to abscesses or ulcers, were recorded. Monthly lactation records were collected from December 2006-April 2009 with weekly hoof health evaluations. Data on cows (n = 2247), in addition to hoof information, included birth date, freshening date, lactation number, and sire (n = 235) and dam information; total animals including those to build pedigrees were 5809. Lesions had a prevalence of 7.0% and abscess/ulcer lameness had a prevalence of 16.5%. The probability of any lameness (both conditions considered together) increased with increasing lactation number (0.018, 0.055, 0.082, 0.168 for first, second, and third plus lactations, respectively). Using a threshold model with a genetic term, σ_G^2, a permanent environment term, σ_{PE}^2, and residual term, σ_E^2, $h^2 = (\sigma_G^2)/(\sigma_G^2 + \sigma_{PE}^2 + \sigma_E^2)$ were calculated for each binary trait. The narrow sense heritability for lameness risk was estimated to be 0.24 for hoof lesion and 0.26 for abscess/ulcer lameness. The data suggest a significant genetic contribution to hoof health that is coupled with a greater risk of lameness with increasing lactation number (or age which cannot be ascertained by this study). The genetic component lends support for undertaking a SNP genome wide association study to identify loci contributing to the phenotype.

Key words: lameness, dairy cow, heritability

W18 Effects of cold pasteurizing colostrum with formic acid on bacteria counts and calf IgG absorption. L. A. Vickers*[1] and D. M. Veira[2], *[1]Animal Welfare Program, University of British Columbia, Vancouver, British Columbia, Canada, [2]Agriculture and Agri-Food Canada, Agassiz, British Columbia, Canada.*

Colostrum is vital to the health of the newborn calf; however, farm practices often lead to bacterial contamination. We set out to determine if 'cold' pasteurizing colostrum with formic acid (FA) in combination with refrigeration would lower bacteria counts; further, we tested the effects of feeding FA treated colostrum on IgG absorption by newborn calves. Fresh colostrum from 8 cows was subjected to 1 of 4 treatments: 1) addition of FA to achieve a pH of 4.3 and refrigerated; 2) addition of FA to a pH of 4.3 and left at 20°C; 3) no FA and refrigerated; or, 4) no FA and left at 20°C. Samples from each treatment were frozen at 0, 24, 48, 96 and 192 h. The addition of FA immediately lowered aerobic bacteria counts (2.7 ± 0.2 vs 4.2 ± 0.2 $\log_{10}$ cfu/ml; $P < 0.001$) and continued to do so for up to 192 h (1.1 ± 0.4 vs. 7.6 ± 0.42 $\log_{10}$ cfu/ml; $P < 0.001$) compared with untreated colostrum. Untreated colostrum had lower aerobic bacteria counts over 192 h when refrigerated compared with being left at 20°C (5.2 ± 0.22 vs. 7.7 ± 0.2 $\log_{10}$ cfu/ml; $P < 0.0001$). Colostrum IgG was not affected by the addition of FA (62.9 ± 15.2 g IgG/L $P = 0.99$). In a separate trial, 24 Holstein bull calves were fed 3L of colostrum through an esophageal feeder 2 h after birth from to 1 of 3 treatments: A) harvested and frozen immediately B) left at 20°C for 4 h then frozen or C) left at 20°C for 4hr then treated with FA to a pH of 4.3. IgG level of colostrum fed to calves did not differ between treatments (69.7 ± 18.1 g IgG/L; $P = 0.99$). A blood sample was taken 24 h after feeding to determine serum IgG. The addition of FA lowered bacteria counts compared with untreated colostrum (2.0 ± 0.3 vs 4.9 ± 0.3 $\log_{10}$ cfu/ml; $P < 0.0001$). There was no difference in 24 h calf serum IgG (20.1 ± 6.6 mg/L; $P = 0.9$) or apparent efficiency of absorption (41.6 ± 6.2%; $P = 0.8$) between treatments. In conclusion, the use of formic acid as a way to cold pasteurize colostrum is effective at lowering aerobic bacteria counts in colostrum and does not interfere with IgG levels or absorption in calves.

Key words: colostrum, formic acid, dairy calf

W19 Allelic variations in the bovine vitamin D receptor gene: Correlations with periparturient hypocalcemia? M. Reiche, C. Deiner, A. Mösch, and H. Martens*, *Institute of Veterinary Physiology, Faculty of Veterinary Medicine, FU Berlin, Institute of Veterinary Physiology, Faculty of Veterinary Medicine, FU Berlin, Berlin, Germany.*

Periparturient hypocalcemia (milk fever) is a disorder of the Ca metabolism in dairy cattle primarily affecting multiparous cows. The major reasons of the rapid decrease of blood Ca concentration are the prompt

increase of Ca secretion into the colostrum and the delayed activation of Ca regulation mechanisms including calcitriol, a metabolite of vitamin D. Vitamin D receptor (VDR) gene polymorphisms are reported to be associated with variations of Ca metabolism in man. The present study investigated the potential existence of VDR gene polymorphisms in German Holstein Friesian cows and correlated resulting variations with the incidence of hypocalcemia. Blood DNA was isolated from 26 high-yielding cows in their 4th to 6th lactation, out of which 17 had experienced hypocalcemia with ionized serum calcium levels < 0.9 mmol/l at least once, whereas nine cows had never undergone periparturient hypocalcemia in their lifetime. The 10 VDR exons and parts of adjacent introns were sequenced and compared with the *Bos taurus* VDR sequence published on NCBI based on breed Hereford. In total, 8 sequence alterations were detected in the fragments, which were primarily heterozygous. However, only 4 of them were located on exons with a potential change of the encoded amino acid. Calculated *P*-values (Fisher's exact probability test) were all >0.05, hence, the sequence variations found in this study were not correlated with the incidence of periparturient hypocalcemia.

Key words: periparturient hypocalcemia, vitamin D receptor, gene polymorphism

W20 Strategies to control the cattle tick, *Rhipicephalus microplus*, in dairy herds in the Brazilian Southwestern Amazon region: Technical recommendations. L. G. Brito*[1], F. da Silva Barbieri[1], and M. C. de Sena Oliveira[2], [1]*Embrapa Rondônia, Porto Velho, RO, Brazil,* [2]*Southeast Embrapa, Sâo Carlos, SP, Brazil.*

One of the most serious sanitary problems faced by dairy farmers in Brazil is infestation of their herds by the cattle tick *Rhipicephalus microplus*. This infestation is closely related to the region's climate conditions, mainly the high average temperature and rainfall. During the period between October 2004 and November 2009, 14 dairy cows (cross-breeds) were monitored at the Porto Velho experimental field of the Embrapa Rondônia research center, and climate data were obtained from the local weather station. From October 2004 to March 2006 the animals were not treated with any pesticides, to enable obtaining the seasonal fluctuation of *R. microplus* under the prevailing climate conditions of the Brazilian Southwestern Amazon region. Multiple linear regression analysis was used to reveal the influence of climate factors on the tick infestation in the herds. During this period without use of pesticides, the cattle had mean infestation of 201 ticks/animal. There was a significant decline in this rate during the dry season (May to September), when it was 72 ticks/animal, as opposed to 237 ticks/animal in the rainy season. Rainfall was the climate factor with the greatest influence on the tick infestation rate ($R^2 = 0.64$). In April 2006 integrated control strategies were implemented for the entire herd at the experimental station, composed of 111 animals of variable genetic composition, including *B. taurus* × *B. indicus* and *B. indicus*. The integrated tick control strategies entailed application of high-efficacy pesticides, as demonstrated by the adult immersion test, utilization of animals to attract larvae and pasture rotation of lactating cows. After implementing these integrated control measures, the mean infestation of *R. microplus* on the lactating cows fell from 201 ticks/animal to only 1.1 ticks/animal. By using the strategies listed was obtained an effective control of the cattle tick population in CEPV, where in the period between October 2007 and October 2009 did not require any treatment directed to control of ticks in the dairy herd in this period.

Key words: control, cattle tick, Brazilian Southwestern Amazon

W21 Ruminal binding characteristics of Mycopurge against various aflatoxins in in vitro. M. R. Akkaya[1], M. A. Bal[1], and V. Akay*[2], [1]*Kahramanmaras Sutcu Imam University, Turkey,* [2]*Global Nutritech Ltd., Kocaeli, Turkey.*

The objective of this experiment was to determine the ruminal binding characteristics of modified yeast extract and HSCAS containing mycotoxin adsorbent (MP, Mycopurge) against various aflatoxins in an in vitro study. Ninety milliliters of certified aflatoxin mixture [aflatoxins B1 (AFB1), B2 (AFB2), G1 (AFG1), G2 (AFG2)] in a liquid form was mixed with 30 mL of ruminal in vitro medium providing the final concentrations of 6 ng AFB1, 1.5 ng AFB2, 6 ng AFG1 and 1.5 ng AFG2, respectively. Treatments were: 1) aflatoxin mixture + water (Control); 2) aflatoxin mixture + rumen fluid (AR); 3) aflatoxin mixture + MP (6 mg) + rumen fluid (ARMP). Wheat starch was used as a substrate for AR and ARMP treatments. After various incubation time points (0, 3, 6, 12, 24 h) at 39°C, aflatoxin concentrations in ruminal medium were detected with HPLC. Although AFB1 concentration at 0 h was 6 μg/L, it was reduced to 2.50 and 1.68 μg/L in Control, 0.86 and 0.50 μg/L in AR, and 0.34 and 0.20 μg/L in ARMP at 3 and 12 h, respectively ($P < 0.001$). In addition, AFB1 concentration in ARMP treatment was in a steady-state after 3 h of incubation compared with Control and AR treatment where AFB1 concentrations became stabilized after 12 h of incubation ($P < 0.001$). Similar type of binding pattern was observed for ARMP treatment in ruminal incubation of AFB2, where the concentration was reduced down to the lowest level at 6 h (0.21 μg/L) compared with Control (0.74 μg/L) and AR (0.36 μg/L) treatment. In addition, concentrations of both AFG1 and AFG2 were in a steady-state condition for AR (0.67 and 0.48 μg/L) and ARMP (0.46 and 0.38 μg/L) treatments after 12 h of ruminal incubation. However, binding capacity of MP for AFG1 and AFG2 was always in favor of ARMP treatment at all time points ($P < 0.001$). There was no treatment effect on ruminal in vitro gas production across all treatments, averaging 53.5 mL at 24 h. Results indicate that aflatoxins can be degraded by the heat of incubation medium along with microbial degradation. In addition, MP can help to bind those respective aflatoxins and reduce their concentrations in the rumen before they enter into the blood stream.

Key words: modified yeast extract, aflatoxin, ruminal binding

W22 Factors affecting the selling price of calves sold in Texas livestock markets. K. J. Stutts, M. M. Beverly*, S. F. Kelley, and B. M. Freel, *Sam Houston State University, Huntsville, TX.*

Most cow-calf producers in Texas market their calves through local livestock auctions. When calves enter the sale ring, buyers must rapidly assess many physical and management factors to determine a value for the calves. The objective of this study was to determine which factors affect the selling price of calves in Texas livestock markets. Data were collected from 9 Texas livestock auctions on 1,420 lots consisting of 7,073 head. The data collected included gender, weight, breed type, color, muscle thickness, horn status, frame score, fill, condition, health, and selling price. An ANOVA was performed using SPSS. Calf characteristics were analyzed individually as dependent variables in which the model included BW as a covariate. Least squares means were generated for each variable and separated based on predicted differences. All selling prices are reported in US dollars per 45.45 kg of BW. Selling prices for steers ($132.34), heifers ($118.46), and bulls ($107.63) were different from each other ($P < 0.01$). Polled calves ($127.78) sold for a higher ($P < 0.01$) price than horned ($104.91) calves. Regarding breed type, British calves ($128.440) sold for the highest ($P < 0.03$) price, and calves that appeared to be predominantly American ($111.08) received the lowest price. Black ($122.51) calves sold for a higher ($P < 0.02$) price than red ($117.67) or yellow ($115.29) calves. Calves advertised as preconditioned ($131.38) and healthy ($121.27) calves sold for the highest ($P < 0.01$) price, and calves that were sick ($86.14) sold for the lowest ($P < 0.01$) price. Selling price of calves increased incrementally as lot size increased. Calves sold in groups of 20 or more ($129.07) had the highest ($P < 0.01$) selling price and calves sold as singles ($109.03) had the lowest selling price. These results indicate that many factors affect the selling price of calves in Texas livestock auctions. Some of these factors are associated with management and others are genetic. Producers could increase the value of their calves by changing their management strategy and through selection or modification of their breeding objectives.

Key words: feeder cattle, livestock auction, selling price

W23 Sources of sire-specific genetic variance for birth weight and weaning weight in the Bruna dels Pirineus beef cattle breed. M. Fina*[1], L. Varona[2], J. Piedrafita[1], and J. Casellas[1], *[1]G2R, Departament de Ciència Animal i dels Aliments, Universitat Autònoma de Barcelona, Bellaterra, Spain, [2]Departamento de Anatomía, Embriología y Genética Animal, Universidad de Zaragoza, Zaragoza, Spain.*

The Bruna dels Pirineus is an autochthonous beef cattle breed reared under traditional valley-mountain grazing systems in the Pyrenees Mountains of Catalonia (Spain). The breeding program of the Bruna dels Pirineus focused on birth weight (BWT) and weaning weight standardized to 185 d (WW185) since its implementation in 1990. Within this context, our analyses were performed on 8,130 BWT and 1,245 WW185 records from 12 and 2 purebred herds, respectively, collected between years 1986 and 2010. All animals included in the study were registered in the Yield Recording Scheme of this breed. This research investigated 2 sources of sire-related genetic effects on BWT and WW185, the influence of genes located in the non-autosomal region of the Y chromosome and the effect of paternal imprinting. Both BWT and WW185 were analyzed using a univariate Bayesian linear animal model and the relevance of paternal imprinting and Y chromosome-linked effects were checked by the deviance information criterion (DIC). In addition to sire-specific and direct genetic effects, our model accounted for random permanent effects (dam and herd-year-season) and 3 systematic sources of variation, sex of the calf (male or female), age of the dam at calving (2, 3, 4, 5, 6 and > 6 years), and birth type (single or twin). Both traits evidenced remarkable effects from the Y chromosome, whereas paternal imprinting was only revealed in WW185. Note that differences in DIC between the preferred model and the remaining ones exceed 39,000 and 2,800,000 DIC units for BWT and WW185, respectively. It is important to highlight that Y chromosome accounted for ~2% and a ~6% of the total phenotypic variance for BWT and WW185, respectively, and paternal imprinting accounted for ~13% of WW185 phenotypic variance. These results revealed 2 relevant sources of sire-specific genetic variability with potential contributions to the current breeding scheme of the Bruna dels Pirineus beef cattle breed.

Key words: Bruna dels Pirineus, paternal imprinting, Y chromosome

W24 Relationships between feed efficiency traits and body weight, age, backfat, rumpfat and circulating serum metabolites in pregnant beef cows. K. M. Wood*[1], Y. R. Montanholi[1], B. W. McBride[1], and K. C. Swanson[2], *[1]Dept. of Animal and Poultry Science, University of Guelph, Guelph, Ontario, Canada, [2]Dept. of Animal Sciences, North Dakota State University, Fargo.*

Sixty-three mature pregnant beef cows, primarily of Angus and Simmental breeding, were used to investigate the relationship between feed efficiency traits with ultrasound measures of backfat (BF), rumpfat (RF) and serum metabolites. Cows were randomly assigned to pen and individually fed a haylage/wheat straw-based TMR for 105 d leading up to parturition. Cows were weighed every 28 d and ultrasounded for backfat and rumpfat. Blood samples were obtained via jugular venipuncture on d 1, 56, 105, and serum was frozen for later analysis of urea, glucose, BHBA, NEFA and total cholesterol. Pearson correlations were conducted in SAS between performance and feed efficiency traits and ultrasound measures and serum metabolite concentrations and P-values adjusted using Benjamini Hochberg false discovery rate correction. Residual feed intake (RFI) was calculated using PROC GLM in SAS. Dry matter intake was not ($P \geq 0.14$) correlated with average body weight (BW), cow age, initial BF and RF, change in BF or RF, or serum metabolites. Average daily gain was negatively correlated ($P = 0.02$) with average BW but not ($P \geq 0.08$) with age, ultrasound measures or serum metabolites. Feed to gain was not ($P \geq 0.07$) correlated with BW, age, ultrasound measures or serum metabolites with the exception of d 56 serum glucose concentration, which was positively correlated ($P = 0.02$). The basic model for RFI ($R^2 = 0.08$) was not correlated ($P \geq 0.17$) with age, BW, ultrasound measures or circulating serum metabolites. Body weight, age, ultrasound measures and blood metabolites may not be good indicators of differences in feed efficiency traits, and there is considerable variation in measures of feed efficiency in mature pregnant cows.

Key words: beef cows, feed efficiency, serum metabolites

W25 Effect of preconditioning days, feeder cattle grade, and sire breed type on growth performance and carcass characteristics of beef cattle participating in a calf to carcass program in southwest Louisiana. D. M. Gandy*, D. R. Goodwin, T. H. Shields, W. A.

Storer, and F. M. LeMieux, *McNeese State University, Lake Charles, LA*.

One hundred 30 - one weanling steer calves (initial BW = 280 ± 78 kg) of various breeds were enrolled in a preconditioning program in southwest Louisiana. Steers were identified by sire breed, tagged, and assigned a USDA feeder calf grade. Calves entered the program in mid-September of 2008 and 2009 and were preconditioned for 36 ± 6 d. Cattle were grouped by weaning age and housed (25- 30 calves) in 0.81 ha paddocks with a mixture of bermudagrass, bahiagrass and carpetgrass and free choice alicia and bermudagrass hay (≥8% CP). A 14% CP preconditioning diet fed in troughs was provided with DMI of 1–2% of live BW. After preconditioning, calves were shipped 1,283 km to Henry C Hitch feedyard in Guymon Oklahoma. Calves were fed to an average harvest weight of 602 kg (range 445 to 727 kg) and harvested at a commercial processing facility. Feeder calf grade, steer sire breed, and preconditioning d were used to determine differences in growth and carcass performance. Large framed calves with at least moderate muscling had increased ($P < 0.05$) preconditioning ADG, harvest weight, and carcass weight when compared with medium framed calves with at least moderate muscling. Growth (preconditioning and feedlot ADG) were not different ($P > 0.05$) when steers were grouped by sire breed American (n = 29) or British (n = 101). Steers with British sires had heavier ($P < 0.05$) harvest weights than steers born of American sires. Steers that were maintained on a preconditioning routine for 37 to 42 d had increased ($P < 0.05$) harvest weight, carcass backfat and numerical USDA yield grade. When calves were preconditioned 36 d or less numerical yield grade was lower ($P < 0.05$). Feeder calf grades continue to be a reliable source for predicting harvest and carcass weights. Breed of sire did not affect carcass characteristics and preconditioning d influences carcass yield grade.

Key words: feeder calf grade, preconditioning, growth

W26 Effect of castration status on arrival of ultra-high risk calves on feedlot performance and health during a 61-d preconditioning program. L. Clark[1], C. Flaig[1], O. C. Schunicht[1], M. L. May[1], R. E. Peterson[1], C. W. Booker[1], C. R. Krehbiel[2], G. K. Jim[1], and L. O. Burciaga-Robles*[1], *[1]Feedlot Health Management Services Ltd., Okotoks, Alberta, Canada, [2]Department of Animal Science, Oklahoma State University, Stillwater.*

Ultra-high risk calves (n = 80; BW = 242.5 ± 4.2 kg) were allocated to evaluate the effect of castration status on arrival on feedlot performance and health during a 61-d preconditioning program. Upon arrival, 40 intact males (BULLS) were identified as candidates for the trial. Based on initial weight (±2.5 kg) and hide color, a matched pair was identified as a castrated male (STEERS) from the same truckload and was allocated as a case control. Arrival processing included a metaphylactic treatment for control of BRD and proprietary health procedures based on animal health risk assessment (Feedlot Health Management Services, Ltd. Okotoks, Alberta, Canada). Individual number and electronic ear tags were also applied. Intact males were band castrated. After initial processing, cattle were allocated to one of 2 pens (20 case controls/pen) equipped with individual feed intake data collection systems (GrowSafe Systems Ltd., Airdrie, Canada) and fed for 60 d. Cattle were observed by trained personnel for detection and treatment of disease during the trial. Cattle were re-weighed on d 30 and d 61. Animal performance was analyzed using PROC GLIMMIX (SAS Institute, NC). Animal was the experimental unit, and the model included the fixed effect of treatment and the random effects of block and pen. Animal health parameters were analyzed using a chi-squared procedure of SAS. A total of 6 animals (3 BULLS, 3 STEERS) were removed from the trial and not included in the analysis. In addition, 2 (5.0%) BULLS and 1 (2.5%) STEERS died ($P = 0.52$) and were removed from the analysis; no difference in animals treated for BRD was detected (15.5 vs 20.0% for BULLS and STEERS respectively; $P = 0.20$). No differences were observed for BW, ADG, DMI, or GF ($P > 0.05$) from d 0 to 30. However by d 60, BULLS had lower BW (305 vs 315 kg; $P = 0.05$), ADG (1.02 vs 1.18 kg/d; $P = 0.02$), and tended to have lower G:F (0.171 vs 0.185; $P = 0.09$) when compared with STEERS. Thus, purchase price discounts for bulls when compared with steers should consider a 13.5% decrease in ADG and a 7.6% decrease in G:F in addition to increased mortality.

Key words: castration, feedlot performance, BRD

W27 Effects of *Bos indicus* breeding on plasma pregnancy-associated glycoprotein (PAG) concentrations and fetus size in early gestation. P. M. Morelli*[1], D. O. Rae[2], S. E. Johnson[1], and A. D. Ealy[1], [1]*University of Florida, Department of Animal Sciences, Gainesville,* [2]*University of Florida, Department of Large Animal Clinical Sciences, Gainesville.*

Cross-breeding *Bos indicus* and *Bos taurus* breeds improves various production traits for cattle maintained in hot climates. Limited information exists describing pregnancy specific events that are influenced by these cross-breeding strategies. In this study, transrectal ultrasonography was used to measure fetal size at 52 to 55 d of gestation in cows composed of Angus (>80% Angus; n = 17), Brangus (n = 15) and Brahman (≥25% Brahman; n = 58) genetics. Blood was collected for the measure of plasma pregnancy associated glycoprotein (PAG) content by ELISA. Multiparous cows were used in a timed AI protocol for this study. Multiples sires were used to generate fetuses with varying degrees of Angus/Brahman cross-breeding. Blood was harvested once between d 52 and 55 post-TAI. Day of blood collection and ultrasonography was used as a covariate. PAG concentrations were greater ($P \leq 0.05$) in Brangus and Brahman cows than Angus cows (9.8, 10.4 and 5.9 ng/ml, respectively; SE = 1.93). Fetus size was smaller ($P \leq 0.05$) in Brangus and Brahman cows than Angus cows (27.7, 28.8 and 34.8 mm, respectively; SE = 3.24). No differences in PAG concentrations and fetus size were observed based on the amount of Angus, Brangus and Brahman genetics in the fetus. In summary, both PAG concentrations and fetus size differed based on the degree of Angus/Brahman cross-breeding of the cow but not the fetus. This suggests that the maternal system plays an active role in controlling placental activity and early fetal development, and Brahman-based cows control these events differently than Angus cows during early pregnancy.

Key words: cross-breeding, pregnancy associated glycoprotein (PAG), fetus size

W28 Genetic parameters and genetic trends for growth and reproductive traits in a Colombian multibreed beef cattle population. O. D. Vergara[1] and M. A. Elzo*[2], [1]*University of Cordoba, Monteria, Colombia,* [2]*University of Florida, Gainesville.*

Genetic parameters and trends for weaning weight adjusted to 240 d of age (WW240; n = 9,668), and weight gain from weaning to 24 mo of age (GW730; n = 1,357), age at first calving (AFC; n = 1,615), and interval between first and second calving (CI1; n = 1,189) were estimated in a Colombian beef cattle population composed of Blanco Orejinegro, Romosinuano, Angus, and Zebu straightbred and crossbred animals. Variance components and genetic parameters were estimated by Restricted Maximum Likelihood. The 4-trait mixed model included the fixed effects of contemporary group (herd-year-season-sex; sex = sex of progeny for CI1), age of dam (WW240 only), breed direct genetic effects, breed maternal genetic effects (WW240 only), individual heterosis, and maternal heterosis (WW240 only). Random effects for WW240 were calf direct genetic, dam maternal genetic, permanent environmental maternal, and residual. Random effects for GW730 were calf direct genetic and residual; and random effects for AFC and CI1were cow direct genetic and residual. Program AIREML was used to perform computations. Heritabilities estimates for additive direct genetic effects were 0.19 ± 0.003 for WW240, 0.53 ± 0.004 for GW730, 0.11 ± 0.007 for AFC, and 0.05 ± 0.001 for CI1. Maternal heritability was 0.11 ± 0.002 for WW240. The high direct heritability for GW730 suggests that selection for this trait is feasible in this population. The genetic correlation between direct and maternal additive effects for WW240 was negative (−0.18 ± 0.009). Correlations between additive direct genetic effects for all traits were close to zero. Calf and cow weighted yearly means showed negative trends for direct growth traits (−0.53 ± 0.19, $P < 0.05$ for WW240; −2.64 ± 0.55, $P < 0.001$ for GW730), and AFC (−0.04 ± 0.02, $P < 0.05$). Cow direct genetic CI1 yearly means showed positive trends (3.01 ± 0.42, $P < 0.001$). This suggests that some selection for AFC existed in this population during these years and other traits were neglected.

Key words: cattle, growth, reproduction

W29 Combining ability of nine tropically adapted and temperate breeds for growth and ultrasound traits in Colombia. C. A. Martinez[1], C. Manrique[1], M. A. Elzo*[2], and A. Jimenez[1], [1]*Universidad Nacional de Colombia, Bogota, Colombia,* [2]*University of Florida, Gainesville.*

Colombia is currently using crossbreeding strategies involving tropically adapted and temperate cattle breeds to improve beef cattle productivity for growth and carcass traits under pasture conditions. The objective of this research was to compare the combining ability of sires from 2 tropically adapted *Bos taurus* breeds (Blanco Orejinegro: BON; Romosinuano: RS), 3 tropically adapted *Bos indicus* breeds (Gray Brahman: GB; Guzerat: GZ; Red Brahman: RB), and 4 temperate *Bos taurus* breeds (Braunvieh: BV; Limousin: LIM; Normand: NM; Simmental: SIM) when mated to Gray Brahman cows for birth weight (BW), and adjusted weights (W), ultrasound ribeye area (REA) and backfat (BF) measured at 4 (W4, REA4, BF4), 7 (W7, REA7, BF7), 12 (W12, REA12, BF12), and 15 (W15, REA15, BF15) mo of age. Data were from 352 calves from 2 herds (22 to 100 per breed group) sired by 37 bulls (3 to 12 sires per breed). The model included breed group of calf, contemporary group (herd-year-season-sex) and age of calf (ultrasound traits only) as fixed effects, and sire and residual as random effects. Least squares means (LSM) for BW, W4 and W7 were similar across breed groups, whereas calves from SIM sires were heavier than calves from GB sires at 12 (42.8 ± 9.9 kg; $P < 0.0009$) and 15 mo of age (35.0 ± 7.9 kg; $P < 0.0008$). The LSM for REA were similar for crossbred calves from sires of all breeds, except for calves from LIM sires whose REA were larger than those of calves from GZ (11.4 ± 3.0 mm^2; $P < 0.0078$), NM (11.0 ± 2.9 mm^2; $P < 0.0103$), SIM (10.3 ± 2.8 mm^2; $P < 0.0143$) and RB sires (11.3 ± 2.4 mm^2; $P < 0.0002$) at 4 mo of age, and from GB sires at 4 (11.3 ± 2.4 mm^2; $P < 0.0002$), 7 (6.8 ± 1.9 mm^2; $P < 0.0174$), 12 (9.7 ± 1.8 mm^2; $P < 0.0224$), and 15 mo of age (11.3 ± 2.8 mm^2; $P < 0.0051$). The LSM for BF were similar across breed groups and calf ages.

Key words: crossbreeding, growth, ultrasound

W30 Genetic parameters and trends for age at first calving in Brahman cows raised in Brazil. J. C. DeSouza*[1], M. Silveira[2], M. A. Pereira[3], P. B. Ferraz Filho[4], J. A. DeFreitas[5], R. M. DaSilva[2], C. H. M. Malhado[6,10], C. H. M. Cavalari[3], M. F. Mota[7], H. J. Fernandes[8], and W. R. Lamberson[9], [1]*Mato Grosso do Sul Federal University, CPAQ/Animal Science, MS, Brazil,* [2]*Student of MSc. of animal science course, UFMS, Campo Grande, Brazil,* [3]*Brazilian Association of Zebu Breeders, Uberaba, Brazil,* [4]*Mato Grosso do Sul Federal University, Tres Lagoas, Brazil,* [5]*Paraná Federal University, Palotina, Brazil,* [6]*South*

Bahia State University, Jequie, Brazil, [7]Paranaense University - UNIPAR, Umuarama, Brazil, [8]State University of Mato Grosso do Sul, Aquidauana, MS, [9]University of Missouri, Columbia, [10]Scholarship - CNPQ, Brazil.

In 1997 the Brahman breed was introduced in Brazil to potentially increase at Brazilian beef cattle production. For this to occur, reproductive traits are very important. The objective of this study was to estimate genetic parameters and genetic trend for age at first calving in Brahman Beef cattle. The data were 5,432 ages at first calving from 1997 at 2008 provided by the Brazilian Zebu Cattle Association and included information on different regions of the country. The genetic parameters were estimated by using the MTDFREML package with an animal model and included the fixed effects of contemporary group (year, season, conception type (1: not in vitro fertilization; VF; 2: in vitro fertilization), nutrition type (1: Pasture, 2: pasture + concentrate, 3: Feed lot) and a random animal effect. The genetic trend was estimated by linear regression of the breeding value of calving interval on cow birth year. The genetic trend was −0.053 d/year ($P = 0.03$) and the R2 of model was 0.38. The estimated genetic variance was 8.89 and phenotypic variance was 49.67 yielding a heritability of 0.18 ± 0.05 and the environmental proportion of the total variance was 0.82 ± 0.05. The genetic gain was small, but in the favorable direction. Breeding values averaged −0.107 in 1997 and improved to −0.707 in 2008 for a total reduction in the age at first calving of 0.599 mo. The genetic variance for age at first calving is small and suggests that the trait not a good candidate for direct selection.

Key words: beef cattle, age at first calving, Zebu

W31 Allometric growth study of Guzerá cattle under a performance test on grazing regimen. R. C. Sousa*[1], I. G. Pereira[1], P. V. R. Paulino[2], S. D. J. Villela[1], R. A. M. Oliveira[1], A. P. L. Tonaco[1], F. S. Coelho[1], and F. A. Carvalho Neto[3], *[1]Universidade Federal dos Vales do Jequitinhonha e Mucuri, Diamantina, MG, Brazil, [2]Universidade Federal de Viçosa, Viçosa, MG, Brazil, [3]Colorado State University, Fort Collins.*

A performance test of Guzerá cattle grazing on *Brachiaria brizantha* pasture was conducted on a private ranch in Brazil during 294 d. The study was assisted by the Brazilian Association of Zebu Breeders. During this performance test the development of the animals were measured by morphometric traits (rump height, body length, and heart girth), scrotal circumference, rib eye area (by ultrasound) and body weight. Forty-five Guzerá bulls were used with an initial body weight of 219.9 ± 38.05 kg and age of 325.8 ± 28.0 d old. The animals grazed on *Brachiaria brizantha* pastures and were supplemented with loose supplements during the performance test duration to overcome protein deficiencies in the pasture. A 70 d adaptation period was allowed and thereafter the animals were weighed and evaluated every 56 d. An exponential model was used to study the allometric growth of these animals. A log-transformation of the initial model was performed to produce a linear model. Growth was considered isogonic when $b = 1$ and heterogonic when $b \neq 1$ ($b > 1$, positive and $b < 1$, negative). The allometric growth of all traits evaluated was heterogonic and negatively correlated to body weight and age of the animals (Table 1). However, coefficients of determination from the allometric equations had moderate values, suggesting that more studies with larger group of animals should be conducted to gather greater amount of information to describe the growth pattern of Guzerá bulls under tropical grazing conditions.

Table 1. Allometric coefficients of morphometric traits, scrotal circumference and rib eye area related to BW of Zebu bulls

Trait	a	b	s(b)	R^2	*P*-value
RH	54.09	0.16	0.01	0.63	*
BL	32.43	0.24	0.01	0.65	*
HG	31.64	0.28	0.01	0.75	*
SC	0.43	0.71	0.02	0.80	*
REA	1.78	0.51	0.02	0.74	*

*$P < 0.01$. a = intercept of linear regression; b = allometric coefficient; s(b) = standard error of the allometric coefficients; R^2 = coefficient of determination; RH = rump height; BL = body length; HT = heart girth; SC = scrotal circumference, REA = rib eye area.

Key words: beef cattle, morphometric measurements, Zebu

W32 Growth curves of Guzera bulls on grass regimen under performance test. R. C. Sousa[1], I. G. Pereira*[1], P. V. R. Paulino[2], A. V. Pires[1], F. F. Silva[1], R. A. M. Oliveira[1], A. P. L. Tonaco[1], and F. A. Carvalho Neto[3], *[1]Universidade Federal dos Vales do Jequitinhonha e Mucuri, Diamantina, MG, Brazil, [2]Universidade Federal de Viçosa, Viçosa, MG, Brazil, [3]Colorado State University, Fort Collins.*

Data derived from a performance test of Guzera bulls on pasture regimen was used to analyze the growth pattern. Forty-five post-weaning bulls (325.8 ± 28 d old) with initial body weight of 219.9 ± 38.05 kg were used. The animals grazed on *Brachiaria brizantha* pastures and were also supplemented to attain a body weight gain of up to 1.5 kg/d. All animals were maintained under the same feed regimen for a period of 294 d. Body measurements were taken every 56 d throughout the study. The objective of the study was to develop a nonlinear function that could best describe the growth pattern of these animals. All models tested converged, but it was observed that there was a significant variation on asymptotic weights and mean square error (MSE) between models. The models of Von Bertalanffy and Brody showed more realistic values compared with the other models (Table 1). We observed that the values produced by the Bertalanffy model were slightly lower than the values from the Brody model when comparing the estimates of the asymptotic weights from the 2 models (Table 1). The asymptotic weight estimated by the Gompertz model proved to be a little lower, while the value was much lower than the others in the Logistic model (Table 1). In most studies in the available literature, the Brody model presents the largest estimates of asymptotic weight, and the Logistic model consistently produces lower estimates. It can be observed that the growth curves fitted by Von Bertalanffy and Brody models had lower mean square error (MSE) and higher coefficient of determination when compared with the other models. The Von Bertalanffy model was chosen as it best represented the growth curve of the Guzerá animals as it had the best fit to the data considering the criteria used.

Table 1. Parameter estimates of growth curves of grazing Guzera bulls under performance test

Model	A	B	K	r^2	MSE
Von Bertalanffy	627.97	0.60	0.00	0.97	641.98
Brody	787.71	0.95	0.00	0.97	681.16
Gompertz	568.26	2.53	0.00	0.97	703.73
Logistics	466.39	7.51	0.01	0.96	939.39

MSE = mean square error; A = asymptotic weight when t tends to plus infinity; B = an integration constant, related to the initial BW; K = maturation rate, an indicator of the speed with which the animal approaches its mature; r^2 = coefficient of determination.

Key words: nonlinear models, age, Zebu

W33 Variance components in growth traits of Guzera cattle breed with different models. I. S. Silva*[1], I. U. Packer[2], C. M. R. Melo[3], L. O. C. Silva[4], and R. A. A. Torres Junior[4], *[1]University of Brasília - UnB, Brasília /DF, Brazil, [2]University of São Paulo - USP/ESALQ, Piracicaba/SP, Brazil, [3]University of Santa Catarina - UFSC, Florianópolis/SC, Brazil, [4]Embrapa Gado de Corte, Embrapa Gado de Corte, Campo Grande/MS, Brazil.*

A total of 130,424 body weight records of Guzera cattle collected in 8 periods every 90 d were used to estimate (co)variance components. REML was used with 4 models: model 1 included genetic direct (GA), genetic maternal (GM) environmental permanent maternal (AM) and residual random effects; model 2 excluded GM; model 3 excluded AM and model 4 excluded both GM and AM. Likelihood ratio test did not show significant differences ($P < 0.05$) between models 1 and 2 in almost all ages. Estimates of direct heritabilities h^2 in models 1 and 2 were similar. The values of h^2 decreased from birth to second age then maintained the same value until the weaning and increased after that. Direct heritability estimates for weight in age classes close to 205, 365 and 550 d, by models 1 and 2, were respectively 0.15, 0.12 and 0.14. Estimates of the same parameter obtained by models 3 and 4 were respectively 0.15, 0.14, 0.15 and 0.26, 0.19, 0.17. Heritability estimates from model 3 were larger due to the exclusion of the AM term of the analysis. Estimates of additive variance were greater with model 4. Model 2 adjusted better the data and required lesser processing time. The model comparison indicated that the GM effect did not improve fit.

Key words: beef cattle, maternal effects, estimates of variances

W34 Estimates genetic parameters for growth traits of Guzera cattle breed by single-trait and two-trait analysis. I. S. Silva*[1], I. U. Packer[2], C. M. R. Melo[3], L. O. C. Silva[4], and R. A. A. Torres Junior[4], *[1]University of Brasília - UnB, Brasília /DF, Brazil, [2]University of São Paulo - USP/ESALQ, Piracicaba/SP, Piracicaba/SP, Brazil, [3]Federal University of Santa Catarina - UFSC, Florianópolis/SC, Brazil, [4]Embrapa Gado de Corte, Campo Grande/MS, Brazil.*

The study aimed to estimate components of (co)variance and genetic parameters, comparing different single-trait and 2-trait models, for weight adjusted for the age-standard. A total of 55,063 body weights records adjusted to 120 (W120), 205 (W205), 365 (W365) and 550 (W550) days of age, from 22,949 animals belonging to 46 herds of Guzera breed, referring to the period of 1975 to 2001. In the single and 2-trait analyses 2 models were used to estimate the genetic parameters by the REML: model 1, as a complete model,, included direct and maternal genetic effects, as well as, maternal permanent environmental and residual effects; the model 2, as a reduced model, included the direct genetic effect and the maternal permanent environmental and residual effects. Likelihood ratio test did not show significant differences ($P < 0.05$) between models 1 and 2 in almost all ages. Estimates and behavior of variances for models 1 and 2 were similar, by the single-trait and 2-trait analyses. In the model 1 the maternal genetic variance estimates were low, mainly before the weaning. Direct heritability estimates by single-and 2-trait analysis for W120, W205, W365 and W550 were 0.15, 0.10, 0.17, 0.14 and 0.13, 0.10, 0.16, 0.15, respectively. Direct heritability estimated by models 1 and 2 were similar in the single-trait and 2-trait analyses. Estimates of maternal heritability were low for all ages. The genetic correlations were similar for models 1 and 2. The direct genetic correlation by models 1 and 2 for W120/W205, W120/W365, W120/W550, W205/P365, W205/W550 and W365/W550 were 0.80, 0.54, 0.54, 0.74, 0.62, 0.95 and 0.80, 0.54, 0.53, 0.74, 0.62, 0.95, respectively. Phenotypic and environmental correlations presented lower values when birth weight was involving. Overall it was observed a good agreement between the results for both models. The comparison between the models indicates that the reduced model was equivalent to the complete model.

Key words: beef cattle, maternal effects, variance components

W35 Real-time ultrasound measurements for the selection of growing animals of Bruna dels Pirineus beef cattle breed. M. Fina, J. Tarres, and J. Piedrafita*, *Grup de Recerca en Remugants, Departament de Ciència Animal i dels Aliments, Universitat Autònoma de Barcelona, Bellaterra (Barcelona), Spain.*

The application of ultrasound technology as a research tool allows the evaluation of carcass attributes in live animals. In addition, these measurements have potential to increase the rate of genetic progress including estimation of heritabilities and genetic correlations in genetic evaluation programs for carcass merits. The objective of this study was to estimate genetic parameters for real-time ultrasound measurements of loin area (LA), loin depth (LD) and subcutaneous fat thickness over the rump (SF) in Bruna dels Pirineus beef cattle, a breed selected for meat from the old Brown Swiss and similar to the American Braunvieh. The measurements were obtained using a Sonovet 2000 ultrasound unit equipped with a 3.5-MHz 17 cm linear transducer. A unique ultrasound technician preformed all measurements. Every animal (n = 352) was scanned 2 to 5 times for each variable to estimate the accuracy of ultrasonic records. The weight at scanning ranged from 158 kg to 608 kg. Intraclass correlations for LA, LD and SF measurements were 0.964, 0.988 and 0.875, respectively. Heritabilities and genetic correlations were estimated using multiple-trait restricted maximal likelihood. The final animal model included only one ultrasonic measurement per animal (the closest to the mean for each animal), fixed effects for year-season (7 breeding year-seasons over a 2.5-yr period) and feedlot, and the interaction of weight by sex as a linear covariate. The pedigree included 936 animals. Heritabilities for LA, LD and SF were 0.37 ± 0.13, 0.36 ± 0.12, and 0.27 ± 0.13, respectively. Genetic correlations between LA and LD, LA and SF, and LD and SF, were 0.63 ± 0.17, 0.36 ± 0.28, and -0.41 ± 0.42, respectively. The estimates of heritabilities and genetic correlations indicate that a relevant additive genetic variance exists for all 3 traits and supports the use of live animal ultrasonic measurements as a selection tool in breeding cattle.

Key words: real-time ultrasound, beef, selection

W36 Linear B-splines to model longitudinal weight records in Tabapuã cattle. G. R. O. Menezes*[1,2], R. A. Torres[2], R. A. A. Torres Júnior[1], L. O. C. Silva[1], A. Gondo[1], and R. F. Euclydes[2], *[1]Embrapa Beef Cattle, Campo Grande, MS, Brazil, [2]Federal University of Vicosa, Vicosa, MG, Brazil.*

This work was aimed at evaluating the feasibility of a random regression model with linear B-splines (RRM) to estimate (co)variance components and breeding values for body weight in beef cattle. Data comprised 359,707 body weight records from 1 to 600 d of age on 84,215 animals of the Tabapuã breed. RRM included as fixed effects contemporary group, age of dam and deviation of the animal's birth date to the average day of the calving season. As random effects, direct and maternal additive genetic and direct and maternal permanent environment effects were included. Six residual variance classes were assumed: 1–60, 61–180, 181–300, 301–420, 421–540 and 541–600 d. Six knots located at ages 0, 120, 240, 360, 480 and 600 d were considered. To compare the results obtained with RRM, a multi-trait model (MTM) was applied to standard pre-adjusted weights at 120, 240, 360 and 480 d of age. MTM's fixed and random effects were almost the same of the RRM, except for the direct permanent environment random effect. (Co)variance components were estimated using a Bayesian approach with Gibbs sampling. RRM presented good results, providing reliable (co)variance components and genetic parameters along the range of ages evaluated. Additionally, RRM showed no convergence problem. (Co)variance components and genetic parameters estimates generated by RRM and MTM were similar for all ages evaluated. For instance, direct heritabilities for body weights at 120, 240, 360 and 480 d of age, estimated by RRM and MTM, were 0.20 and 0.18; 0.21 and 0.18; 0.21 and 0.19; 0.24 and 0.19, respectively. These estimates were close to the ones obtained in other studies with Tabapuã cattle. For the ranking based on estimated breeding values, the models were similar, with larger differences among animals with less information, i.e., cows and calves. RRM allowed for better and greater use of available data. Data file used for RRM was 67% larger than the one used for MTM what can improve accuracies of the genetic evaluations. Thus, RRM is a feasible and interesting alternative to be applied in genetic evaluations for longitudinal growth traits in beef cattle.

Key words: random regression, beef cattle, growth

W37 Genetic variability for calf mortality in Nellore cattle. L. C. Magalhães Silva*, F. Baldi, L. G. Albuquerque, and M. J. R. Paranhos da Costa, *São Paulo State University, Unesp, Jaboticabal, São Paulo, Brazil.*

The objective of this work was to estimate genetic parameters for calf mortality in Nellore cattle. Calf mortality (CM) was defined as a binary trait, with 1 = success, indicating a calf born alive after the pregnancy diagnosis and 0 = failure, indicating a calf failing to reach the end of gestation, stillborn, or dead within the first 48 h after calving. Pregnancy diagnoses were performed on cows 90 d after the end of breeding season. After consistency checks 68,307 records for calf mortality from 31,583 cows and 646 sires belonging to Agropecuaria Jacarezinho Ltda, Sao Paulo, Brazil, were available for subsequent analyses. The mortality frequency obtained from the data was of 2.0%. CM was analyzed using a sire model. The age of the cow at the beginning of the breeding season (in classes, ranging from 1 to 13 years) was included as fixed effect in the model, while contemporary group (CG), defined by year, farm and breeding season of the cow and the additive genetic effect of the sire were fitted as random effects. The pedigree file contained 861 sires. Bayesian inference using a threshold model was applied and a Gibbs Sampler was employed to obtain the marginal posterior mean and standard deviation of all variance components. A single Markov chain of 500,000 cycles was generated with a sampling interval of 100 iterations, using the THRGIBBS1F90 software. The posterior distribution for CM heritability was obtained from effective samples (10,000 samples). The descriptive statistics (mean and standard deviation) and the highest posterior density (HPD at 95%) region were estimated for CM heritability using the BOA package (R program). For CM heritability, the mean h2 ± standard deviation and HPD [lower bound – upper bound] were 0.21 ± 0.07 and [0.087- 0.37], respectively. The results of the present study pointed out that, applying a sire model to evaluate CM, there is enough genetic variability to select for decreased calf deaths in beef cattle. Financial support: FAPESP.

Key words: calves, heritability, mortality

W38 Selection effect for growth traits on energy requirements in reproduction females of three production cycles. I. D. P. Solar Diaz*[1], F. R. de Araujo Neto[1], G. M. Ferreira de Camargo[1], R. Barbosa Lobo[2], and H. N. de Oliveira[1], *[1]Sao Paulo State University, Jaboticabal, Sao Paulo, Brasil, [2]Sao Paulo University, Ribeirao Preto, Sao Paulo, Brasil.*

The objective was to evaluate the effect of selection for growth traits on energy requirements in reproductive females from 3 production cycles (C). Records of weights from Nellore cows were used to calculate the average weights in the reproductive stage (after 730 d). The average number of days that females remain in each category (pregnant lactating, non-pregnant lactating, pregnant nonlactating and empty and dry) for the period of one year considering the average calving interval of 365 (C1), 450 (C2) and 550 (C3) days were calculated as well. The energy requirement was measured by total net energy (T.N.E.) which was obtained by the sum of net energy for maintenance, activity, pregnancy and lactation. The prediction equations of NRC were used. The selection effect was analyzed using the estimates of coefficients of regression which were obtained from a previous analysis (not shown) of genetic parameters from birth to mature ages of cows. A selection intensity of 1.76 u.d.p was used. The following selection criteria were used: weights of 120, 210, 365, 450, 550 and 730 d and the weights gains between these phases. The increase of N.E. was not significant when different selection criteria were used, however the increase was observed between the production cycles. There is a tendency of increase in T.N.E. from C1 (4,864–5,070 Mcal) to C2 (4,935–5,148 Mcal), however the C3 (4,503–4,700 Mcal) was relatively inferior compared with the others. As expected, the nutritional requirements, on an annual basis, decreases with an increasing calving interval, as part of the T.N.E. is assigned to less productive classes (or nonproductive in the case of C3) and therefore less demanding. However, when considering the production of calves, the cost-effectiveness is impaired. In general, considering the genetic parameters used in this study, we conclude that the selection criteria used did not interfere in the females energy requirements regardless of their reproductive efficiency.

Key words: beef cattle, net energy

W39 Effect of model structure on direct and maternal (co)variance and heritability estimates for 210 d weight in Nellore cattle. L. Pascoa*[1,2], A. de los Reyes[2], M. A. Elzo[3], J. L. Ferreira[4], L. A. F. Bezerra[5], and R. B. Lobo[5], *[1]Federal Institute of Brasilia, Planal-*

tina, Distrito Federal, Brazil, [2]Federal University of Goias, Goiânia, Goiás, Brazil, [3]University of Florida, Gainesville, [4]Federal University of Tocantins, Araguaina, Tocantins, Brazil, [5]National Association of Farmers and Researchers, Ribeirão Preto, São Paulo, Brazil.

Actual and adjusted weights to 210 d of age from 72,731 male and female Nellore calves born in 40 PMGRN Nellore Brazil herds from 1985 to 2005 were used to compare the effect of different models on direct and maternal (co)variance and heritability estimates. Four structures of contemporary groups (CG) were defined: CG1: CG_B – semester of birth; CG2: CG_B – trimester of birth; CG3: CG1 – SC; CG4: CG2 – SC, where CG_B: herd – year of birth – management group at each age. Four analytical models were defined: M1: Weight = α + CG1 + SC + DAC + ε; M2: Weight = α + CG2 + SC + DAC + ε; M3: Weight = α + CG3 + DAC + ε; M4: Weight = α + CG4 + DAC + ε; where, α = constant; SC = sex of calf; DAC = class of cow age at calving, ε = random residual effect. (Co)variances were estimated using a derivative-free restricted maximum likelihood procedure, considering CG fixed (F) or random (R). Estimates of additive direct and maternal genetic variance (σ^2_d, σ^2_m) and direct and maternal heritability (h^2_d, h^2_m) were larger in models with semester than with trimester of birth in CG (Table) likely due to greater variation among weights when the season of birth considered in CG was longer. These estimates were similar in models with and without sex of calf in CG. Models with random CG yielded higher estimates of σ^2_d, σ^2_m, h^2_d and h^2_m and lower estimates of residual variance (σ^2_e) than models with fixed CG.

Table 1. Estimates of direct and maternal (co)variances (kg^2) and heritabilities for adjusted / actual weights at 210 days of age in Nellore cattle

M	CG	σ^2_d	σ^2_m	σ^2_e	h^2_d	h^2_m
M1	F	145/153	49/52	234/292	0.31/0.29	0.11/0.10
	R	146/155	49/52	233/291	0.32/0.29	0.11/0.10
M2	F	119/127	42/45	231/290	0.27/0.25	0.10/0.09
	R	121/130	42/45	229/287	0.28/0.27	0.10/0.09
M3	F	142/151	49/51	230/287	0.31/0.29	0.11/0.10
	R	144/153	49/52	229/286	0.32/0.29	0.11/0.10
M4	F	116/123	41/44	226/285	0.27/0.25	0.10/0.09
	R	121/129	42/45	224/281	0.28/0.26	0.10/0.09

Key words: cattle, contemporary group, weaning

W40 Age of dam as phenotypic source of variation for body weight in Nellore beef cattle. D. A. Lino*[1,2], S. Tsuruta[1], I. Misztal[1], E. N. Martins[2], and L. O. C. Silva[3], *[1]University of Georgia, Athens, [2]State University of Maringa, Maringa, PR, Brazil, [3]Embrapa Gado de Corte, Campo Grande, MS, Brazil.*

Prior to the inclusion of effects in genetic evaluation models, tests should be carried out to quantify their influence. The objectives of this study were to verify the trend caused by age of dam (AOD) on weight and on phenotypic variance of weight in Nellore beef cattle from birth until 385 d. Data from the Brazilian Association of Zebu Breeders were used. A total of 2,915,879 body weight records from 1975 to 2009 were divided into 5 periods of measurement: birth weight (BW), weight taken at age 91 ± 59 d (W1), 188 ± 53 d (W2), 290 ± 86 d (W3), and 383 ± 82 d (W4). The AOD at measurement was divided into 11 categories, ranging from 4 to 14 years. A model separate for each weight considered AOD as a fixed effect. The adjusted phenotypic variance was obtained from the residual variance of the model separately for each AOD class. To compare the effect of AOD in all periods, the estimated values were standardized by phenotypic variance. The effect of AOD on BW, W1, W2, W3, and W4 explained 1.5, 7.3, 6.3, 4.4, and 3.1% of the differences in weight, respectively. When the standardized values were considered, the changes were basically the same for all periods. The AOD at measurement accounted for 8.9% of the phenotypic variance observed in BW with the highest variance at 4–7 years of age and declining variance outside of this range. For W1, the phenotypic variance was 468 at AOD = 4, increased to 483 at AOD = 7, and declined to 446 at AOD = 14. Therefore, the AOD was responsible for 8.8% of the changes in phenotypic variance for W1. For weight and phenotypic variance of weight, the BW showed a linear trend, whereas W1 showed a quadratic behavior. For W2, W3, and W4, the change in phenotypic variance ranged from 2.9 to 6.0%, without any special trend along AOD. The age of dam influences the phenotypic variance up to 130 d of age but less afterward.

Key words: age of dam, phenotypic variance, beef cattle

W41 Additive genetic variation of residual feed intake and its components in Nellore cattle. M. E. Zerlotti Mercadante*, A. C. Del Claro, S. F. Martins Bonilha, J. N. dos Santos Gonçalves Cyrillo, and R. H. Branco, *Instituto de Zootecnia, Sertãzinho, São Paulo, Brazil.*

The objective was to investigate the importance of additive genetic effects on residual feed intake (RFI) in Nellore cattle. Performance tests for individual feed intake were conducted at Instituto de Zootecnia, Sertãzinho-SP, Brazil. Records of 491 animals (247 males and 244 females), born from 2004 to 2009, progeny of 50 sires and 345 dams, were analyzed. The pedigree file included up to seventh generation of animals with records, and contained 1,652 animals, with 3 sires and 24 dams with own performance and progeny. The averages of test duration, initial age and BW, ADG, DMI and ME were 86 ± 23 d, 290 ± 43 d, 224 ± 53 kg, 0.923 ± 0.220 kg/d, 6.645 ± 1.169 kg/d and 2.151 ± 0.083 Mcal/kg. ADG was estimated as the slope of regression of BW on test d. Phenotypic RFI (RFI_P) was obtained as residuals of linear regression of DMI on MBW ((mid-test BW)$^{0.75}$) and ADG. The model included contemporary group (CG, n = 8), defined by birth yr and sex, as fixed effect and initial age as linear covariate. Variance components were estimated by REML. Genetic RFI (RFI_G) was obtained from linear regression of DMI on EBV of MBW and EBV of ADG, including also the effects of CG and age in the model. EBV were obtained in a 2-trait animal model analysis of MBW and ADG, including CG and age. The heritabilities of DMI, RFI_P and RFI_G were estimated in one-trait animal model analysis, including CG and age (only for DMI). EBV for RFI_P and RFI_G ranged from −0.329 to 0.490 kg/d (SD = 0.136) and from −0.410 to 0.435 kg/d (SD = 0.120), and the average of accuracy values were 0.573 and 0.491 for RFI_P and RFI_G EBV, respectively. The rank correlation between RFI_P and RFI_G EBV was 0.694.

Table 1. Variance components and heritability ± SE for ADG, MBW, DMI, RFI_P and RFI_G

Trait	σ^2 additive genetic	σ^2 phenotypic	h^2±SE
ADG	0.010	0.021	0.464±0.106
MBW	18.853	61.821	0.305±0.094
DMI	0.449	1.000	0.449±0.116
RFI_P	0.037	0.209	0.178±0.098
RFI_G	0.053	0.283	0.186±0.092

Key words: beef cattle, *Bos indicus*, genetic evaluation

W42 Relationships among beef cattle temperament and tenderness traits using repeated performance records. T. T. Taxis*[1], W. R. Shafer[2], L. L. Berger[3], D. B. Faulkner[4], J. E. Beever[4], M. M. Rolf[1], D. L. Dow[1], J. F. Taylor[1], C. L. Lorenzen[1], and R. L. Weaber[1], *[1]University of Missouri, Columbia, [2]American Simmental Association, Bozeman, MT, [3]University of Nebraska, Lincoln, [4]University of Illinois, Urbana.*

Beef cattle temperament has been associated with a variety of performance measures, including steak tenderness. The American Simmental Association provided performance data and pedigree records to elucidate the relationship between temperament (exit velocity; EV) and tenderness (Warner-Bratzler shear force; WBSF) in *Bos taurus* breeds. EV were recorded on d 0 (EV1) and d 42 (EV2) of a feeding trial. The edited data set included 2,819 WBSF, 917 EV1 and 976 EV2 phenotypes in 176 contemporary groups (CG) with 13,418 pedigreed animals. Four different statistical models were analyzed. A trivariate and repeated records model were utilized to assess EV, and 2 bivariate models were utilized to assess WBSF. The trivariate animal model with fixed effects (CG, sire and dam breed composition) and a random animal effect was fit revealing a 0.99 genetic correlation between EV observations. A repeated records analysis of EV using the same fixed effects provided a better model fit ($P < 0.0001$; via likelihood ratio). Heritabilities were 0.19 (0.06) and 0.39 (0.08) for WBSF and EV, respectively, with a −0.10 (0.20) genetic correlation. Animals with multiple WBSF measurements, were analyzed using 2 bivariate models (both included WBSF and EV) to elucidate the effects of within animal WBSF variation. WBSF was analyzed using average peak shear force (APSF) and individual core values as repeated records. EV was analyzed using repeated records in both models. Heritability for WBSF using APSF was 0.06 (0.06) and 0.06 (0.05) from the repeated records model. Heritabilities for EV were unchanged in both models. Genetic correlations between WBSF and EV were −0.62 (0.47) and −0.63 (0.47). The analysis using individual core values provided a better model fit (p, 0.00001; via likelihood ratio). A whole genome association study using BovineSNP50 genotypes is planned for WBSF and EV.

W43 Carcass and meat palatability trends in cattle ranging from 100% Angus to 100% Brahman. M. A. Elzo*, D. D. Johnson, J. G. Wasdin, and J. D. Driver, *University of Florida, Gainesville.*

Carcass and meat palatability characteristics constitute key factors for the success of beef cattle operations. Consumers prefer meat that has desirable levels of tenderness, marbling, juiciness, and flavor. Cattle in the Southern region of the US contain some Brahman to enable them to cope with hot and humid climatic conditions, thus decreasing meat tenderness and affecting the desirability of these animals for branded beef products. The objective of this research was to estimate additive genetic differences between Angus (A) and Brahman (B), heterosis, and least squares means (LSM) for 6 carcass and 6 meat palatability traits for groups of cattle ranging from 100% Angus (A) to 100% Brahman. Carcass traits were hot carcass weight (HCW), dressing percent (DP), ribeye area (REA), fat over the ribeye (FOE), kidney, pelvic and heart fat (KPH), and marbling score (MAB). Meat palatability traits were Warner-Bratzler shear force (WBSF), and tenderness (TEND), connective tissue (CTI), juiciness (JUIC), flavor (FLAV), and off-flavor (OFLAV) scores. Data came from 1367 steers from the Angus-Brahman multibreed herd of the University of Florida collected from 1989 to 2009. Estimates of additive genetic breed differences indicated that B carcasses had higher DP ($P < 0.0001$), lower MAR ($P < 0.0001$), smaller REA ($P < 0.0001$), and less FOE ($P < 0.0001$) than A carcasses. Brahman beef was also tougher ($P < 0.0001$), had more connective tissue ($P < 0.0001$), and it was less juicy ($P < 0.001$) than A beef. Heterosis increased HCW ($P < 0.0001$), DP ($P < 0.017$), REA ($P < 0.0001$), FOE ($P < 0.0001$), and KPH ($P < 0.01$) in crossbred steers. The LSM for HCW, REA, FOE, and KPH increased from A to 1/2 A 1/2 B, and then they decreased toward B. The LSM for MAB, TEND, CTI, and JUIC decreased whereas the LSM for WBSF increased from A to B. Results indicated that crossbred steers with percentage Brahman up to 50% showed limited negative impact on meat quality while maximizing meat yield due to heterosis.

Key words: carcass, meat quality, multibreed

W44 Role of cytoplasmic inheritance on preweaning traits in a closed breeding nucleus Angus herd. J. A. Carrillo* and F. Siewerdt, *University of Maryland, College Park.*

The importance of cytoplasmic inheritance was investigated in an elite Angus herd that has been closed to outside breeding for 70 years. Historical data included full pedigree information on 10,838 animals and phenotypic information (up to 7,986 animals) on body weights collected at birth (WB) and weaning, hock length (HL) at birth and scrotal circumference at weaning (SC). Adjusted body weights to 205 d (W205) were obtained and individual average daily gain from birth to 205 d was also computed. Each animal was traced back to one of 18 founder cows, all from distinct female lineages. Data were analyzed with an animal model that included contemporary group and the random effects of animal, maternal, permanent environment, and cytoplasmic line. The ratios of cytoplasmic variances to phenotypic variances ranged from 0.000 ± 0.002 (WB) to 0.005 ± 0.006 (SC) indicating a very small participation in the determination of genetic and phenotypic variability. In contrast, the much higher genetic maternal variances had ratios to the phenotypic variances ranging from 0.044 ± 0.046 (SC) to 0.156 ± 0.029 (WB) and were typically 50 times higher than the cytoplasmic variances. The observed ranges for cytoplasmic breeding values (BV) for W205, SC, and HL were of 2.62kg, 0.252cm, and 0.053cm, respectively, suggesting that a small but not negligible amount of genetic gain could be amassed by including cytoplasmic BV in the selection index. Selection indexes were computed for all traits individually, with or without inclusion of the cytoplasmic BV. A 20-fold weight on the desired genetic gain was placed on the cytoplasmic BV compared with the direct and maternal BV. Inclusion of the cytoplasmic information in the index reduced the predicted genetic gain in direct and maternal BV by less than 1.5% indicating that this small reduction in genetic gains could be compensated by gains in cytoplasmic BV. Selection for cytoplasmic effects can lead to increased inbreeding by focusing on few maternal lines of animals. Rapid exhaustion of what little cytoplasmic genetic variation is present will happen, unless new variation is created by mutations.

Key words: animal model, quantitative genetics, beef cattle

W45 Heritability and effect of breed and diet on complementary feed utilization traits in Simmental, Angus and crossbred steers. N. V. L. Serão*[1], J. E. Beever[1], D. B. Faulkner[1], M. Pérez-Enciso[2], and S. L. Rodríguez-Zas[1], *[1]University of Illinois at Urbana-Champaign, Urbana, [2]Universitat Autònoma de Barcelona, Barcelona, Catalonia, Spain.*

Phenotypic data from 1,488 steers were used to estimate genetic parameters for average daily gain (ADG), dry matter intake (DMI), gain to feed (GF), residual feed intake (RFI), residual average daily gain (RADG), carcass backfat (BF) and rib-eye area (REA). RADG

was adjusted for DMI and mid-test metabolic weight (MMW), whereas RFI was adjusted for ADG and MMW. All analyzes were carried out using Qxpak v 5.03, with an animal model including the pedigree (3,786 animals), the fixed effects of breed (5 levels; Angus (AN), 3/4 AN, 1/2 AN 1/2 Simmental (SM), 3/4 SM and SM), diet (5 levels), breed- diet interaction, days on feed (covariate) and the random effect of harvest group within contemporary group (32 levels). The heritabilities were estimated using maximum likelihood and fixed effects were considered significant at 0.05. ADG presented low heritability estimate ($h^2 < 0.20$), whereas GF, RADG and REA showed moderate estimates ($0.20 < h^2 < 0.40$) and DMI, RFI and BF presented high heritabilities ($h^2 > 0.40$). Breed-diet interaction was significant for BF, REA and RFI. The main effect of diet was significant for RADG and GF, and the main effect of breed was significant for ADG and DMI. The heritability of RADG ($h^2 = 0.30$) was higher than that for ADG ($h^2 = 0.16$). This suggests that genetic selection for RADG would result in higher genetic improvement than for ADG in this population, since the adjustments for DMI and MMW decrease the phenotypic variation of the trait. In contrast, RFI showed a similar heritability to DMI, respectively $h^2 = 0.43$ and $h^2 = 0.42$, suggesting that the adjustment for ADG and MMW did not offer major gains in estimating the heritability in this population. Although the selection for either trait may result in similar genetic gains, RFI represent a more suitable indicator of feed efficiency than DMI. Finally, the estimates for RADG and RFI indicate that, for the population studied, selection based on intake-based indicators is expected to result in superior genetic improvement for feed utilization than selection based on gain-based indicators with lower undesirable increase in body weight.

Key words: genetic parameters, RADG, RFI

W46 Comparison of body weight genetic evaluation accuracy by random regression with splines and multi-trait model in Limousins. M. Lukaszewicz*[1,2], I. Misztal[1], A. H. Nelson[1], J. P. Sánchez[1], and J. K. Bertrand[1], *[1]University of Georgia, Athens, [2]Institute of Genetics and Animal Breeding, Jastrzebiec, Poland.*

This study compared multibreed EPDs obtained by multi-trait (MT) and random regression (RRS) models. RRS allows using weight records outside standard ranges in MT but EPDs by RRS may contain artifacts. The data on birth (BW), weaning (WW), and yearling (YW) weights were provided by the North American Limousin Foundation. After editing, data comprised 1,382,305 BW; 986,777 WW; and 412,977 YW RRS-analysis-ready records. Both models fit direct and maternal additive genetic, contemporary group, animal's age, direct and maternal heterosis effects, and direct and maternal additive genetic means of the breed effects. The RRS fit additionally the direct permanent environment effect. WW and YW record numbers in MT were 94% and 93% of those in RRS. The validity of using RRS was assessed by correlating EPDs from both methods. Correlations between BW direct EPDs, computed on all animals, were 0.99 in both sexes. They dropped to 0.95–0.97 for the later weights. For maternal EPDs the correlations for BW and WW were 0.95 and 0.90 in bulls and 0.96 and 0.92 in cows. In bulls with the RRS EPD accuracy > 0.6 for given trait, the correlations between BW, WW, and YW EPDs for direct effect increased to 1, 0.98, and 0.98 while those between maternal EPDs to 0.99 and 0.96, for BW and WW. For bulls with accuracy < 0.6 under MT and > 0.6 under RRS (for each trait at a time) the correlations between direct EPDs were 0.99, 0.97, and 0.97. For cows with accuracy < 0.45 under MT and > 0.45 under RRS (for each trait at a time) the correlations between direct EPDs were 0.99, 0.93 and 0.91 for BW, WW, and YW while between maternal EPDs 0.71 and 0.86, for BW and WW. When few additional records are available for RRS, RRS and MT provide nearly identical EPD for most animals. Most changes are for animals with additional information beyond that possible with MT.

Key words: body weight EPD accuracy, multi-trait vs. random regression, Limousin

W47 Growth curves for buffaloes (*Bubalus bubalis*) using random regression mixed models with different structures of residual variances. D. M. Bolivar[1,2], M. F. Cerón-Muñoz[2], M. A. Elzo*[3], E. J. Ramirez[2], and D. A. Agudelo[4], *[1]National University of Colombia, Medellin, Colombia, [2]University of Antioquia, Medellin, Colombia, [3]University of Florida, Gainesville, [4]Lasallian University Corporation, Caldas, Colombia.*

The objective of this study was to analyze buffalo growth based on body weight (BW), Longissimus dorsi muscle area (AOL), and fat deposition over the hip (FOH) using random regression mixed models of first (FORRM) and second order (SORRM), each with 9 different variance structures. Ten measurements for each trait were taken on 26 animals during the first performance test (93 d test plus 23 d adaptation period) developed for buffaloes in Colombia. Computations were performed using the lme procedure of the nlme library of program R. Preliminary analyses determined that an SORRM was appropriate for BW and FOH and an FORRM was suitable for AOL. The maximum likelihood ratio (MLR), the Akaike information criterion (AIC) and the Bayesian information criterion (BIC) were used to compare models. The best models were an SORRM with homogeneous residual variances for BW, an FORRM with heterogeneous animal residual variances for AOL, and an SORRM with heterogeneous residual variances among farms times an exponential function of age for FOH. Heterogeneity of residual variances was likely due to environmental differences among farms, and to genetic differences among buffaloes not accounted for by FORRM and SORRM. Fixed intercepts with the best models for each trait were 227 ± 7.90 kg for BW, 34.82 ± 0.99 cm2 for AOL, and 4.19 ± 0.229 mm for FOH. Fixe linear regression coefficients were 1.289 ± 0.073 g/d for BW, 0.0584 ± 0.0042 cm2/d for AOL, and 0.0035 ± 0.0032 mm/d for FOH. The fixed quadratic regression coefficient indicated that BW rate decreased after one year of age whereas FOH rate continued to increase until the end of the test. Random regression coefficients suggested that there was considerable variability among trait curves for individual buffaloes, particularly for FOH.

Key words: buffalo, growth curve, performance test

W48 Estimates of genetic and phenotypic trends for body weight traits of Zandi sheep obtained by a univariate and multivariate animal model analysis. H. Mohammadi* and M. Moradi Shahrebabak, *Department of Animal Science, University College of Agriculture and Natural Resources, University of Tehran, Karaj, Tehran, Iran.*

The objective of the present study was to estimate genetic changes for body weights at different ages in Zandi sheep. Traits included were birth weight (BW, n = 8366), 3 mo weight (3MW, n = 6360), 6 mo weight (6MW, n = 4350), 9 mo weight (9MW, n = 2890), and yearling weight (YW, n = 2430). The data and pedigree information used in the current research were collected at the Breeding Station of Zandi sheep (Tehran province, Iran) during 1991–2007. Variance components were estimated from a 5-trait analysis, based on the best model of analysis

for each trait, using the ASReml program. The final model included the fixed effects of year-season, sex of lamb and parity of dam, birth type, and the linear covariate effect of age of dam 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 genetic trends were obtained by regressing the means of predicted breeding values on year of birth for each trait. Direct genetic trends were positive and significant ($P < 0.05$). The additive genetic trends for BW, WW, 6MW, 9MW, and YW using univariate and multivariate analysis were estimated 2.1 and 3.9, 98.5 and 106.28, 89.63 and 95.47, 26.35 and 32.22, 41.53 and 49.83 g/year, respectively. Also, maternal genetic trend for BW was 5.40 and 4.92 g/year. The phenotypic trends for traits were estimated −8.5 and −8.9, −422.2 and −427.2, −90.60 and 90.53, −357.1 and −359.2, −133.32 and −134.31 g/year, respectively. The environmental trends for traits were −11 and −11.5, −444 and −447, −387 and −395, −212 and −215, −296 and −302 g/year, respectively. The results showed that improvement of body weights of Zandi sheep seems feasible in selection programs.

Key words: Zandi sheep, growth traits, genetic and phenotypic trends

W49 Genetic and phenotypic correlations between reproduction and production traits in Zandi sheep. H. Mohammadi* and M. Moradi Shahrebabak, *Department of Animal Science, University College of Agriculture and Natural Resources, University of Tehran, Karaj, Tehran, Iran.*

The objective of this study was to estimate heritabilities and genetic and phenotypic correlations among production and reproduction traits over 4 parities in the Zandi sheep to formulate a breeding plan for this breed. Genetic and phenotypic correlations were estimated between production and reproduction traits in a flock of Zandi sheep reared at the Khojir Research Station by ASREML procedures using bivariate mixed models, included fixed effects (year of mating and age of ewe; for BW traits, additionally sex of lamb; for weaning weight (WW), additionally number of d to weaning as a covariate) and random effects of animal direct genetic, permanent environment (repeated records of ewes) and residual. Production traits investigated were birth weight (BW) and WW, and reproduction traits, including 2 basic and 2 composite traits. The basic traits were conception rate (CR) and total number of lamb born (NLB).The composite traits were total litter weight at birth per ewe lambing (TLWB/EL) and total litter weight at weaning per ewe lambing (TLWW/EL). Direct additive estimates of heritability (h2 ± S.E.) were: 0.24 ± 0.03; 0.26 ± 0.02; 0.05 ± 0.02; 0.14 ± 0.02; 0.11 ± 0.02; 0.10 ± 0.02; for BW, WW, CR, NLB, TLWB/EL and TLWW/EL, respectively. Estimates of the direct genetic and phenotypic correlations between the reproductive and growth traits are shown in Table 1. Genetic correlation estimates between the investigated traits ranged from −0.05 for BW–CR to 0.45 for WW–TLWW/EL. Phenotypic correlations ranged from 0.03 for BW–CR to 0.19 for WW–TLWW/EL. This study provides estimates of genetic correlations that will improve the accuracy of genetic evaluation and prediction of the outcomes from breeding programs for meat objective that include reproduction.

Table 1. Estimates of genetic and phenotypic correlations (±SE) between reproductive and growth traits in Zandi ewe

Genetic correlations	CR	NLB	TLWB/EL	TLWW/EL
BW	–0.05 ± 0.07	0.24 ± 0.10	0.35 ± 0.06	0.13 ± 0.06
WW	0.10 ± 0.04	0.16 ± 0.08	0.23 ± 0.05	0.45 ± 0.07
Phenotypic correlations				
BW	0.03 ± 0.02	0.07 ± 0.01	0.09 ± 0.05	0.05 ± 0.06
WW	0.07 ± 0.02	0.03 ± 0.02	0.09 ± 0.06	0.19 ± 0.06

Key words: covariance components, composite reproductive traits, growth traits

W50 Estimation of genetic trend for some reproductive traits in Zandi sheep breed. H. Mohammadi* and M. Moradi Shahrebabak, *Department of Animal Science, University College of Agriculture and Natural Resources, University of Tehran, Karaj, Tehran, Iran.*

Knowledge of genetic parameters and trends is necessary to optimize animal breeding schemes. An estimate of the genetic progress achieved by selection programs is necessary to describe the genetic changes progress, to assess the benefits of the selection program and to introduce necessary adjustments. The aim of this study was to estimate genetic parameters and genetic trends of reproductive traits. Genetic parameters from both single-trait and bivariate analyses for reproductive traits were estimated using REML with animal models for Zandi sheep from data collected from 1991 to 2007 at the Breeding Station of Zandi sheep in Tehran province, Iran. Traits included were litter size (LS, n = 5025), litter mean weight per lamb born (LMWLB, n = 4338), litter mean weight per lamb weaned (LMWLW, n = 4172), total litter weight at birth (TLWB, n = 4338) and total litter weight at weaning (TLWW, n = 4172). Estimates of heritability with ASREML software analyses were 0.05 for LS, 0.13 for LMWLB, 0.08 for LMWLB, 0.11 for TLWB, and 0.10 for TLWW. The genetic trends were calculated by regression of the average predicted genetic values per year for each trait versus the dam year of birth. Estimated genetic trends of LS, LMWLB, LMWLW, TLWB and TLWW were −0.001, 0.02, 0.013, 0.023 and 0.26, respectively. From 1991 to 2007, average estimates of breeding values from the multiple-trait analysis increased at a greater rate than average estimates from the single-trait analysis. The rate of yearly genetic improvement was very small for LS, LMWLB, LMWLW, and TLWB traits. However, the reproductive traits of Zandi breed may still be improved by selection. Positive genetic correlations between reproductive traits and growth traits showed that simultaneous genetic improvement of the traits may be possible.

Key words: genetic trends, reproductive traits, Zandi sheep

W51 Estimates of genetic and phenotypic trends for body weight traits of Zel sheep obtained by univariate and multivariate animal model analysis. H. Mohammadi* and M. Sadeghi, *Department of Animal Science, University College of Agriculture and Natural Resources, University of Tehran, Karaj, Tehran, Iran.*

The objective of the present study was to estimate genetic trends for body weight traits at different ages in Zel sheep. Traits included were birth weight (n = 10723), 3 mo weight (n = 8108) and 6 mo weight (n = 5236). The data and pedigree information used in the current research were collected by Jahad-e-Keshavarzi organization (Mazandaran province, Iran) during 1994–2009. Variance components were

estimated from a 3-trait analysis, based on the best model of analysis for each trait, using the ASREML software. The final model included the fixed class effects of year-season, sex of lamb and parity of dam, birth type, the linear covariate effect of age of dam 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 genetic trends were obtained by regressing the means of predicted breeding values on year of birth for each trait. Direct genetic trends were positive and significant for BW, WW and 6MW ($P < 0.05$). The direct genetic trends for BW, WW, and 6MW using univariate and multivariate analysis were estimated 1.90 ± 0.07 and 2.53 ± 1.1, 98.5 ± 10.4 and 105.38 ± 25.2, 73.23 ± 21.2 and 78.46 ± 33.40 g per year, respectively. The maternal genetic trend for BW was 2.94 ± 1.21 and 3.07 ± 2.49 g per year. The phenotypic trends for traits were estimated −6.5 ± 22.60 and −6.9 ± 22.50,-152.2 ± 251 and −147.2 ± 239, −100.60 ± 48 and 100.53 ± 45 g per year, respectively. The environmental trends, measured as the difference between phenotypic and genetic trends, were −21.1 ± 0.02 and −21.5 ± 0.05, −244 ± 16 and −247 ± 19, −287 ± 30 and −295 ± 26 g per year, respectively. Negative phenotypic and environmental trends could be due to bad environmental conditions, especially to nutrition of the sheep in an unsuitable climate during the study years.

Key words: Zel sheep, growth traits, genetic and phenotypic trends

Breeding and Genetics: Genomic Selection and Whole-Genome Association

W52 Accuracy and bias of multiple-trait genomic evaluations for linear type traits in US Holsteins. S. Tsuruta*[1], I. Misztal[1], I. Aguilar[2], and T. Lawlor[3], *[1]University of Georgia, Athens, [2]Instituto Nacional de Investigación Agropecuaria, La Piedras, Canelones, Uruguay, [3]Holstein Association USA Inc., Brattleboro, VT.*

The objectives of this study were to conduct multiple-trait (MT) genomic evaluations and to compare bias and accuracy of genomic breeding values (GBV) with those from single-trait (ST) genomic evaluations, using different genomic relationship matrices (G). Genomic evaluations were conducted for 18 linear type traits of US Holsteins using genomic and phenotypic combined data. For each of 6931 bulls, 38,416 SNP markers were used as genomic information. A single-step approach was used to predict GBV with G that assumed various allele frequencies: equal (p = q = 0.5) (GE), base (GB), current (GC), and current with scaled G (GCS). Data sets contained 8,865,120 records for 5,657,787 cows from 2009 data and 7,715,925 records for 4,813,726 cows from 2004 data. Coefficients of determination (R^2) and regressions (δ) of 2004 GBV on 2009 daughter deviations were calculated, as statistics of accuracy and bias, respectively, for 1307 young bulls. Parent averages (PA) were also calculated for 2004 data with no genomic information. With MT (ST) models, average R^2 (%) were 20.5 (18.6) and 37.9 (34.6), 37.3 (34.1), 35.9 (34.2) and 37.7 (34.5), and average δ (× 100) were 76.7 (77.3) and 79.8 (79.4), 76.3 (75.0), 74.7 (73.8) and 76.7 (76.2), for PA and for GBV with GE, GB, GC and GCS, respectively. When the weight for the inverse of the numerator relationship matrix for genotyped animals was reduced to 0.7, R^2 remained almost identical while the average δ increased to 92.7 with GE, 90.7 with GB, 89.2 with GC, and 91.9 with GCS for MT models. The ST models required a stricter convergence criterion of 10^{-14} than that of 10^{-11} for MT models to achieve the same accuracy. The GBV obtained from MT models are more accurate than those from ST models. Modifying the weight for pedigree relationships of genotyped animals reduces bias in GBV. Multiple trait large-scale genomic evaluation is computationally feasible.

Key words: genomic evaluation, linear type trait, US Holstein

W53 Genomic imputation and evaluation using 342 high-density Holstein genotypes. P. M. VanRaden[1], D. J. Null*[1], G. R. Wiggans[1], T. S. Sonstegard[2], and E. E. Connor[2], *[1]Animal Improvement Programs Laboratory, ARS, USDA, Beltsville, MD, [2]Bovine Functional Genomics Laboratory, ARS, USDA, Beltsville, MD.*

Genomic evaluations for 73,749 Holsteins were computed using 636,967 of the 777,000 markers on the Illumina high density (HD) chip. Observed data included 342 animals with HD genotypes, 54,676 animals with 42,503 marker (50K) genotypes, 17,371 animals with 2,614 marker (3K) genotypes, and 1,360 nongenotyped dams (0K) with >90% of haplotypes imputable from progeny. The HD genotypes were from 180 influential sires, 138 Beltsville research cows, and 24 other females. Percentages of correctly imputed genotypes were estimated using an example simulated chromosome for this same population structure with 1% of genotypes missing and 0.02% incorrect initially from each chip. Over all animals, 94.4% of genotypes were missing initially. After imputation of missing markers, 99.9% of genotypes were correct from HD, 98.0% from 50K, 88.4% from 3K, and 93.8% from 0K genotypes. These imputation rates with version 2 of program findhap.f90 are several percent higher than with version 1. Version 2 begins with long segments to improve haplotype matches for close relatives and ends with short segments to detect matches from more remote ancestors instead of choosing just one optimal segment length. Evaluations were tested using imputation of actual genotypes and August 2007 phenotypes to predict deregressed evaluations of bulls proven after August 2007. For 29 traits tested, estimated genomic reliability averaged 54.3% using 636,967 markers vs. 54.8% using 42,503 regressions vs. 29.9% from traditional parent average. Squared correlations with future data were higher for 10 traits and lower for 19 with HD than with 50K evaluations. The largest marker effects were located at very similar positions, but new markers from the HD chip often had larger effects than the best markers from the 50K chip. Results were less favorable than the 1.6% increase in reliability expected from simulation, but more animals with HD genotypes will improve imputation and reliability. Also, multi-breed evaluation could produce larger gains than the single-breed evaluation investigated here.

Key words: genomic evaluation, imputation, marker density

W54 Genomic evaluation of Angus-Brahman multibreed cattle for feed efficiency and postweaning growth using the Illumina 3k chip. M. A. Elzo*[1], G. C. Lamb[2], D. D. Johnson[1], M. G. Thomas[3], I. Misztal[4], D. O. Rae[1], J. G. Wasdin[1], and J. D. Driver[1], *[1]University of Florida, Gainesville, [2]North Florida Research and Education Center, Marianna, [3]New Mexico State University, Las Cruces, [4]University of Georgia, Athens.*

Lower density chips provide an affordable alternative to evaluate animals and characterize traits. The objective of this research was to evaluate 620 bulls, steers, and heifers ranging from 100% Angus to 100% Brahman (B) using phenotypes from for 4 postweaning feed efficiency and growth traits, pedigree, and SNP genotypes from 2900 loci (Illumina3k chip). Traits were residual feed intake (RFI), daily feed intake (DFI), feed conversion ratio (FCR), and weight gain (WG). Data was collected in a GrowSafe automated feeding facility from 2006 to 2010. Calves remained in pens for the 21-d pre-trial and 70-d trial periods. Animals were assigned to pens by sire group and sex. Concentrate consisted of cottonseed hulls, corn, molasses, and a protein, vitamin, and mineral supplement. Calves were evaluated using a polygenic-genomic mixed model. Fixed effects were contemporary group (year-pen), age of dam, sex of calf, age of calf, B fraction of calf, and heterozygosity of calf. Random effects were animal polygenic (AP; mean zero; variance = A*Vg; A = additive relationship matrix, Vg = additive genetic variance), additive SNP (AS; mean zero; variance = additive SNP variance), and residual effects (mean zero, common residual variance). Variance components and heritabilities were estimated using option VCE (Markov Chain Monte Carlo) of program GS3. Heritabilities were 0.18 for RFI, 0.30 for DFI, 0.16 for FCR, and 0.33 for PWG. The fraction of the additive genetic variance explained by the 2900 markers of the Illumina3k chip was 15% for RFI, 11% for DFI, 37% for FCR, and 20% for PWG. The AS, AP, and TA EBV for all traits tended to decrease as B fraction increased, suggesting that high percent B calves were genetically more efficient (lower RFI), but had lower WG.

Key words: feed efficiency, genomic, multibreed

W55 A neural network approach for association between a low-density whole genome SNP marker panel for 19 traits in beef

cattle. E. Hay*[1], 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, back fat, carcass weight, rib eye area, yearling weight, and heifer pregnancy rate was evaluated for 19 traits (residual feed, intake, dry matter intake, birth weight, weaning weight, docility, milk yield, average daily gain, yearling weight, carcass weight, marbling scores, rib eye area, back fat, mature weight and height, scrotal circumference, calving ease direct, calving ease maternal, heifer pregnancy). Data consisted of the genotypes of 2,245 Angus animals and their corresponding EPDs with missing rate (on phenotypes) ranging from 0 to 54% (heifer pregnancy). 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 both approaches, the lowest correlation between true and estimated breeding values was for docility and (0.52) and scrotal circumference (0.57). The highest accuracy was for yearling weight (0.82 for LR and 0.83 for NN). Across the 19 traits, the differences in performance between LR and NN range from 2 to 5% with superiority for the NN approach, except for weaning weight where the LR was slightly superior (0.27%), 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, beef cattle

W56 Whole genome association analyses for ultrasound and carcass merit traits in beef cattle. H. Li*, Z. Wang, P. Stothard, and S. S. Moore, *University of Alberta, Edmonton, Alberta, Canada.*

Carcass merit traits in beef cattle are of high interest in the beef industry and are quantitative in nature. The goal of this study was to identify genetic markers and potential candidate genes associated with meat quality traits in beef cattle. A genome-wide association study (GWAS) for 40,809 single-nucleotide polymorphism (SNP) markers using Bayesian methods was conducted in a total of 922 steers. Five carcass merit traits including carcass weight (CWT), carcass average backfat (CABF), carcass rib eye area (CREA), carcass grade fat (CGF), carcass lean meat yield (CLMY) and 3 ultrasound measurement traits including ultrasound marbling (UMAR), ultrasound backfat (UBF) and ultrasound ribeye area (UREA) were analyzed. The proportion of phenotypic variance explained by markers was 0.50 for CWT, 0.25 for CABF, 0.37 for CREA, 0.27 for CGF, 0.24 for CLMY, 0.39 for UBF, 0.63 for UMAR and 0.37 for UREA. SNPs with large substitution effects indicated that major genes exist for meat quality traits in beef cattle. For instance, the largest SNP on BTA6 explained 6.67% of the phenotypic variance for CWT. Many of the large effect SNPs coincided with previously identified QTL. Positional candidate genes (e.g., 49 for CWT) were identified within 1 Mbp windows flanking the top 10 SNP markers. Potential functional genes (e.g., *NCAPG*, *MED28* on BTA6 and *LYN* on BTA14 for CWT) were selected from these positional genes based on predicted and known functional information associated with the genes or their orthologs. Overall, this WGAS provides a list of markers and potential functional candidate genes associated with beef carcass merit traits that could be used to improve beef production and quality via marker-assisted selection.

Key words: beef cattle, genome-wide association study, carcass merit

W57 Large-scale SNP association analyses for somatic cell score in Canadian Holstein cattle. H. Li*[1], Z. Wang[1], F. S. Schenkel[2], M. Sargolzaei[3], S. S. Moore[1], and P. Stothard[1], *[1]University of Alberta, Edmonton, Alberta, Canada, [2]University of Guelph, Guelph, Ontario, Canada, [3]L'Alliance Boviteq, Saint-Hyacinthe, Québec, Canada.*

Genetic studies in dairy cattle have found that selection for higher milk production brings with it slightly higher rates of mastitis. Mastitis is the most common and most costly disease of dairy cattle and there are no affordable or prevailing methods for directly measuring mastitis. Somatic cell score (SCS) is an excellent indirect trait for selection for mastitis as the genetic correlation between SCS and mastitis is 60% to 80%. The goal of this study was to identify genetic markers and potential candidate genes associated with SCS in dairy cattle. A genome-wide association study for 29,552 single-nucleotide polymorphism (SNP) markers was conducted in a total of 647 Canadian Holstein bulls. The analyses used a combination of Bayesian models to predict individual SNP effects. The proportion of the variance of the bulls' deregressed SCS EBVs explained by markers was 0.76. SNPs with large substitution effects indicated that major genes exist for SCS. The10 SNPs with largest effects were on BTA6, 14, 21, 18, and 19. Many of the large-effect SNPs coincided with previously identified QTL. One hundred and 32 positional candidate genes were identified within 2 Mbp genomic regions flanking the top 10 SNPs. Potential functional genes (e.g., GC and NPFFR2 on BTA6, LY6D on BTA14, MFGE8 and AP3S2 on BTA21, and FOXL1, CYLD and NOD2 on BTA18) were selected from these positional genes based on predicted and known functional information associated with the genes or their orthologs. Functional annotation revealed that these genes are involved in the regulation of immune system activity and inflammation. For instance, the CYLD gene on BTA18 is a crucial negative regulator of inflammation and subsequent immune response in antibacterial defense. This finding reinforces the role of the genetic control on immune response to bacterial infections. The list of SNPs and potential functional candidate genes may prove useful for prevention of mastitis via marker-assisted selection.

Key words: Holstein cattle, genome-wide association study, somatic cell score

W58 Comparison of selective genotyping strategies for prediction of breeding values in a population undergoing selection. A. A. Boligon*[1,2], N. Long[2], L. G. Albuquerque[1], K. A. Weigel[3], D. Gianola[2,3], and G. J. M. Rosa[2], *[1]Department of Animal Sciences, Sao Paulo State University, Jaboticabal, SP, Brazil, [2]Department of Animal Sciences, University of Wisconsin, Madison, [3]Department of Dairy Science, University of Wisconsin, Madison.*

A simulation study was used to evaluate the predictive ability of genomic selection under different strategies of selective genotyping. The genome consisted of 10 chromosomes, each with 202 markers and 100 QTLs evenly spread across 100 cM. After 5,000 generations of random mating with an effective population size of 100 (50 males

and 50 females), a reference population (G0) was generated by a full factorial mating between the 50 males and 50 females. In G0 animals were selected based on their phenotypes (highest phenotypic values) or at random, at different selection intensities, to produce generation G1. Five genotyping strategies were considered to choose 500 animals in G0 as a training set: random sampling (R); highest phenotypic values (H); lowest phenotypic values (L); extreme (low and high) phenotypic values (E); and subset of less related animals (I). The number of individuals in G0 and G1 was fixed at 2,500, and heritability was set to 0.10, 0.25 and 0.50. Additionally, all 5 genotyping strategies were applied also to an indicator trait with a genetic correlation of 0.5 with the target trait. The selective genotyping strategies were compared in terms of their ability of predicting the genetic values of the animals in G1, using a Bayesian Lasso model with all 2020 markers simultaneously. For all simulated traits, the lowest correlation between predicted and true breeding values (GEBV and TBV, respectively) was obtained when using the L genotyping strategy. For E, R, and I strategies, the correlation between GEBV and TBV became slightly higher as selection intensity decreased, and was largest when no selection occurred. These 3 strategies were better than H. In addition, the E, R, and I approaches had lower prediction mean squared errors (PMSE), followed by H and then by L. Overall, genotyping strategy E led to the best predictive ability of breeding values, indicating that animals with extreme phenotypic values in a reference population are the most informative when training genomic selection models.

Key words: Bayesian Lasso, molecular markers, predictive ability

W59 Estimating genomic breeding values in crossbred animals. E. H. Hay*, S. Smith, and R. Rekaya, *University of Georgia, Athens.*

For several livestock species and traits, the accuracies of predicted molecular breeding values are significantly higher than those obtained using parent averages and similar to those obtained for proven animals. These exciting results are unfortunately valid only when animals of the same breed are used in the training and validation sets. Unfortunately, in several applications admixture and crossbred animals are present making the training and validation sets very heterogeneous. Several studies have shown that using SNP estimates from pure breeds on other breeds or crossbred animals have little success. Alternative solutions using different mixture of animals (pure breeds, crossbreds) in training and validation sets were proposed with promising results in some cases. In this study a different approach is adopted where estimates of SNP effects in pure breeds are used to predict molecular breeding values in crossbred animals via the projection of these effects based on the percentage contribution of each pure breed in the crossbred individual. To test the performance of the proposed procedure, a simulation was conducted involving 2 breeds (A and B) with 1,500 animals each and 3 crosses 50/50, 75/25, and 25/75% of A and B breeds, respectively. Genotypes for a low density panel of 384 SNPs were also simulated for all animals without missing. Four analyses were conducted for estimating the SNP effects: 1) using only data from breed A, 2) using only data from breed B, 3) used data from breeds A and B, and 4) using data from A, B and the crossbreds. The results indicated that estimating SNP effects in analysis 4 led to the highest accuracies in crossbreds compared with the other 3 alternatives. However, when our approach was used based on the projection of the SNP estimates from analyses 1 and 2 as a function of the breed composition of the crossbreds, the best results were obtained. In fact, the accuracies in crossbreds increased by 28% compared with the results obtained in analysis 4. Based on this results, it seems that there a possibility of using pure bred estimates of SNP marker effects to predict the molecular breeding values of some crossbred animals.

Key words: genomic, SNP, crossbreds

W60 Accounting for new mutations in the genomic relationship matrix. J. Casellas*, *G2R, Departament de Ciència Animal i dels Aliments, Universitat Autònoma de Barcelona, Bellaterra, Spain.*

In this abstract, procedures for calculating the genomic relationship matrix are adapted to accommodate the occurrence of new mutations in the autosomal genome, i.e., the mutational genomic relationship (G_m) matrix. These algorithms derived from the original development by N. R. Wray for the additive numerator relationship matrix and accommodated genomic data from massive genotyping technologies. Assume as starting point g non-overlapping generations with n individuals per generation, all of them being genotyped for m single nucleotide polymorphism (SNP) markers spread across the whole autosomal genome. Moreover, assume $p_{k(l)}$ as the allelic frequency of the kth SNP in the lth generation and $\pi_{k(l)} = 2(p_{k(l)}\text{-}0.5)$ as a correcting factor to set mean values of allele effects to 0; the genotype of the ith individual at the kth SNP (γ_{ik}) was assumed as −1, 0 or 1 (i.e., homozygote, heterozygote and other homozygote, respectively). The general structure of the G_m matrix can be defined as $G_m = G_1 + G_2 + \ldots + G_g$, G_q being a genomic relationship matrix where individuals from generation q were treated as founders and the rows and columns linked to ancestors from previous generations were fixed to 0. To avoid the successive computation of all intermediate G_q matrices, the final mutational genomic relationship between individuals i and j (ρ_{ij}; i being older than j) reduced to the following expression $\rho_{ij} = \sum_{0>r>m}\sum_{0>s>g^*}[(\gamma_{ir} - \pi_{r(s)})(\gamma_{jr} - \pi_{r(s)})]/[2\sum_{0>q>m}p_{q(s)}(1 - p_{q(s)})]$, where g^* was the generation of origin of individual i. This matrix could be straightforwardly implemented within the structure of the genomic BLUP model in order to account for the genetic variability originated from young mutations.

Key words: genomic relationship, matrix, mutation

Dairy Foods: Cheese

W61 Effect of the use of rennet substitute on composition and yield of Minas Padrão cheese. J. Camisa[1], S. T. Di Cicco[1], K. Sivieri[2], P. C. B. Vianna*[1], and C. M. V. B. De Rensis[1], *[1]UNOPAR, Londrina, PR, Brazil, [2]UNESP, Araraquara, SP, Brazil.*

The objective of this research was to determine the effect of the use of rennet substitute on composition and yield of Minas Padrão cheese. Pasteurized and standardized milk (3.0% fat) was divided into 2 parts and prepared for each treatment varying the rennet: batch 1(BOV), commercial calf rennet (Chymosin and pepsin) and batch 2 (QPF), commercial rennet substitute Chy-max (Chymosin) and converted to cheese following traditional cheese making procedure. Milk, whey and cheese compositions were determined according official methods. Fat and protein recoveries and yield were determined. Differences on the rennet had no significant influence ($P > 0.05$) on chemical composition of the cheeses. Cheeses made with QPF and BOV showed no significant difference on fat and protein recoveries but QPF showed tendency for higher fat and protein recoveries. The use of Chy-max showed no significant influence on cheese actual yield. The adjusted yield also showed no significant difference with the use of Chy-max, although it had a tendency of increase yield with the rennet substitute.

Key words: calf rennet, chymosin, fat and protein recoveries

W62 Effects of gelation temperature and cutting time on the rheology and quality of curd made from buffalo milk: A comparison with cows' milk. I. Hussain*, J. Yan, A. E. Bell, and A. S. Grandison, *Department of Food and Nutritional Sciences, University of Reading, Reading, Berkshire, UK.*

The rheology and overall quality of curds made from buffalo and cows' milks were measured at gelation temperatures of 28, 34 and 39°C, and cutting times of 45, 60, 75 and 90 min after chymosin addition. The maximum curd firmness (G′) was obtained at a gelation temperature of 34°C in both types of bovine milk. The viscoelasticity (Tan δ) of both curds were increased with the increasing gelation temperature. The rennet coagulation time was reduced with increase of gelation temperature in both types of milk. Frequency sweep (0.1–10 Hz) was used 90 min after of chymosin addition, and both milk samples showed characteristics of weak viscoelastic gel systems. When both milk samples were subjected to shear stress to break the curd system at constant shear rate, 95 min after chymosin addition, the maximum yield stress was obtained at the gelation temperatures of 34°C and 28°C in buffalo and cows' curd respectively. The curd yield and moisture content were decreased with the increase in gelation temperature, while whey fat losses increased. The different cutting times slightly affected the yield and overall quality of curds made from both milk types. Two different curd drainage methods were used to compare the final overall curd quality.

Key words: rheology, gelation temperature, cutting time

W63 Cheese making properties of milk protein concentrate powder as affected by storage at high temperature. N. Rémillard and M. Britten*, *Food Research and Development Centre, Agriculture and Agri-Food Canada, St-Hyacinthe, (QC), Canada.*

Milk protein concentrate is extensively used to fortify cheese milk and increase cheese plant productivity. Long-term storage is known to alter the physicochemical properties of spray dried protein ingredients and might reduce their ability to produce high quality cheeses. To accelerate the storage effect, spray dried milk protein concentrate was stored at 50°C for up to 28 d. After various storage periods, the powder was dispersed in water and characterized for solubility, average particle size, rheology (flow curves) and kinetics of rennet gel formation. Model cheeses were also produced from milk standardized to 3.0% casein and 4.4% milk fat. The casein fraction originating from milk protein concentrate was fixed to 25%. Cheese composition, yield, protein and fat retention coefficients were determined. The solubility of milk protein concentrate decreased during storage at 50°C. Solubility loss averaged 1.8% per day. Casein micelles showed evidence of aggregation with average particle diameter increasing from 200 to 800 nm after 28 days. With increasing storage time, lower flow index and higher consistency were measured on milk protein dispersions. Rennet clotting time was increased and gelation rate was reduced after 7 days storage. These changes are explained by the adsorption of whey protein to casein micelles during storage. Long-term storage of milk protein concentrate slightly increased protein retention in cheese but also increased fat losses in whey, resulting in reduced cheese yield. This study suggests that during the storage of milk protein concentrate powders, mixed aggregates can form between casein micelles and whey proteins, which act as passive fillers and interfere with cheese matrix formation.

Key words: milk protein powder, storage, cheese

W64 Influence of different cheese matrix structures on lipid digestion in a simulated gastro-intestinal environment. S. Lamothe[1], M.-M. Corbeil[1], S. Turgeon[2], and M. Britten*[1], *[1]Food Research and Development Centre, Agriculture and Agri-Food Canada, St-Hyacinthe, (QC), Canada, [2]Dairy Research Centre STELA, Faculty of Agriculture and Food Science, Université Laval, Quebec, (QC), Canada.*

In normal individuals, lipid digestion and absorption are highly efficient processes but in diseases such as short gut, cystic fibrosis and pancreatic deficiencies, the bioavailability of lipids is greatly reduced. Hence, it could be relevant to increase bioavailability of ingested lipids. On the other hand, it could be advantageous to reduce lipid bioavailability for populations with high blood lipid levels and at a high risk of cardiovascular disease and obesity. The objective of this study was to compare the kinetics of fatty acids release and matrix degradation of different cheeses in a gastro-intestinal environment. The relation between physical characteristics of the cheeses (microstructure, texture) and matrix degradation during simulated digestion was also studied. Compositional analysis, rheological measurements and microstructure by SEM were measured on mild cheddar, aged cheddar, light cheddar and mozzarella cheese. Cheese (4.5 g) was cut into small cubes and submitted to simulated digestion. Matrix degradation index, free oil, free fatty acids and microstructure by optical microscopy were analyzed on chime after 5, 30, 60, 120, 150, 180 and 240 min digestion. Fatty acids release kinetics varied markedly according to the type of cheese. Mozzarella showed higher rate and extent of fatty acids release compared with other cheeses. This was paralleled by a greater rate of matrix degradation and amount of free oil. This result could be attributed to the higher moisture content of mozzarella cheese combined with the lower mineral content that weakened the protein network, as shown by a decrease of the firmness, elasticity and cohesiveness. Rate and concentration of fatty acids released from mild

cheddar was markedly lower compared with other cheeses. Limited degradation of the matrix was observed during the digestion. Higher mineral and lower moisture content of mild cheddar resulted in a more cohesive and firm matrix that made it more resistant to degradation. These results suggest that kinetic of fatty acids release is modulated by cheese matrix structure and rheological characteristics.

Key words: cheese, lipids, digestion

W65 Effects of high pressure processing on the chemical, functional and rheological properties of fresh Queso Fresco. D. L. Van Hekken*, M. H. Tunick, R. Kwoczak, and P. M. Tomasul, *USDA, ARS, Wyndmoor, PA, USA.*

Although Queso Fresco (QF), a popular high moisture Hispanic-style cheese sold in the US, is made from pasteurized milk it is subject to post pasteurization bacterial contamination. High pressure processing (HPP) of cheese is being considered because of its lethality to bacteria and potential to extend shelf life. However, little research has been performed to determine the effects of HPP on the functional and rheological properties of QF. Fresh QF, made from pasteurized homogenized milk without starter cultures, was cut into 45x45x150mm^3 blocks, double packaged in vacuum bags, and received the following HPP treatments: 200, 400, or 600 MPa for either 0, 5, 10, or 20 min; samples were stored at 4°C but were warmed to an internal temperature of either 22 or 40°C just before HPP treatment. Between d 6 and 10, samples were assayed for compositional, functional (meltability, initial color, and change in color after heating) and rheological (texture profile, torsion, and small oscillatory shear analyses) properties. The moisture content of the cheese was stable when QF was processed at 22°C but whey was forced out of the cheese matrix and accumulated in the packaging when processed at 40°C. HPP of QF at 22 or 40°C did not affect the non-melt property, the initial bright white color, or the changes in color after heating of QF. Compared with HPP at 22°C, conducting HPP at 40°C resulted in QF having higher values for hardness, chewiness, cohesiveness, shear stress and shear strain. Cheese samples had variable responses to HPP as pressure and length of treatment increased; springiness and cohesiveness were lowest for 600 MPa treatments, shear rigidity at the point of fracture was highest at 600 MPa, and HPP treatment had little effect on viscoelastic properties. High pressure processing altered the rheological properties of QF and, when conducted at 40°C, resulted in excessive wheying-off. As new safety intervention processes are explored, it is essential that the quality traits of the cheese be maintained.

Key words: cheese, high pressure processing, Queso Fresco

W66 ACE-inhibitory activity of commercial Wisconsin Cheddar cheeses during ripening. Y. Lu*, S. Govindasamy-Lucey, and J. Lucey, *University of Wisconsin - Madison.*

ACE-inhibitory (ACEI) peptides have been found in cheeses that have been reported to have anti-hypertensive properties. More types and concentrations of ACEI peptides may be produced with ripening. The objective of this study was to quantify the ACEI activity of Cheddar cheeses during ripening and determine the types of ACEI peptides formed in these cheeses of different ages. Water soluble extracts (WSE) were prepared from commercial Wisconsin Cheddar cheeses at ages of 3–6 d, 2, 6 and 9 mo, 1 and 2 years manufactured from the same plants. Centrifugation and ultra-filtration were used to remove fat and to fractionate the WSE into 3 molecular weight (MW) fractions: <3000 Da, 1000–3000 Da and <1000 Da, respectively. The fractions were subjected to HPLC-Tandem mass spectrometry (MS) and HPLC-electrospray ionization (ESI)-time-of-flight (TOF) MS to identify the ACEI peptides. The fractions with MW <3000 Da were used to conduct ACE-inhibitory activity tests. With age, higher ACEI activity was observed in the WSE of cheese and more types of ACEI peptides were also found. Some of the ACEI peptides, such as, IPP, VPP, EKDERF, VRYL and YPFPGPIPN were synthesized and quantified using HPLC-MS. The concentration of these ACEI peptides increased up to a certain ripening time. The maximum contents of IPP, VPP and EKDERF were 2.8, 7.4 and 5.3 mg/100g cheese, respectively and these levels were found in a 1-year Cheddar cheese. The maximum content of VRYL was found in a 2-year Cheddar cheese with amounts as high as 7.5 mg/100g cheese while the maximum content of YPFPGPIPN was 6.8 mg/100g cheese, which was found in a 6-mo Cheddar cheese. Aged Cheddar cheese is a good source of ACEI peptides and we predicted (based on previous clinical studies with these purified ACEI peptides) that a measurable anti-hypertensive effect in individual consumers would be expected if around ~100 g/day of this 1-year Cheddar cheese was consumed.

Key words: ACE-inhibitory activity, ACE-inhibitory peptides, mass spectrometry

W67 Influence of cooking temperature on the behavior of enterococci and the production of diacetyl in Coalho cheese. P. L. Mamede, J. M. Perri, A. Y. Kuaye, and W. H. Viotto*, *UNICAMP, Campinas, São Paulo, Brazil.*

Coalho cheese, a typical Brazilian cheese, is a semi-hard, white-colored cheese made from cow′s milk. Its elastic or rubbery texture and its low melting capacity are the principal attributes of Coalho cheese in the grilled form, but flavor also plays an important role. Bacteria of the genus *Enterococcus* were the predominant micro biota in Coalho cheeses that displayed a buttery flavor and aroma. The behavior of the *Enterococcus* genus during the different stages of cheese making, and the influence of cooking temperatures on the diacetyl/acetoin content of Coalho cheeses during refrigerated storage were evaluated. Three vats of cheese were made at different curd cooking temperatures (40, 45 and 50°C), using pasteurized milk previously standardized to casein: fat ratio = 0.83 ± 0.04. Cheese making was repeated on 3 different days, resulting in 9 experiments. Cheeses were stored at 4°C during 90 d. The milk pasteurization process was not effective to eliminate the enterococci. Both the steps of curd cooking and curd salting selectively favored the growth of this genus, known to tolerate high salt concentrations, resist high temperatures and lowering of the pH. The growth of *Enterococcus* was favored by curd cooking, but was not affected by variations in the cooking temperature. The *Enterococcus* population and the production of diacetyl/acetoin increased significantly with the storage time of the Coalho cheeses. The production of diacetyl/acetoin and the consequent development of a buttery flavor and aroma in Coalho cheese can be associated with the development of *Enterococcus*. The authors are grateful to CNPq (Brazilian Natl. Research Council) for their financial support.

Key words: cheese, *Enterococcus*, diacetyl

W68 Identification of the main esterase involved in lipolysis by *Propionibacterium freudenreichii*. M. C. Abeijón Mukdsi[3,4], H. Falentin[1,2], M.-B. Maillard[1,2], R. B. Medina[3,4], S. Parayre[1,2], S.-M. Deutsch[1,2], S. Lortal*[1,2], and A. Thierry[1,2], *[1]INRA, UMR1253, Rennes, France, [2]Agrocampus Ouest, Rennes, France, [3]CERELA-CONICET,*

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Free fatty acids are important flavor compounds in cheese, where they bring pungent, rancid, cheese, and fruity notes. They mainly result from the lipolytic activity of cheese microorganisms. *Propionibacterium freudenreichii*, a species used as a ripening culture in Swiss cheese, is the main agent of Swiss cheese lipolysis, with 96% of the free fatty acids released during the ripening resulting from *P. freudenreichii* activity [Dherbécourt et al. 2010 J. Agric. Food Chem. 58:11732-11739]. Our aim was to identify the most probable lipolytic esterase(s) involved in cheese lipolysis by *P. freudenreichii*. Since cheese lipolysis mainly occurs during *P. freudenreichii* growth, we focused our study on surface-exposed or secreted esterases. Out of the 12 putative esterases previously predicted from the genome sequence of *P. freudenreichii* CIRM-BIA1 [Dherbécourt et al. 2008 Microb. Cell Fact. 7], the lipolytic esterase PF#279 was shown to be secreted, and the putative esterase PF#774 was predicted to be anchored in the plasma membrane [Dherbécourt et al. 2010 Appl. Environ. Microbiol. 76:1181-1188]. To evaluate the respective role of these 2 proteins in lipolysis, *P. freudenreichii* CIRM-BIA1 was knocked out and then complemented for the genes encoding these 2 proteins, separately. Each of these genes was also overexpressed in *P. freudenreichii* CIRM-BIA1. All these genetically modified strains were assessed for their lipolytic activity during their growth in a medium containing an emulsion of milk fat. Results showed that the mutants inactivated for PF#279 showed a very low residual lipolytic activity, whereas inactivating or overexpressing PF#774 had no impact on lipolysis level. This study shows that only one lipolytic esterase, PF#279, is involved in milk fat hydrolysis in *P. freudenreichii* CIRM-BIA1 and is a key component in Swiss cheese lipolysis.

Key words: lipolysis, *Propionibacteria*, Swiss cheese

W69 Characteristics of the chemical composition and lipolysis during ripening of Emmental cheese. N. S. Oh*, Y. K. Shin, J. P. Ok, and Y. H. Park, *Institute of Dairy Food Research, Seoul Dairy Co-op., Institute of Dairy Food Research, Seoul Dairy Cooperative, Ansansi, Kyunggi, South Korea.*

The objective of this study was to characterize the lactate metabolism and lipolysis in Emmental cheese made of Korean raw milk throughout the ripening periods; 14 d at 10°C, 42 d at 23°C, and 30 d at 4°C. Emmental cheese was made using commercial starter culture with propionic acid bacteria (PAB) and without PAB as control at the pilot plant scale. The changes in contents of 5 organic acids, which were citric acid, lactic acid, formic acid, acetic acid and propionic acid, and individual free fatty acids (FFAs) were measured using HPLC/PDA and GC/FID. As a result of propionic fermentation by PAB, the concentration of acetic and propionic acid was increased up to 1.6 and 5.7 g/kg, respectively and mainly increased dramatically in the stage of hot room (23°C). Lactic, citric and formic acid contents were 2.6, 2.5 and 0.8 g/kg at the end of ripening. As a result of lipolysis, the amount of total free fatty acids (FFAs) was 7.2 g/kg. Compared with control, levels of individual FFAs from butyric (C4:0) to linoleic (C18:2) acids increased significantly ($P < 0.05$) during ripening period. Especially in the 23°C room, 79% of total FFAs was released and most abundant FFAs are palmitic (C16:0) and oleic acid (C18:1). Then, it showed that the lipolysis of Emmental cheese was strongly affected by bacterial lipase from PAB.

Key words: Emmental cheese, organic acids, lipolysis

W70 Oxidative stability of Prato cheese added with lutein. D. Maus, A. A. O. Xavier, M. T. K. Kubo, R. A. Jorge, A. Z. Mercadante, and W. H. Viotto*, *UNICAMP, Campinas, São Paulo, Brazil.*

The carotenoid lutein has been associated to the reduction and prevention of age-related macular degeneration (AMD), the leading cause of irreversible blindness in the elderly people. Since this carotenoid is not synthesized by the human body, its addition to cheese is an option of lutein supplementation in the diet, and it can also act to prevent photo-oxidation of cheese. The storage conditions of cheese in supermarkets may lead to changes in the product due to the presence of riboflavin (RBF), which under light stimulus promotes oxidation of vitamins, lipids and proteins, leading to nutrient losses and sensory changes. The objective of this work was to evaluate the stability of lutein added to the cheese and RBF, in the presence and absence of light, during 56 d of refrigerated storage. The formulation of lutein used was Lutein 20% FS - natural coloring of lutein for food, from DSM Nutritional Products (Basel - Switzerland). Prato cheeses without addition and with addition of 0.04% formulation of lutein on the mass of milk (estimated content of 80 μg/g milk) were evaluated as the behavior of RBF and lutein during storage at 12°C. A split-split-plot design was used for analyses of lutein and riboflavin contents and the results were evaluated by ANOVA. There was degradation of 35.3% of riboflavin in cheese without the addition of lutein exposed to light. For cheeses with added lutein, there was no degradation of riboflavin in both the absence and presence of light. In all cheeses, the levels of lutein remained virtually constant throughout the period of storage, allowing the assumption that all added lutein remained available at the end of storage period. These facts indicate that lutein, when present in cheese, has a protective role by preventing the degradation of riboflavin.

Key words: carotenoids, cheese, photo-oxidation

W71 Comparison of texture and sensory attribute between Gouda cheese and cholesterol-removed Gouda cheese during ripening. H. J. Jung*, E. J. Ko, and H. S. Kwak, *Sejong University, Seoul, South Korea.*

The present study was carried out to examine the texture and sensory evaluation between Gouda cheese and cholesterol-removed Gouda cheese made by crosslinked β-cyclodextrin (β-CD). Both cheeses were ripened at 14°C, 85% RH for 6 mo. The texture and sensory characteristics of the cheeses were measured during ripening (0, 1, 2, 3, 4, 5 and 6 mo). To analyze the texture properties, the 2-bite compression test was performed using by texture analyzer, and to evaluate sensory properties, 9-trained panelists examined the cheeses. In chemical composition analyses, moistures were significantly different between cheese (42.96%) and sample cheese (48.44%) ($P < 0.05$). But fat and protein in the control and the sample were 32.99, 22.51 and 31.45, 20.45%, respectively, and were not significantly different ($P < 0.05$). The amount of cholesterol was 82.41 mg/100 g and the percentage of cholesterol removal was 91%. In the texture analysis, hardness, gumminess and chewiness were significantly increased, but cohesiveness and springiness were not increased in both cheeses during ripening periods ($P < 0.05$). In comparison of the control and sample cheeses, hardness and springiness were not significantly different, but cohesiveness, gumminess and chewiness were different ($P < 0.05$). In sensory properties, appearance (yellowness and dryness), aroma (butyric, fruity, musty and nutty), flavor and taste (butyric, sour, salty, bitter and after taste) and texture (hardness, springiness, crumbliness, sticky, dryness and mouth coating) were significantly increased except buttery,

nutty in aroma and sweetness in taste in both cheeses during ripening ($P < 0.05$). And appearance, aroma, flavor and taste, and texture were not significantly different between the control and sample cheeses ($P < 0.05$). Therefore, this study may suggest that the quality of cholesterol-removed Gouda cheese is not different from the control cheese.

Key words: Gouda cheese, cholesterol removal, sensory evaluation, texture

W72 Influence of pH on flavor of low fat Cheddar cheese. M. M. Motawee*[1] and D. J. McMahon[2], *[1]National Organization for Drug Control and Research, Cairo, Egypt, [2]Western Dairy Center, Utah State University, Logan.*

Low fat cheddar cheese typically lacks flavor characteristic of full fat cheddar cheese. This study investigated whether flavor or low fat cheese could be improved by modifying cheese pH and lowering storage temperature. Cheese was made from 700 kg of 0.6%-fat milk using lactococcal starter culture and lactobacilli adjunct culture. Milk was renneted at 31°C, cooked to 35°C, drained, curd washed with cold water, dry stirred, salted, and pressed into 9-kg blocks and stored at 3, 6, and 10°C. Make procedure was varied to produce cheese with pH (at 60 d) from 5.08 to 5.55 with similar moisture, salt and fat. Sensory descriptive analysis was performed using the Spectrum scale after 4 mo on cheese aged at 3 and 6°C and compared with retail-purchased full fat cheeses. Scores for cooked, fruity, oxidized, pineapple, rancid, sulfur and whey flavors were negligible (≤0.5) for both low fat and full fat cheeses. There were few differences in flavor scores of low fat cheese attributed to pH or storage at 38 or 42°F. There was a consistent tendency for cheese aged at 3°C to receive slightly lower scores, such as 2.4 vs. 2.9 for sour and 1.4 vs. 1.7 for umami flavor. Sour, umami and salty flavors of low fat cheeses were not influenced by pH and these were all slightly less compared with full fat cheese, i.e., 2.7 vs. 4.4, 1.6 vs. 2.1, and 2.9 vs. 3.8, respectively. Low fat cheeses also scored lower for lactone (0.8 vs. 1.6), nutty (0.8 vs. 1.4) and buttery (0.8 vs. 1.8) flavors. Cheese microflora was studied by plating on Elliker agar for total lactic acid bacteria, and on Rogosa agar for lactobacilli, with the difference between them being attributed to lactococci. Starter culture levels were about 10^7 cfu/g initially and between 10^6 to 10^7 by d 30, and stayed about 10^6 cfu/g through 90 d then dropped off by 120 d to being much less than the nonstarter bacteria (this occurred earlier in cheese stored at 10°C). Lactobacilli levels were about 105 after 5 d of storage, increased to 10^6 by 30 d for all cheeses, and reached 10^7 cfu/g by 90 d in the 10°C cheese. Levels of thermophilic bacteria stayed relatively constant at 10^3 to 10^4 cfu/g throughout storage irrespective of temperature.

Key words: Cheddar, low fat, flavor

W73 Free fatty acid compositions of low-fat and full-fat goat milk cheeses stored under refrigeration for three months. W. Nouira[1], Z. Guler[2], and Y. W. Park*[1], *[1]Fort Valley State University, Fort Valley, GA, [2]Mustafa Kemal University, Hatay, Turkey.*

Amount of free fatty acid (FFA) is an indicative of degree of lipolysis in dairy foods. The objective of the study was to determine differences in composition and total FFA contents between low-fat (LF) and full-fat (FF) plain soft goat milk cheeses stored for 3 mo at 4oC. The 2 types of cheeses were manufactured using a bulk tank goat milk collected from the Fort Valley university farm. LF cheese was manufactured after cream removal from the whole milk. FFAs of all LF and FF cheeses were extracted in diisopropyl ether using polypropylene chromatography column, and FFA concentration was determined using a gas chromatography, equipped with a fused silica capillary column. Moisture, fat, protein contents (%) and pH of fresh LF and FF cheeses were: 55.1, 52.3; 1.30, 25.6; 3507, 22.5; 5.40, 5.42, respectively. The concentrations (mg/g cheese) of FFAs in the fresh FF and LF cheeses before the storage for C4:0, C6:0, C8:0, C10:0, C12:0, C14:0, C16:0, C18:0, C18:1, and C18:2 were: 0.020, 0.072; 0.070, 0.035; 0.061, 0.055; 0.181, 0.167; 0.073, 0.047; 0.174, 0.112; 0.579, 0.152; 0.308, 0.202; 0.521, 0.174; and 0.057, 0.026, respectively. The respective FFA to total fatty acids ratios for 0, 1 and 3 mo aged FF and LF cheeses were 8.44, 12.4; 6.31, 16.91; 12.03, 14.19. Total FFA contents of LF cheeses at 0, 1 and 3 mo aging were 48.0, 96.8 and 36.4% of those in FF cheeses. It was concluded LF cheese generated more FFA than FF cheese although total FFA amount was significantly ($P < 0.05$) lower in LF cheese.

Key words: lipolysis, free fatty acid, goat milk cheese

W74 Increasing functionality of low fat mozzarella cheese using polysaccharides. E. N. Oberg*, W. R. McManus, and D. J. McMahon, *Utah State University, Logan.*

We examined the ability of polysaccharides to function as fat mimetics in low fat mozzarella string cheese to improve functionality by acting to form protein fibers during cheese extrusion. Low fat (LF) mozzarella cheese curd made from 273 kg of 0.7%-fat milk was salted at a rate of 10 g/kg then divided into 3.6-kg batches that were hand-stretched in hot (80°C) 5% brine and formed into a homogeneous mass. The hot cheese was hand mixed with a hot (80°C) polysaccharide slurry and 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. From preliminary trials using starches (waxy corn, waxy rice, and instant tapioca starch), xanthan and guar gum, and polydextrose we determined that LF string cheese made using xanthan gum most resembled retail string cheese. Cheese was then made using 10% xanthan gum slurry added at 0.25%, 0.5%, 1.0%, 1.5%, and 2.0% levels as well as a control with no added gum. Cheeses were analyzed for fat, salt, pH, and moisture. After 2 wk of 4°C storage, the cheese was analyzed for extent of stringiness by pulling apart the cheese longitudinally, visually observing and photographing size, length and appearance of individual strings of cheese, consumer liking, and hardness using a penetrometer shear test. Using a hedonic scale (1 to 9) for overall liking the LF with 1% added xanthan slurry (score = 6.8) was liked more ($P < 0.05$) than a retail comparison string cheese (score = 6.2) and the LF cheese with no added gum scored lower (5.9). When considered on a JAR scale, 71% of panelists scored the LF cheese with added xanthan as having the right texture, while only 49% did so for the retail cheese. The no added gum LF cheese was considered too firm. By visual comparison, adding the xanthan gum slurry produced greater fiber formation with the longest and best string separation. After 8 wk storage, the LF cheeses had softened extensively with fracture stress for LF cheese decreasing from 11.8 to 20.5 kg at 2 wk to 2.22–3.45 kg at 8 wk. Extent of stringiness also decreased considerably during storage.

Key words: mozzarella, string cheese, low fat

W75 The effects of incorporating sweet potato and peanut flours on sensory properties of probiotic yogurt in Mwanza, Tanzania. S. Hekmat* and S. Varriano, *Brescia University College, London, Ontario, Canada.*

Yogurt is a nutrient-dense product that serves as an excellent vehicle to transfer probiotic microorganisms and other nutritional additives to consumers. Vitamin A deficiency and protein-energy malnutrition are the 2 common dietary deficiencies in some resource-poor African communities. Addition of sweet potato and peanut flours in certain African staples has been an effective method to increase the pro-vitamin A content of the diet and to alleviate protein-energy malnutrition, respectively. The objective of this study was to evaluate the effects of incorporating sweet potato and peanut flours on sensory properties of probiotic yogurt in Mwanza, Tanzania. Standardized milk (3.5% fat) with 4 and 6% sweet potato flour (SPF), 4% peanut flour (PF), 3 and 5% milk powder (MP), and one with no additives (C) were prepared. The samples were heat treated at 85°C for 30 min, cooled to 37°C and inoculated with standard yogurt cultures and *Lactobacillus rhamnosus* GR-1 (4%). All yogurt samples were fermented and cooled to 4°C. Consumer taste panels were conducted. A 9-point hedonic scale was used to evaluate and compare the samples. The SPF (4%) sample was rated significantly ($P < 0.05$) higher for flavor and overall acceptability compared with MP (5%), PF (4%), and SPF (6%) samples. However, the SPF (6%) yogurt had a significantly ($P < 0.05$) lower appearance score compared with MP (3%) and C samples. The addition of PF (4%) was not desirable and resulted in low flavor and overall acceptability scores. This study suggests that addition of moderate amount of sweet potato flour to yogurt improves the flavor and overall acceptability of the product and can potentially be used as a nutritional additive to combat vitamin A deficiency in Africa.

Key words: yogurt, sweet potato flour, peanut flour

W76 Riboflavin photodegradation in yogurt with added lutein. L. D. Domingos, A. A. O. Xavier, R. A. Jorge, A. Z. Mercadante, A. J. Petenate, and W. H. Viotto*, *UNICAMP, Campinas, São Paulo, Brazil.*

Lutein is a carotenoid possessing biological activity against degenerative diseases, such as the decrease and prevention of the occurrence of age-related macular degeneration. It also shows antioxidant properties and can exert a protective function in foods. Dairy products are light sensitive due to the presence of riboflavin, a sensitizer capable of absorbing luminous energy and transferring it to reactive oxygen molecules, unleashing oxidative components on the milk components, resulting in nutritional losses and sensory alterations. The current work evaluated the oxidative stability of yogurt with an added lutein-based preparation, in the presence and absence of light and stored for 35 d under refrigeration. The 0.3% lutein formulation used was obtained from Vegex Lutein WS and is a natural dye from Christian Hansen (Horsholm, Denmark) used for food purposes. Yogurts were manufactured with and without the addition of 1.5 mg per 120g portion (estimated value of 11.5 µg/g yogurt) in the final product, and characterized with respect to their total carotenoid and riboflavin contents. Degradation of the riboflavin and lutein were monitored during refrigerated storage at 5°C. A split-split-plot design was used for analyses of lutein and riboflavin contents and the results were evaluated by ANOVA. In the yogurts without lutein and exposed to light, there was a reduction in the riboflavin content and the formation of oxidized riboflavin products. In the yogurts with lutein, the riboflavin and lutein contents remained constant throughout the entire storage period in the light, the same occurring in the samples stored in the dark. The dye lutein impeded the photo-degradation of riboflavin in the yogurt exposed to light. All the samples presented constant lutein contents throughout the entire refrigerated storage period, signifying that all the lutein added remained available up to the end of the storage period.

Key words: yogurt, lutein, riboflavin

W77 The physicochemical and sensory properties of milk supplemented with dispersable nanoginseng during storage. Y. J. Ahn* and H. S. Kwak, *Sejong University, Seoul, Korea.*

This study was carried out to investigate the dispersibility of nanoginseng (600 ~1,000 nm) in milk and to determine the effects of the addition of the ginseng into the milk on the physicochemical and sensory attributes of the milk during storage. To be dispersable nano- ginseng, 0.5% nano ginseng powder was added into the sterilized water, swelled at 80°C for 2 h, added 0.3% polyglycerol monostearate, stirred at room temperature with 800rpm for 24 h and obtained the supernatant after centrifugeting. The dispersable nanoginsengs (2, 4, 6, 8%) were added into milk and stored at 5°C for 16 d, and pH, DPPH for antioxidation, color and sensory evaluation were studied. The pH was ranged from 6.65 to 6.79 during storage. DPPH showed that the additions of 2, 4, 6 and 8% dispersable nanoginseng increased 1.3, 1.7, 2.0 and 2.2 times higher activity, respectively. The color value, L, in the milk, was not significantly influenced by adding the nanoginseng solution (2 ~8%, v/v) ; whereas the a and b values significantly increased with the solution ($P < 0.05$). In sensory attribute, earthy, bitterness, astringency and overall acceptability were not significantly different between control and 4% addition of the solution ($P < 0.05$). Based on the data obtained from this study, it is concluded that the low concentrations (2 ~4%) of the nanoginseng solution could be used to develop a nanopowdered ginseng-added milk without significantly adverse effects on the physicochemical and sensory properties.

Key words: nanoginseng, dispersibility milk

W78 Optimum condition for crosslinked β-cyclodextrin and recycling for cholesterol removal in milk and cream. Y. K. Lee* and H. S. Kwak, *Sejong University, Seoul, South Korea.*

This study was carried out to investigate the optimum condition of crosslinked β-cyclodextrin (β-CD) and the recycling for cholesterol removal in milk and cream. The crosslinked β-CD was prepared with 15% adipic acid solution, and water solubility of the β-CD was measured for the optimum condition based on mixing temperature (20, 40, 60 and 80°C), mixing time (1, 2, 3 and 4 h), crosslinking temperature (20, 40, 60 and 80°C), crosslinking reaction time (24, 36, 48 and 60 h) and cooling time (48, 72, 96 and 120 h). For recycling study, recyclable yield and cholesterol removal rate were measured by 2 and 15% adipic acid added crosslinked β-CD in milk and cream, respectively. In the results of this study, optimum condition was 80°C mixing temperature, 2 h mixing time, 60°C crosslinked temperature, 24 h crosslinking reaction time and 48 h cooling time. After being determined the optimum condition, the recyclable yields of the crosslinked β-CD ranged from 90.01 to 55.17% in 6 times of recycling and the percentage of cholesterol removal by 15% crosslinked β-CD was over 90% till 8th time recycling. On the basis of the results, this study suggested that

15% adipic acid added crosslinked β-CD maximized recyclable yield and during recycling cholesterol removal was improved.

Key words: optimization, crosslinked β-cyclodextrin, recycling, milk, cream

W79 Optimization of water in oil in water (W/O/W)-microencapsulated iron for milk fortification (I). S. Y. Lee*, S. I. Ahn, and H. S. Kwak, *Sejong University, Seoul, South Korea.*

This study was designed to examine the microencapsulation efficiency of iron and to measure the stability and bioavailability of iron microcapsules in vitro. Core material was ferrous sulfate and coating materials were medium-chain triglyceride (MCT) for W/O and whey protein isolate (WPI), arabic gum (AG) or maltodextrin (MD, DE 18) for W/O/W. The highest emulsion stability index (ESI) for W/O iron emulsion was 98% when the ratio of water to oil was 4:6 and 1% polyglycerol polyricinoleate (HLB 0.6) was added as primary emulsifier. The highest yield of W/O/W iron emulsion was 93% when the ratio of W/O to water was 2.5:7.5, coating material was 30% WPI, 1% ferrous sulfate as a core material and 1% (w/v) polyoxyethylene sorbitan monolaurate (HLB 16.7) as a secondary emulsifier. The smallest size of spray dried microcapsule was 10.1Î1/4m with WPI and the largest 22.6Î1/4m with AG. The moisture content of the capsules were within 2% with all coatings used. The maximum absorbed moisture contents were 28, 24 and 30% with MD, WPI, and AG, respectively, under 98% relatively humidity. In the in vitro study only 1.0~2.1% of iron was released in simulated gastric fluid at 37°C pH 2 for 0, 30, 60, 90 and 120 min. Comparatively, iron release increased dramatically to 70, 60, and 46% with WPI, MD, and AG, respectively, in the simulated intestinal fluid at 37°C pH 7 for 0, 30, 60, 90 and 120 min. Based on our results, WPI was the most efficient, stable and bioavailable.

Key words: W/O/W, microencapsulation, iron

W80 Water in oil in water (W/O/W)-microencapsulation iron for milk fortification (II). S. Y. Lee*, S. I. Ahn, and H. S. Kwak, *Sejong University, Seoul, South Korea.*

This study was carried out to investigate the fortification of iron into milk by means of W/O/W microencapsulation technique. Coating materials were medium-chain triglyceride (MCT) for W/O and whey protein isolate (WPI) for W/O/W. Core material was ferrous sulfate. Spray dried iron microcapsules were made and added (0.1, 0.3, 0.5 and 0.7%) into milk and the pH, released iron, TBA, color and sensory attributes of iron microcapsules in milk were measured during storage at 4C for 0, 4, 8, 12 and 16 days. All experiments were run in triplicate. Iron fortified milk had kept pH between 6.78 and 6.88 during storage. The amounts of the released iron from the capsules in the milk were 0.17~0.20, 0.48 and 0.71ng/ml from 0.1~0.3, 0.5 and 0.7%, respectively. The TBA value for fat oxidation showed in the range of 0.17 to 0.22 absorbance at 450nm, which has no significant difference between control and samples during storage ($P < 0.05$). In color, b- and a- values of the sample milk containing 0.5~0.7% iron microcapsules were significantly different from control ($P < 0.05$). In sensory evaluation, rancidity, cooked and metallic parameters revealed significant differences with increased iron encapsulated microcapsules, however, overall acceptability did not show significant difference during storage ($P < 0.05$). Based on the data obtained from this study, it is concluded that 0.3% powdered iron microcapsule could be applicable for iron-fortified milk.

Key words: W/O/W, microencapsulation, iron fortification, milk

W81 Development and characterization of synbiotic quark cheese. A. F. Carvalho*[1], M. M. Gonçalves[1], G. M. Tavares[1], J. Y. Suda[1], N. F. Nogueira Silva[2], and J. B. P. Chaves[1], *[1]Federal University of Viçosa, Viçosa, MG, Brazil, [2]Institut National de la Recherche Agronomique STLO, Rennes, Bretagne, France.*

A current food market trend is the consumers search for healthier, low fat, low sugar and more nutritious products. In this context, functional dairy products often added with probiotics and prebiotics stand out among other products of similar nature. Probiotic bacteria are live microorganisms which when consumed promote health benefits to the host. Prebiotics are non-digestible ingredients that stimulate the selective growth of beneficial bacteria in the intestine. This work aimed to develop a symbiotic skimmed Quark cheese, using a new manufacturing technology, which is feasible for small volume production. The prebiotic ingredient inulin (BENEO Raftiline) and 3 probiotics (*Lactobacillus acidophilus* LA5, *Bifidobacterium animalis* BB12 and *Lactobacillus delbrueckii* UFV H2b20) were used. Three formulations were produced, differing in the probiotic added to the fermented mass, in 3 replications. Microbial cell viability was monitored during storage at refrigerated temperature. Effects of probiotic addition on the cheese physico-chemical and rheological characteristics and sensory acceptance were determined at 5, 15 and 25 d. Regression analysis did not detect significant change ($P > 0.05$) in microbial count up to 25 d storage, with high counts as log cfu.g-1 in the range of 6.4 to 6.9. There was no significant change ($P > 0.05$) in cheese acidity over time. The product was characterized as a pseudoplastic fluid and its rheological characteristics did not vary significantly ($P > 0.05$) in cheeses with different probiotics. Addition of stabilizers, thickeners and fiber raised consistency and apparent viscosity levels of the product. The new technology allowed the production of a type cheese with good sensory acceptance and probiotics addition did not cause any change perceived by consumers. This product can be considered, therefore, a potential carrier for probiotic microorganisms.

Key words: prebiotic, probiotic, cheese

W82 Comparison of quantitative neutral volatile compounds in regular cream cheese and cholesterol-removed cream cheese. S. S. Jeon*, S. J. Lee, and H. S. Kwak, *Sejong University, Seoul, Korea.*

This study compared quantitative flavor compounds in regular cream cheese (RCC) and cholesterol-removed cream cheese (CRCC), which was treated by crosslinked β-cyclodextrin, and were stored at 7°C for 4weeks. To quantify the volatile compounds, the cheeses (0, 1, 2, 3 and 4weeks) were extracted and analyzed by solid-phase microextraction (SPME) and gas chromatography (GC), respectively. Tentatively identified flavor compounds were mainly 11 from fatty acid. One amine was present in RCC, and 2 lactones and miscellaneous were in CRCC and one was in RCC, respectively. However, 2 ketones were present in both cheeses. In quantitative analysis, hexanoic acid and octanoic acid were not significantly developed ($P < 0.05$) in both cheeses. N-Decanoic acid was produced higher in RCC (0.158 ppm) than in CRCC (0.155 ppm). Benzoic acid appeared at 3 week storage and developed from 0.1321 to 158 ppm in RCC and from 0.106 to 0.130 ppm in CRCC. Dodecanoic acid was found at an insignificant amount in both samples. Tetradecanoic acid kept ranged from 0.151 to 0.161 ppm in both cheeses. However, z-11-tetradecanoic acid produced in only CRCC from 0.120 to 0.135 ppm. Tridecanoic acid was lower than

other acids. N-hexadecanoic acid was produced at 0.153 ppm in RCC and 0.139 ppm in CRCC and remained constant. Oleic and 9, 12-octadecadienoic acid developed only from 0.118 to 0.144 ppm and from 0.034 to 0.073 ppm in CRCC, respectively. The ketone, 2-tridecanone was produced 0.032 and developed to 0.050 ppm only in RCC and 2-pentadecanone produced 0.060 and developed to 0.083 ppm in both cheeses. The lactone, 2H-pyrane-2-one, tetrahydro-6-pentyl, was produced 0.050 ppm and developed to 0.074 ppm in both cheeses. However, 2H-pyran-2-one, 6-heptyltetrahydro kept 0.140 ppm only in CRCC. As amine, 5-(p-aminophenyl)-4-(o-tolyl)-2-thiazolamine and as other, phenol, 4, 6-di (1, 1-dimethylenthyl)-2-methyl kept 0.050 ppm only in RCC. On the basis of our results, we conclude that the quantity of flavor compounds in regular cream cheese and cholesterol-removed cream cheese was similar except for a few components.

Key words: cream cheese, cholesterol removal, flavor

W83 Comparison of lipolytic and proteolytic changes between commercial bovine milk and caprine milk yogurts stored under refrigeration. J. Oglesby and Y. W. Park*, *Fort Valley State University, Fort Valley, GA.*

In European and Asian countries, there is a long tradition of consumption of fermented milks such as yogurt, which is associated with good nutrition and health benefits of the products. A study was conducted to determine storage stability of caprine milk yogurt compared with bovine milk counterpart in relation to lipolysis and proteolysis. Commercial bovine milk yogurt (CBY) and commercial caprine milk yogurt (CCY) were purchased from local retail stores, and Fort Valley State University plain caprine milk yogurt (FVCY) were manufactured using direct vat set (DVS) lactic culture (YC-180, Chr. Hansen, Inc., Hoersholm, Denmark). The caprine milk used was the late lactation bulk milk from the University dairy goat herd consisted of Saanen, Alpine, and Nubian breeds. All experimental yogurt samples were subjected to 4°C refrigeration storage for 4 weeks. Acid degree value (ADV), pH, water soluble nitrogen (WSN) and basic nutrient contents of all yogurt samples were analyzed to compare lipolytic and proteolytic changes between the products during 0, 2 and 4 weeks of storage. Mean dry matter and fat content (%) of CBY, CCY and FVCY products were 11.28, 3.05; 13.1, 3.65; 11.03, 3.40, respectively, indicating the CCY contained the highest total solids and fat contents among all tested varieties. The initial and final ADVs of CBY, CCY and FVCY were 0.503, 1.009; 0.756, 0.685; 0.707, 1.094, respectively, showing significant lipolysis occurred in the CBY and FVCY, while CCY showed a minimal lipolytic change. The pHs of all 3 products ranged from 4.05 to 4.12, suggesting no significant changes occurred in pH, while the respective WSN (%) of CBY and CCY at 0, 2, and 4 weeks were 3.40, 5.55; 3.93, 4.77; 5.07, 6.75, showing proteolysis was increased in the products. It was concluded that the commercial caprine yogurt had less lipolysis than the CBY and FVCY, probably due to the added stabilizer, whereas proteolysis of all 3 products steadily increased during the storage.

Key words: yogurt, lipolysis, proteolysis, caprine milk

W84 impact of protein content, total solids, and milk protein solids on the functionality of nonfat yogurt. K. N. Shah* and L. E. Metzger, *Midwest Dairy Foods Research Center, Dairy Science Department, South Dakota State University, Brookings.*

Nonfat yogurt is a popular fermented product available in various forms. In the US, the Code of Federal regulations requires >8.25% milk solids in the yogurt base. NDM is a common ingredient utilized to provide milk solids in yogurt produced in the US. However, in International markets, skim milk powder (SMP), milk protein concentrate (MPC), and dried permeate are utilized in yogurt formulations. The protein content, total solids (TS) and source of milk protein may have an impact on the functionality of yogurt. Additionally, storage of dairy ingredients can result in quality deterioration. For example, the storage of high protein MPC at > 20°C for more than 6 mo results in loss of solubility of MPC. The objective of this study was to evaluate the effect of different milk solids sources at various protein/TS ratios and impact of storage of powders on the viscosity and whey separation of nonfat yogurt. Three different lots of SMP, NDM, MPC40 and MPC70 were collected from US manufacturers and each lot was divided into 3 portions. A portion was analyzed after 3, 9, and 15 mo of storage at 25°C. A Rapid Visco Analyzer method was utilized to produce yogurt from each formulation. At each storage time, yogurt formulations with protein (%)/TS (%) ratios (4/12.5, 4.5/13.5 and 5/15.5) were produced from each lot of SMP, NDM, MPC40, and MPC70.Varying amounts of deprotonized whey powder were included to standardize the TS content. The data was analyzed by repeated measures using PROC GLM in SAS. SMP and NDM yogurt viscosity were significantly ($P < 0.05$) higher than MPC40 and MPC70 at each protein/TS ratio. Additionally, MPC70 yogurt viscosity was significantly ($P < 0.05$) lower than MPC40 yogurt viscosity at each protein/TS of yogurt. Whey separation values of SMP were significantly ($P < 0.05$) higher than NDM at each protein/TS of yogurt. The viscosity of yogurt manufactured from all powders were significantly ($P < 0.05$) affected by storage. However, the change in viscosity during storage was small in all treatments at all protein/TS ratios. The usage of various milk protein sources significantly affects the functional attributes of nonfat yogurt.

Key words: nonfat yogurt, viscosity

W85 Sensory evaluation of various probiotic yogurts in Mwanza, Tanzania. S. Hekmat*[1,2], J. Hemsworth[1], H. Soltani[1], and G. Reid[2], *[1]Brescia University College, London, Ontario, Canada, [2]Canadian Research and Development Center for Probiotics, London, Ontario, Canada.*

Yogurt fermented with *Lactobacillus rhamnosus* GR-1 has shown therapeutic properties and its introduction into a dietary regimen of certain population in Mwanza, Tanzania has been an effective method in treating and preventing urogenital infections and in improving the nutritional status of people living with HIV/AIDS. The objective of this study was to evaluate sensory properties of various probiotic yogurts containing local fruits and vegetables found in Mwanza, Tanzania. The yogurt mother culture was prepared by fermenting a milk mixture (3.25% fat) containing 0.33% yeast extract and 0.4% inulin. Four flavors of probiotic yogurt containing at least 10^7 cfu/ml of *Lactobacillus rhamnosus* GR-1 were made using widely available fruits and vegetables in Mwanza such as mango, pineapple, cucumber, and orange at the rate of 10% w/v. Consumer taste panels were conducted using a Hedonic scale of 1–9 (1 = dislike extremely; 9 = like extremely). The results showed that the mango yogurt had the highest overall mean score (7.3) and the cucumber yogurt had the least overall mean score (6.1). The mango and orange yogurts were rated significantly higher than the cucumber yogurt ($P < 0.05$). The appearance and texture of cucumber yogurt were rated significantly lower ($P < 0.05$) than the other yogurts with the mean scores of 6.0 and 5.6, respectively. These findings will be used as a guide to formulate a probiotic yogurt that is feasible and acceptable by consumers in Mwanza, Tanzania.

Key words: probiotics, yogurt, sensory

W86 Effect of pasture feeding and dairy cattle breed on vitamin E and β-carotene content in milk. V. M. Marino[1], I. Schadt[1], S. La Terra[1], M. Caccamo[1], G. Licitra[2,1], and S. Carpino*[1], *[1]CoRFiLaC, Regione Siciliana, Ragusa, Italy, [2]DISPA, Catania University, Catania, Italy.*

It has been shown that several factors such as breed, feed source, and animals′ health status might influence milk vitamin E and β-carotene (AO). The aim of this study was to examine the effects of pasture feeding and dairy cattle breed on AO concentrations in milk. Four dairy farms located in southeastern Sicily were selected; 2 with both Holsteins (H) and Brown Swiss (BS) cows and 2 with only Modicana (M) local breed cows. Bulk milk of each breed per farm was sampled 4 times during 3 experimental periods (P1 = March / April, P0 = June / July, and P2 = November / December). Samplings within period occurred with weekly intervals. Pasture was available in P1 and P2 but not in P0. Periods P1 and P2 differed by botanical composition and plant maturity. During P0 cows were grazing stubble. Additional hay and concentrate was supplemented during all periods. Pasture intakes have been calculated using CPM-Dairy. Milk AO contents were analyzed by HPLC. Both, milk β-carotene and α-tocopherol were highest during P1, lowest during P2 and intermediate during P0 ($P < 0.001$). Least squares means (μg / g fat) ± standard deviations during P1, P2 and P0 of β-carotene were $9.68^{a} \pm 0.07$, $0.84^{c} \pm 0.07$, $2.45^{b} \pm 0.07$, respectively, and relative to α-tocopherol $16.15^{a} \pm 0.05$, $11.15^{c} \pm 0.05$, $13.28^{b} \pm 0.05$, respectively. Milk from BS contained more β-carotene compared with H ($P < 0.05$), but α-tocopherol levels were not affected. Milks from M had the same levels of β-carotene compared with BS cows and had significantly higher levels of α-tocopherol ($P < 0.05$) compared with the milks from the other breeds. However, the latter results might have been confounded by the significant higher pasture intake of M relative to the BS and H. Low AO milk contents measured during P2 could be explained by cows′ vitamin consumptions of body tissue resources during the summer period, when AO were lacking in the diet. Body resources during P2 first had to be restored before AO could be released into milk. Pasture benefits relative to AO milk content might be obtained only after a minimum necessary exposure period of cows to pasture.

Key words: milk, breed, antioxidants, pasture

W87 The fatty acid composition and properties of summer and winter butter. O. Tsisaryk*, *Lviv National University of Veterinary Medicine and Biotechnologies, Lviv, Ukraine.*

The objective of the study was to determine the fatty acid composition, nutritional value and spreadability of summer butter (S) manufactured from milk when dairy cows were grazing and winter butter (W) when cows were fed indoors. Milk was collected from dairy cows in August and December, and butter was manufactured, 3 times for each period. Butter samples were conserved at –20°C until fatty acid analysis by GLC and stored at 4°C per rheological properties and sensory analysis. The fatty acid methyl esters were separated on a column SP-2560 (100 m × 0.25 mm i.d. × 0.20 μm 100% bis-cyanopropyl polysiloxane, Supelco) in a chromatograph Hewlett Packard 6890. The nutritional value of butter was analyzed under the indices. Butter samples were tested for resistance to penetration. The percentage of the sum medium-chain saturated fatty acids (C12-C16) decreased ($P < 0.05$) from 49.5 in W butter to 48.5% in S butter, especially C16:0 – from 32.9 in W butter to 30.9% in S butter. There was an increase ($P < 0.05$) in the ratio of unsaturated to saturated fatty acids in S butter. The sum of unpaired fatty acids and branched-chain ones also increased in S butter. The concentration of cis-9, cis-12, cis-15 C18:3 increased from 0.4 in W butter to 0.9% in S butter, unlike cis-9, cis-12 C18:2, which decreased from 2.3 in W butter to 1.5% in S butter. The ratio of n-3 to n-6 fatty acids increased to 0.63 ($P < 0.05$) in S butter from 0.23% in W butter. The total trans-isomer concentrations were higher in S butter. The concentration of trans-11 C18:1 increased from 1.2 in W butter to 2.0 in S butter and cis-9, trans-11 C18:2 increased from 0.6 to 1.1 respectively. Atherogenicity, thrombogenicity and health promoting indices were 2.82, 1.98 and 0.40 in W butter and 2.69, 1.90 and 0.41 in S butter respectively. Penetrometer readings indicated that S butter was softer at 4°C and the spreadability index also was higher in S butter. Thus, S butter was found to have a higher biological value and a better texture.

Key words: summer and winter butter, fatty acids, properties

W88 Hungarian Trappist (*Trapista*) cheese production from Holstein and Jersey cows′ milk. L. Varga*, *Department of Dairy Science, Institute of Food Science, Faculty of Agricultural and Food Sciences, University of West Hungary, Mosonmagyarovar, Hungary.*

Milk composition is widely known to affect the yield and quality of subsequent dairy foods. Hungarian Trappist (Trapista) is a traditional semi-hard cow′s milk cheese with a mild flavor and good melting properties. Making up approximately 70% of the total ripened cheese consumption, Trapista is by far the most popular cheese in Hungary. The objective of the current experiments was to compare the composition of milk and the quality, yield and production costs of Hungarian Trappist cheese from Holstein and Jersey cows. From November 2008 through July 2009, a total of 260 tonnes of Holstein and Jersey milk were processed in a cheese factory located in the western part of Hungary. Raw bulk milks were analyzed for somatic cell count (SCC), fat, protein and extraneous water. As for Trappist cheese, major chemical components (i.e., total solids, fat and protein) and pH were determined and cheese yield and production cost calculations were also made. The results showed that Jersey milk had higher concentrations of most milk components measured, including protein, fat and SCC, than did Holstein milk. No extraneous water was detected in the raw milk batches processed. The mean total solids and fat-in-DM contents of Trappist cheese from Holstein milk were found to be 56.80% and 50.17%, respectively, whereas the levels of the same components in cheese from Jersey milk were 55.92% and 49.12%, respectively. The 2 cheese products had an identical mean pH value of 5.15 after salting. Jersey milk yielded 4.4% more cheese per kg than Holstein milk using fat standardized cheesemilk. In addition, compared with Holstein Trappist, the manufacture of each kg of Jersey Trappist resulted in the production of 95.2 g more milkfat. All things considered, at October 2009 prices, the production costs of Trappist cheese from Jersey milk were 0.55–0.70 USD/kg lower than those of Holstein Trappist in Hungary.

Key words: Trappist cheese, Holstein milk, Jersey milk

W89 Long-term ethanol or acetic acid supplementation do not impair sensory milk quality. J. L. P. Daniel*, L. G. Nussio, M. H. F. Spotto, T. L. Cardoso, A. Sá Neto, and M. Zopollatto, *University of Sao Paulo, College of Agriculture "Luiz de Queiroz", Piracicaba, SP, Brazil.*

Ethanol and acetic acid are common end products from tropical silages. The objective of this study was to determine whether high dose of ethanol or acetic acid might affect sensory milk quality. Thirty lactating Holstein cows averaging 40 kg/d of milk at beginning of trial were grouped in 10 blocks and fed one of the 3 diets during 7 weeks: Control (33% Bermuda hay + 67% concentrates); Ethanol (control diet + 5% ethanol, DM basis); and Acetic acid (control diet + 5% acetic acid, DM basis). Ethanol and acetic acid were diluted in water (1:2) and sprayed onto total mixed ration twice daily. The same amount of solution was replaced with water in the control diet. During the 1st week of the trial, cows received half-dose of these chemical compounds. Unpreserved and unpasteurized milk was sampled on 6th week of trial and judged immediately after milking for appearance, aroma, taste, and global quality by a sensory panel of 56 non-trained persons. Scores were evaluated on a 9-point scale (where 1 = poor quality to 9 = high quality). Since original data did not fit normal distribution, a Box-Cox transformation was performed. All diets led to well accepted milk batches (score means >6.6). Milk sensory attributes were similar across treatments ($P > 0.15$), except for global quality ($P = 0.02$), where acetic acid and ethanol treatments were slightly improved than control milk (7.56, 7.48 and 7.28 respectively). Long-term ethanol and acetic acid supplementation did not impair sensory milk quality which is in agreement to the blood parameters (not showed).

Key words: aroma, taste, appearance

Forages and Pastures: Improving Forage Conservation and Quality

W90 Dry matter yield and silage nutritive value of winter cereals in the southern High Plains. F. E. Contreras-Govea*[1], H. Gonzalez Garcia[2], D. M. VanLeeuwen[3], and J. Idowu[4], *[1]New Mexico State University, Plant and Environmental Sciences Department, Artesia, [2]Universidad Autonoma de Ciudad Juarez, Departamento de Ciencias Veterinarias, Ciudad Juarez, Chihuahua, Mexico, [3]New Mexico State University, Agricultural Biometrics Service, Las Cruces, [4]New Mexico State University, Extension Plant Sciences Department, Las Cruces.*

This study was conducted to assess DM yield and silage nutritive value of 3 winter cereals harvested at different dates in Southern High Plains. Triticale (× Triticosecale Wittm. Ex A. Camus), wheat (*Triticum aestivum* L.), and barley (*Hordeum vulgare* L.) were sown on 15 October 2009 in a split plot randomized block design with harvest date (HD) as whole plot and cereal as subplot. Cereals were harvested on 20 April, 4 May, and 10 May, 2010. Maturity at harvest ranged from boot to early milk, anthesis to early dough, and caryopsis water ripe to soft dough respectively. Triticale was the most immature and barley the most mature cereal with wheat intermediate. At harvest, 10 kg of each cereal from each plot was chopped to a theoretical length of cut (TLC) of 25 mm. Chopped cereal (500 g) was placed in a plastic bag, vacuum sealed, and stored at room temperature (20°C) for fermentation for 30 d. Pre-ensiled and ensiled cereals were analyzed for nutritive value and fermentation characteristics for the ensiled cereals. Data analysis were conducted using the MIXED procedure of SAS, with HD, cereal, and HD*cereal interaction as fixed effect and replicate as random effect. There was no HD by cereal interaction among variables ($P > 0.05$). Harvesting in April, DM yield was lower (13.2 Mg/ha) than in 4 May (16.5 Mg/ha) or 10 May (16.3 Mg/ha) ($P < 0.05$), but nutritive value was higher. In vitro digestibility and NDF digestibility were greater ($P < 0.05$) in April (862 g/kg and 761 g/kg) than in 4 May (827 g/kg and 713 g/kg) or 10 May (813 g/kg and 688 g/kg). Among cereals, barley had greater ($P < 0.05$) nutritive value, followed by wheat, and triticale. All 3 cereals fermented well, but pH values were high in all 3; barley 5.84, wheat 5.93, and triticale 6.05. Lactic and acetic acid concentration did not differ ($P > 0.05$) among cereals. Harvesting in May increased DM yield by 23%, but decreased nutritive value. Fermentation was similar across cereals, but the high pH may be was an indicator of unstable fermentation.

Key words: winter cereals, silage fermentation, dry matter yield

W91 The effects of substituting corn silage and alfalfa hay with Master Graze on feed intake, milk yield and milk composition. A. Salamone*[1], A. A. AbuGhazaleh[1], C. Stuemke[1], R. Atkinson[1], and B. Dodd[2], *[1]Southern Illinois University, Carbondale, [2]Masterschoice, Anna, IL.*

The objective of this study was to evaluate the effect of using Master Graze (Master's Choice, IL) as a forage source for dairy cows. Sixteen Holstein cows in early-mid lactation (90±19 DIM) were divided into four treatment groups (4 cows/treatment) and fed treatment diets for 4 consecutive periods with each period consisted of 21 days. Cows on the control group (T1) were fed a 60:40 forage:concentrate diet (DM basis) with corn silage and alfalfa hay as forage source (1:1; DM basis). For treatment groups, the Master Graze silage substituted the forage mix at 16% (T2), 33% (T3) and 50% (T4) on DM basis. All diets were formulated to be isonitrogenous. Cows were fed treatment diets as TMR once daily for ad libtium consumption and amounts fed and refused were recorded daily. Substituting the corn silage-alfalfa hay mix with the Master Graze at the three tested levels had no effects ($P > 0.05$) on feed intake (19.4, 19.2, 19.7, and 19.2 kg/d for T1 to T4, respectively) or milk production (23.1, 22.7, 22.7, and 22.9 kg/d). Milk fat percentages (3.91, 3.82, 3.85, and 3.9) and yields (0.89, 0.85, 0.86, and 0.88 kg/d), and milk protein percentages (3.04, 3.06, 3.04, and 3.03) and yields (0.70, 0.68, 0.69, and 0.69 kg/d) were all similar ($P > 0.05$) among treatment diets. Treatment diets had also no effects ($P > 0.05$) on milk urea nitrogen, milk SCC, and cows body weight and body condition score. In conclusion, results from this study show that the Master Graze may replace 50% of dietary corn silage-alfalfa hay mix in dairy cows ration without any adverse effects on feed intake, milk production or milk composition.

Key words: Master Graze, forage, dairy

W92 Ruminal degradability of *Albizia lebbeck* silage. T. Clavero*, R. Razz, and O. Araujo-Febres, *Centro de Transferencia de Tecnologia en Pastos y Forrajes. Universidad del Zulia, Maracaibo, Estado Zulia, Venezuela.*

An experiment was carried out at the tropical western region of Venezuela in order to evaluate *in sacco* dry matter degradability of four levels of supplementation of *Albizia lebbeck* silage. The rations used were: 100% *Brachiaria humidicola* hay (HBH); 75% HBH + 25% silage *Albizia lebbeck* (ALS); 50% HBH + 50% ALS; and 25% HBH + 75% ALS. Samples (10g) milled to pass a 3 mm screen were weighed into 9 x 18 nylon bags, which were incubated for 0, 6, 12, 24, 48, 72 and 96 hours in rumen-fistulated steers. Residues were washed and dried at 65°C to estimate in sacco DM degradation. The animals were fed a diet consisting of *Echinochloa polystachia* ad libitum and 2 kg of a corn-soybean meal based concentrate. Digestion parameters were obtained by means of non linear regression, a randomized model with three replications was analyzed and treatments means separated by the Tukey test. The results showed significant effects ($P < 0.05$) of diets on in sacco degradability kinetics of DM. For ruminal degradation, the lowest soluble fractions (23.42 ± 1.4%) and degradation rate ($0.005h^{-1}$) were observed in HBH. However, positive effects were observed with the other diets, presenting the highest values in maximum degradation (56.39 ± 2.7%), degradation rate ($0.015h^{-1}$) and potential degradation (85.18 ± 3.1%) when 25% HBH + 75% ALS was offered ($P < 0.05$). It can be concluded that *Albizia lebbeck* silage diets had high DM rumen degradability and indicate that these diets could be used as ruminant feed supplements to enhance forage digestibility.

Key words: *Albizia lebbeck*, silages, rumen degradability

W93 Characterization and identification of *Lactobacilli* stains from tropical grasses. J. P. S. Rigueira[1], O. G. Pereira*[1], K. G. Ribeiro[2], A. S. Cezário[1], and W. F. Souza[1], *[1]Federal University of Viçosa, Viçosa, Minas Gerais, Brazil, [2]Universidade Federal dos Vales do Jequitinhonha e Mucuri, Diamantina, Minas Gerais, Brazil.*

The grasses of *Brachiaria* and *Panicum* genera have constituted one of the most important forage for pasture in Brazil. There has been recent interest in using these forages for the silage production. In this work, we characterize and identify lactobacilli strains isolated from grasses *Panicum maximum* 'Mombaça' and *Brachiaria decumbens*. The isolation of predominant lactic acid bacteria (LAB) in forage before ensiling was carried out on Rogosa SL Agar (Difco), at 37°C, for 48 h.

Forage samples were randomly collected from the pasture after 70 d of regrowth. For the 10^1 dilution, 25 g of forage was mixed with 225 mL of sterile phosphate buffer solution and homogenized in a blender for 1 minute. Decimal dilutions were made ranging from 10^1 to 10^6 and plated on sterile Petri dishes. We carried out the Gram stain test reaction to catalase, growth at different pH and temperatures beyond the morphology of the isolated stains. Isolate identification was obtained using the API 50 CH carbohydrate fermentation test kit (bioMérieux, Inc., France). All isolated strains showed negative reaction to catalase and were Gram stain positive. They grew at pH 7.2 and were inhibited at pH 9.6. All the stains showed growth at temperature from 15°C to 45°C.The morphology of the bacillus stains was identified as *Pediococcus pentosaceus* and *Leuconostoc mesenteroides* and showed the coccus form. Table 1 shows the isolated species in tropical grasses. *Lactobacillus fermentum* and *Lactobacillus plantarum* the predominant species in both forages. Financial support by CNPq and FAPEMIG.

Table 1. Species indentified by API 50 CH test in *Brachiaria* (B) and *Panicum maximum* (M) forages and the respective percentage abundance (ID)

Code	Species	%ID	Code	Species	%ID
B3	*Leuconostoc mesenteroides*	88.9	M2	*Lactobacillus lactis* ssp. *lactis*	83.8
B4	*Lactobacillus fermentum*	99.5	M4	*Lactobacillus fermentum*	93.7
B5	*Lactobacillus brevis*	70.7	M16	*Lactobacillus paracasei*	80.8
B6	*Lactobacillus fermentum*	96.2	M21	*Lactobacillus plantarum*	94.9
M1	*Pediococcus pentosaceus*	93.5	M17	*Lactobacillus paracasei*	80.8

Key words: lactic acid bacteria, tropical grass, silage

W94 Milk production response to feeding alfalfa silage inoculated with *Lactobacillus plantarum*. R. E. Muck*[1], G. A. Broderick[1], A. P. Faciola[2], and U. C. Hymes-Fecht[1], *[1]USDA, ARS, US Dairy Forage Research Center, Madison, WI, [2]University of Wisconsin-Madison, Madison.*

In mini-silo trials, silages treated with a *Lactobacillus plantarum* inoculant (Ecosyl, Yorkshire, UK) had increased in vitro rumen microbial biomass production. Our objective was to determine if alfalfa silage treated with this inoculant could produce a milk production response commensurate with the in vitro responses. Alfalfa (240 g CP/kg DM, 300 g NDF/kg DM, 500 g DM/kg) was ensiled with (LP) and without (C) Ecosyl inoculant. Twenty-eight multiparous Holstein cows in early lactation were blocked by DIM and randomly assigned to 2 diets (C or LP-treated silage) in a double crossover design with 4 28-d periods. Diets were formulated to contain 162 g CP and 280 g NDF/kg DM, and the diets fed consisted of (g/kg DM): alfalfa silage (509), corn silage (206), high moisture corn (214), soy hulls (47) and vitamin/mineral mix (25). Milk production and DMI were recorded for the last 14 d of each period. Milk samples were collected from each cow at both milkings on d 20, 21, 27 and 28 for analysis of milk composition. Means for LP were compared against means for C before and after LP using a paired *t*-test in Proc MIXED of SAS. The LP diet increased milk production but did not affect DMI or milk/DMI. Milk composition and production of milk components were largely unaffected by diet except as noted in the table. The increased milk production and reduced MUN in the current study support the hypothesis that the inoculated silage is producing more rumen microbial biomass.

Table 1. Milk production and composition from diets containing alfalfa silage made with (LP) and without (C) inoculant

Item	C	LP	SE	*P*-value
Milk, kg/d	39.6	40.4	0.26	0.03
Milk Protein, %	2.81	2.78	0.009	0.05
Milk Lactose, %	4.82	4.89	0.013	<0.01
Milk Urea N, mg/dL	12.7	11.6	0.17	<0.01

Key words: silage inoculant, milk production, alfalfa

W95 Biomin BioStabil Plus enhances the fermentation characteristics, aerobic stability, and intake by rams of native tropical grass silage. C. Rosario[1], A. A. Rodriguez*[1], and Y. Acosta-Aragon[2], *[1]University of Puerto Rico, Mayaguez, PR, [2]Biomin Holding GmbH2, Herzogenburg, Austria.*

The effect of Biomin BioStabil Plus (BSP, blend of homo and heterofermentative lactic acid bacteria) on the ensiling characteristics, aerobic stability, and intake by rams of native tropical grasses (NTG) silage was determined. Forage (mix of *Panicum maximun*, *Sorghum halapense*, and *Digitaria decumbens*; 6-week regrowth) was chopped and treated with or without BSP. Treatments were applied to weighed portions of forage, manually mixed and packed into PVC micro-silos. Fresh forage and samples of 3 silos for each treatment opened at 4, 7, 14, 21, 28 and 35 d were analyzed for pH and fermentation products. Statistical analysis was performed as a Completely Randomized Design (CRD) with a 2 (treatments) by 7 (d) factorial arrangement. Aerobic stability was determined on 3 silages from each treatment exposed to air. The pH and temperature were measured after 0, 24, 72 and 96 d, and 0, 6, 12, 24, 30, 48, 72, 96 and 120 h of aerobic exposure, respectively. Statistical analysis of pH and temperature data was performed as a CRD with a 2 (treatments) by 4 (d) or 2 by 10 (h) factorial arrangement, respectively. To determine the effects of NTG fermented with BSP on DMI, chopped NTG were ensiled with or without the inoculant in 208-L capacity plastic bags for a minimum of 35 d. Six rams were used in a CRD trial with 3 replicates per treatment. Diets containing 50% grass hay and 50% NTG treated with or without BSP, were offered daily at 3% of ram BW/dry matter basis. Rams were allowed a 6-d diet adaptation, prior to a 5-d data collection period. Forage fermented with BSP had lower ($P < 0.05$) pH and higher ($P < 0.05$) lactic acid content than untreated silage. Vegetative material treated with BSP and exposed to air for 5 d had lower ($P < 0.05$) pH than control, but no effect on temperature was observed. Silage intake as proportion of total DM offered and as percentage of total DMI was improved ($P < 0.05$) by 8.13% and 4.42% when rams were fed with the inoculated silage. The ensiling of NTG with BSP enhanced the fermentation characteristics and improved forage consumption by rams.

Key words: tropical grasses, silage, BioStabil Plus

W96 Fermentation characteristics and aerobic stability of tropical corn ensiled with additives containing homo-fermentative or hetero-fermentative bacterial strains. V. Rivera[1], L. Solorzano[2], and A. Rodriguez*[1], *[1]University of Puerto Rico, Mayaguez, PR, [2]Chr. Hansen, Fitchburg, WI.*

The fermentation characteristics and aerobic stability were determined on tropical corn (TC; *Zea mays*) ensiled with additives containing homo-fermentative (*L. plantarum*) or a blend of homo and hetero-fermentative (*L. buchneri, E. faecium and L. plantarum*) lactic acid-producing bacteria (LAPB). Corn (38% DM) was chopped (2.5 cm), untreated or treated with both products to weighed portions of forage, manually mixed, and packed into PVC microsilos (1.5 kg) to ferment for 0, 15, 30, and 58 d. Three samples of fresh forage and silage for each treatment (trt) and ensiling d were analyzed to determine pH and fermentation products. Statistical analysis was performed as a Completely Randomized Design (CRD) with a 3 (trt) by 4 (d) factorial arrangement. For aerobic stability, 3 samples from each trt and ensiling d were exposed to air for 120 h. The pH and temperature were measured after 0, 1, 3 and 5 d, and 0, 6, 12, 18, 24, 48, 72, 96 and 120 h of aerobic exposure, respectively. Statistical analysis of pH and temperature data was performed as a CRD with a 3 (trt) by 3 (length of fermentation) by 4 (d) or 3 by 3 by 9 (h) factorial arrangement, respectively. Corn fermented with homo-fermentative LAPB tended to have lower ($P < 0.09$) pH and higher ($P < 0.07$) lactic acid content than untreated silage or TC fermented with hetero-fermentative LAPB. After 24 h of aerobic exposure TC fermented with both products had lower ($P < 0.01$) pH than the control. The pH was also higher ($P < 0.01$) in untreated silage than TC treated with additives after 15 and 30 d of ensiling, but similar when fermented for 58 d. Forage fermented with both products resulted in silage with lower ($P < 0.05$) temperature after 1 d of aerobic exposure. Inoculation prevented the start of the temperature rise by 18 and 24 h in TC treated with homo or hetero-fermentative strains, respectively. In summary, homo-fermentative strains improved the fermentation characteristic and delayed the deterioration of TC silage, but a greater response of the product containing hetero- fermentative bacteria on aerobic stability was observed.

Key words: tropical corn, silage, additives

W97 The aerobic stability and dry matter losses of high moisture corn ensiled as whole or ground grain using *Lactobacillus buchneri* alone or in association with *Lactobacillus plantarum*. R. Coudure[1], J. G. Cazaux[1], F. Skiba[1], E. Chevaux*[2], V. Demey[2], and J. Sindou[2], *[1]Arvalis - Institut du végétal, Montardon, France, [2]Lallemand SAS, Blagnac, France.*

The goal of this trial was to study the effect of addition of a single additive or a combination of silage additives on the fermentation, aerobic stability and nutritional value of High Moisture Corn (HMC). The trial was designed as a 3 × 2 × 2 factorial with the following factors: (i) no additive (C) vs *Lactobacillus buchneri* NCIMB 40788 (LB) (300000 cfu/g HMC) vs *L.buchneri*+ *Lactobacillus plantarum* MA18/5U (LBLP) (LB 150000 cfu/g HMC + LP 100000 cfu/g HMC), (ii) whole grain (WG) vs ground(G) (2 mm) and (iii) 36% vs 32% moisture (of the corn). Each experimental group had 6 replicates (microsilos). The anaerobic and aerobic phases lasted 144 and 13 days respectively. Dry matter (DM) losses were determined by weighing all silos individually at the start and end of each phase. Samples were taken for DM, pH and chemical composition determinations at d 11 and 20 of the anaerobic phase, at opening of silos and 13 days after opening. In the case of 36% moisture HMC, lower DM losses were seen with the combination LBLP. For GHMC as well as WGHMC, a higher fraction of the total DM was conserved at the end of the aerobic phase, compared to C (i.e. +5.3% vs. +2.4% resp., $P < 0.01$). The use of LB alone conserved 2.6% more DM in GHMC at the end of the aerobic phase. For WGHMC, little differences were seen in DM losses between C and LB alone. In terms of variations in pH, the values for LB and LBLP treated GHMC were higher ($P < 0.01$) than C at the end of the anaerobic phase (4.5 ± 0.03 and 4.2 ± 0.10 vs. 4.0 ± 0.03 resp.). However at opening, the pH of LB and LBLP treated silos stayed stable, whereas the pH of the C increased ($P < 0.05$) rapidly (4.6 ± 0.05 and 4.3 ± 0.06 vs. 5.5 ± 0.37). In WGHMC the pH measured at opening was 4.5 for all experimental groups and rose by 0.5 units during the aerobic phase. The chemical composition of HMC was not affected by the silage additives when compared to C. Similar trends were observed for the parameters tested for the 32% moisture HMC, however differences observed seemed less pronounced compared to the 36% moisture HMC.

Key words: high moisture corn, *L.buchneri*, *L.plantarum*

W98 Effect of dry matter density on fermentation and nutrient preservation in brown mid-rib (BMR) corn silage within bunker silos. K. Griswold[1], P. Craig[2], J. Graybill[1], and R. Ward*[3], *[1]Penn State Cooperative Extension, Lancaster, [2]Penn State Cooperative Extension, Dauphin, [3]Cumberland Valley Analytical Services, Maugansville, MD.*

The objective was to determine the relationship of dry matter (DM) density to fermentation and nutrient preservation in BMR corn silage within bunker silos. Poly-weave nylon bags (36 per silo) containing chopped BMR corn were buried in 3 bunker silos during filling on the same farm in 2 successive years. Bags were blocked by depth from bunk end, 10.6 m (Front), 27.8 m (Center), and 44.9 m (Back), level from silo floor, 0.6 m (Low), 1.5 m (Middle), and 2.2 m (High), 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). At feed-out, all bags at a specific depth were retrieved, and silage cores for DM density at each bag position were collected with a 5.08 cm diameter stainless-steel coring tube. Corn and silage subsamples were analyzed for nutrient content and fermentation profile by NIR and wet chemistry. Data were analyzed by PROC MIXED and REG within SAS. The model included fixed effects of depth, level, location, all interactions, and random effects of silo and year. Significance was set at $P < 0.05$, and trends at $0.05 \leq P \leq 0.10$. There were no significant interactions. Density was affected ($P < 0.0001$) by depth, level, and location. Density was 221, 274, and 273 kg DM/m^3 for front, center, and back, respectively. Density was 282, 265, and 221 kg DM/m^3 for low, middle, and high, respectively. Density was 238 and 231 kg DM/m^3 for I and IV compared with 279 and 275 kg DM/m^3 for II and III, respectively. Fermentation was affected ($P < 0.05$) by depth and level but not location. Total VFA were 9.7, 10.8, and 10.4% of DM for front, center, and back, and 11.2, 10.3 and 9.5% of DM for low, middle and high, respectively. There was a trend ($P = 0.059$) for NDF content to be affected by level with 37.8, 38.6, and 40.4% of DM for low, middle, and high, respectively. Regression analysis showed a weak linear inverse relationship ($R^2 = 0.05$) between DM density and NDF content. Starch content was unaffected ($P > 0.10$) by DM density across all positions. These results suggest that DM density of BMR corn silage may affect fermentation, but likely does not affect starch and NDF content.

Key words: corn silage, density, fermentation

W99 Effects of the levels of silage additives on the fermentation quality and in situ digestibility of reed (*Phragmites australis* Cav.) silage harvested at different maturity stages. B. W. Kim*, K. I. Sung, and J. S. Shin, *College of Animal Life Sciences, Kangwon National University, Chuncheon, Kangwon-Do, South Korea.*

This study was conducted to determine the optimum levels of silage additives on reed silage harvested at different maturity stages. Reed

plants harvested at early boot (23% DM), late boot (24% DM) and early heading stages (26% DM) were chopped to an average particle length of 1 cm and ensiled in 500 g mini silos, with and without additive treatment. The additives used were formic acid applied at 0.2, 0.4 and 0.6% of the fresh crop weight and molasses applied at 0.5, 1.0 and 2.0% of the fresh crop weight. Treatments were allocated in a randomized complete block design with three replicates. The silage pH, acid and NH_3-N/TN concentrations, and the situ DM disappearance at 0, 12, 24, 48 h of incubation in Korean beef cattle were examined. The silage fermentation quality and in situ digestibility were not affected by the different maturity stages. Silage treated with formic acid had the lower pH (4.5, 4.3 and 4.0 at 0.2, 0.4 and 0.6%, respectively) than the molasses (5.0, 4.8 and 4.4 at 0.5, 1.0 and 2.0%, respectively) and untreated (5.2). While the lactic acid concentrations increased with the higher levels of molasses, the higher levels of formic acid resulted in lower concentrations of lactic acid ($P < 0.05$). The formic acid and molasses treatments were markedly effective for reducing the ammonia production which was similar at most addition levels (less than 10% NH_3-N/TN at all addition levels). Higher in situ digestibility resulted from adding additives, especially with formic acid treatment (about 10% at 0.2% level; $P < 0.05$). No significant difference was found between the addition levels of both additives. It is concluded that formic acid or molasses applied at ensiling produced better fermented silage and enhanced silage digestibility compared with untreated reed silage. The highest quality of reed silage was observed at 0.2% of formic acid and 2.0% of molasses, which are considered as the optimum levels of addition in this study.

Key words: reed, silage, additive

W100 Ruminal parameters of sheep fed corn silage inoculated with *Lactobacillus buchneri* and *L. buchneri* associated with *L. plantarum*. F. C. Basso*, P. A. R. Salvo, F. H. Kamada, J. P. R. Costas, W. L. da Silva, and R. A. Reis, *Animal Science Departament, College Agricultural and Veterinary Sciences, São Paulo State University, Jaboticabal, São Paulo, Jaboticabal.*

Silages inoculated with certain heterofermentative bacteria show improvement in aerobic stability. Many studies are done on silages, however few studies are reported about the effect of microbial inoculants on ruminal parameters in sheep. Therefore, the aim was to evaluate the effect of microbial inoculants in corn silage on sheep ruminal parameters. Three stack silos containing 10 t of corn silage were prepared. The corn silages were treated with nothing (CS, 32% of DM); or with either *L. buchneri* NCIMB 40788 (1×10^5cfu/g of forage; 35.5% of DM, CSB) or with *L. buchneri* (1×10^5 cfu/g; 31.7% of DM) plus *L. plantarum* MA18/5U (1×10^5 cfu/g, CSBP). Silage samples were collected during the experiment. The DM content, pH value, ammonia nitrogen content and yeast and mold counts (log cfu/g) were measured. Six castrated 10 mo-old, rumen cannulated male rams (40kg) were used. The animals were fed 80% of corn silage and 20% of commercial concentrate (57.5% soybean meal, 7% wheat bran, 5% cottonseed meal, 16% ground corn, 12.5% citrus pulp and 2% of mineral salt). The daily dry matter intake (DMI) was measured. Rumen fluid samples were collected 0, 3, 6, 9, 12 hours after feeding to measure pH values and ammonia levels. The experimental design was Latin square (3 × 3) repeated twice. Data was subjected to ANOVA and means compared by the Tukey test ($P < 0.05$). The DM content was different ($P < 0.05$) among treatments (CS: 31.68%; CSB: 33.42% and CSBP: 30.80%), probably because at ensiling, the DM content also was different among the forages. The pH value of CSB was lower (4.03) than CS (4.12) and CSBP (4.11) ($P < 0.05$). Ammonia nitrogen content (CS: 12.94%, CSB: 11.86% and CSBP: 14.51%) and yeast and mold counts (<3.00 log cfu/g of silage) were not different among treatments. Average DMI was 0.930; 0.962 and 0.881 kg/d, respectively for CS, CSB, and CSBP. The difference between CSBP and CSB was significant ($P < 0.05$). Ruminal pH (6.06, 6.12 and 6.07, respectively) and ruminal ammonia (17.09, 13.87 and 15.11 mg/dL) were not affected by the microbial inoculants in silage. In conclusion, addition of microbial inoculant in corn silage did not affect the ruminal parameters evaluated.

Key words: ammonia, microbial additives, pH values

W101 In vitro fermentation on cactus forage (*Opuntia* spp.) inoculated with *Kluyveromices lactis* yeast. C. Rodríguez-Muela*[1], D. Díaz-Plascencia[1], P. Mancillas-Flores[1], O. Ruiz-Barrera[1], F. Salvador-Torres[1], G. Corral[1], S. Mena[2], R. Copado-García[1], and L. Duran[1], *[1]Universidad Autónoma de Chihuahua, Chihuahua, México, [2]Universidad de Guadalajara, Jalisco, México.*

In order to evaluate the effect of use of *Kluyveromyces lactis* yeast (Kl) obtained from apple byproducts by solid state fermentation, on cactus forage (*Opuntia spp*), two treatments (Tr) were used: T1) 10 kg of paste of cactus forage (CF) and T2) 10 kg of CF + 100 ml of an inoculate of Kl (1.2×10^9cells/mL). Each Tr was added with 20 g of urea, 2 g of ammonium sulfate, and 5 g of mineral supplement. There were six replications per Tr and samples were fermented in an aerator for 48h to support the growth of yeasts. Tr was mixed for 15 min every 12h, and samples were taken at 0, 12, 24 and 48h. The variables evaluated were: temperature (T), pH, ammonia (AM), lactic acid (LA), yeasts count (YC), soluble sugars (SS) and crude protein (CP). The statistical design used was a completely randomized design, considering the random effect of the aerator nested in Tr (plot). Data were analyzed with the Proc Mixed procedure of SAS. The results showed that T increased ($P < 0.01$) from 0 to 12h, showing an inoculate*time interaction, with values of 22.4°C and 24.1°C in T1, and 20.7°C and 24.6°C in T2. Values of pH in T1 decreased ($P < 0.04$) from 4.9 to 4.6, and from 4.8 to 4.4 in T2 from 0 to 48h (respectively). Values of AM increased ($P < 0.01$) from 0.31 to 0.44 mM/mL in T1, and from 0.29 to 0.38 mM/mL in T2 from 0 to 48h (respectively). Values of LA increased ($P < 0.01$) from 2.30 to 2.63 mM/mL in T1, and they decreased from 1.55 to 0.91 mM/mL from 0 to 48h in T2. YC increased ($P < 0.01$) from 8.3×10^6 to 1.8×10^7cells/mL in T1 and from 3.2×10^7 to 4.9×10^7cells/mL of 0h to 48h in T2. There was an effect of time ($P < 0.01$) on SS, with a trend to decrease over fermentation time. An interaction was found for inoculate*time on CP ($P < 0.01$) with values in T1 of 9.4, 12.2 and 11.7% at 0h, 24h and 48h, and of 14.7, 19.4 and 18.0% at 0h, 12h and 48h, in T2, respectively. It can be concluded that the use of Kl on the in vitro fermentation of cactus forage increased significantly CP content and yeast counts with a marked reduction of SS and LA.

Key words: yeast, fermentation, cactus

W102 Comparison of an inoculant and enzymes, separate and in combination, on the fermentation of alfalfa silage. S. J. Z. Hansen* and A. H. Smith, *Danisco, Waukesha, WI.*

Fermented feedstuffs are one of the key components of the dairy ration, where stability and digestibility are important characteristics. The objective of this study was to compare the use of inoculants and enzymes, separate and in combination, on alfalfa silage to determine whether a more stable, digestible forage was produced. Treatments tested in the mini-silos were untreated (Ctrl), Agmaster XV inoculant (XV) and 2 enzymes, Clampzyme 20 (C20) and Clampzyme HIGO100

(HG) (Genencor). Agmaster XV contains *Pediococcus pentosaceus* P751, *Lactobacillus plantarum* LP115 and *Lactobacillus brevis* LBR35 and was applied at 1.8 e 11 cfu/ton of haylage. Glucose oxidase and cellulase are the active ingredients of C20 (3500 carboxymethylcellulose (CMC) Units/g) and HG (3600 CMC Units/g) and these were applied at 0.91 g/ton of haylage. Mini-silos used were airtight 5-gallon buckets containing haylage at a density of 240 kg/cubic meter. Alfalfa was wilted for 24 h before it was chopped. The moisture of the alfalfa was 51.4%, within the ideal level for ensiling when packed. Three mini-silos from each treatment, at Day 1, 3, 7 and 14, were opened and homogenized, with samples taken for volatile fatty acid (VFA) analysis, pH, enumeration of lactic acid bacteria and spoilage organisms (coliforms, yeasts, molds), and ADF, aNDF, NDFD48 and CP. Statistics, using 2-way ANOVA analysis, established the inoculant and both enzyme treatments improved fermentation by decreasing pH and increasing lactate (Table 1), however a synergistic effect of the inoculants with enzymes was noted. All treatments decreased spoilage organisms, and the inoculant with enzymes increased digestibility, as measured by NDFD48, on d 7 when compared with the control ($P < 0.001$). The use of inoculants and enzymes improved the fermentation of alfalfa silage, increasing the quality of the feed.

Table 1. Lactate (% DM) accumulation after ensiling

	Days of ensiling			
	1	3	7	14
Ctrl	0.5	1.9[a]	3.9[a]	3.6[a]
XV	0.6	2.5[b]	4.4[b]	4.9[b]
C20	0.5	2.5[b]	4.3[b]	4.7[b]
HG	0.6	2.6[b]	4.9[c]	4.9[c]
XV+C20	0.7	3.7[c]	5.2[c]	5.6[c]
XV+HG	0.9	3.5[c]	5.7[d]	5.4[c]

[a,b,c]Means within a column with unlike superscripts differ ($P < 0.05$).

Key words: fermentation, enzymes, inoculant

W103 Effects of sodium bisulfate on alfalfa silage preservation. M. Terré[1], D. Seale[2], C. Knueven[3], and A. Bach*[4,1], *[1]Institut de Recerca i Tecnologia Agroalimentàries, Caldes de Montbui, Barcelona, Spain, [2]DS AgriTech Ltd., Reading, Berkshire, UK, [3]Jones-Hamilton, Co, Walbridge, OH, [4]Institució Catalana de Recerca i Estudis Avançats, Barcelona, Spain.*

Sodium bisulfate (SBS) is proposed as an acidifier to produce a rapid acid condition during the ensiling process by releasing the bisulphate ion HSO_4^-. The objective of this study was to evaluate the effects of SBS on pH, silage fermentation and aerobic stability of alfalfa silages. Third-cut alfalfa was harvested and chopped mid July 2010, wilted to 43.1% DM, and ensiled in 14 30–L capacity microsilos, and stored at ambient temperature (18–25°C). Half of them were treated with SBS at the dose of 8 g/kg of fresh alfalfa (Jones-Hamilton Co., OH) (SBS) and the other half was not treated with any preservative (C). On d 0, samples were analyzed for pH, DM, water-soluble carbohydrates (WSC), CP, NDF, ash and buffering capacity (BC). On d 3, 3 microsilos per treatment were opened to determine pH, BC, and ammonia–N. On d 100, 4 microsilos per treatment were opened to determine pH, DM, ammonia-N, WSC, lactic, acetic, propionic and butyric acid, ethanol, CP, and aerobic stability was monitored for 7 d. Lactate-assimilating yeasts and molds were enumerated on d 100 and 107. Data were analyzed with an ANOVA with silo treatment as main effect. The pH was lower ($P < 0.05$) in SBS than in C silos on d 0 (4.80 vs. 5.94 ± 0.127, respectively), and this difference was maintained on d 100 (4.52 vs. 4.88 ± 0.041, respectively, $P < 0.001$). Buffering capacity was also modified with the addition of SBS, being lower ($P < 0.05$) in SBS compared with C silos on d 0 (1208 vs. 1478 ± 53.3, respectively) and 3 (1114 vs. 1347 ± 77.5, respectively). All silages were well preserved and no differences in the NDF, WSC, CP and ashes content, the fermentation profile, in yeast and molds counts, in lactate-assimilating yeast counts, or in temperature changes during the aerobic stability measurements were observed between treatments. In conclusion, sodium bisulfate reduced silage pH (in agreement with an observation already made in grass silages) and lowers the buffering capacity of alfalfa silage, both of which could be expected to aid preservation under more difficult ensiling conditions than those encountered in this trial.

Key words: alfalfa, silage, sodium bisulfate

W104 Nutritive value and fermentation parameters of 'Tifton 85' bermudagrass and 'Mulato II' brachiariagrass silage in Florida. A. D. Aguiar*[1], J. M. B. Vendramini[1], A. T. Adesogan[2], L. E. Sollenberger[2], L. Galzerano[1], L. Custodio[1], E. Alves[1], and G. R. Manarim[1], *[1]Range Cattle Research Education Center, Ona, FL, [2]University of Florida, Gainesville.*

The objective of this study was to investigate the nutritive value and fermentation parameters of Mulato II (*Brachiaria* sp.) and Tifton 85 bermudagrass (*Cynodon* sp.) silages treated with sugarcane (*Saccharum officinarum* L.) molasses [M; 1 kg molasses (DM)/50 kg forage (As fed)], inoculants [I; EcoSyl, MTD/1; 100 mg/50 Mg forage (As fed)] (I), molasses plus inoculants (MI), and control (C). The experiment was conducted in Florida and harvested in the summer (21 July) and fall (6 October) 2010. Tifton 85 plots were distributed in a randomized complete block design with 4 replicates, and Mulato II plots in a complete randomized design with 4 replicates. The data were analyzed using PROC MIXED with treatment as fixed effect, and block and replicates as random effects. Forage was harvested, wilted on the field for 4 h, packed into a mini-silo at a density of approximately 382 kg fresh forage/m^3, and ensiled for 90 d. In the summer, there were no differences ($P > 0.10$) among treatments for the parameters evaluated in Mulato II silage. In Tifton 85 silage, treatments C and I had greater concentrations of acetic acid than M ($P = 0.05$, 0.33 vs. 0.55%), however, the C treatment had greater NH3-N and lesser NDFD concentration than M and I ($P = 0.03$, 8.0 vs. 6.0% total N). During the fall, the I treatment had lesser lactic acid ($P = 0.09$, 1.8 vs. 3.9%), and NH3-N concentrations than the C ($P = 0.03$, 7.0 vs. 11.0% total N) in Mulato II silage. The M treatment had greater concentrations of water-soluble carbohydrates than C and I ($P = 0.06$, 9.9 vs. 6.7%) and the NDFD was greater ($P = 0.09$) for MI (61%) than C, I, and M (Mean = 54%). Tifton 85 fall silage treated with molasses had greater water-soluble concentration than C and I ($P = 0.04$, 3.8 vs. 1.9%). The NH3-N concentration was greater for I than C ($P = 0.04$, 17 vs. 10% of total N) but there was no difference ($P > 0.10$) between C and M, and M and I. The effects of molasses and inoculants were inconsistent in this study and further investigation is necessary to evaluate the benefits of those management practices on warm-season grasses silage.

Key words: warm-season grass, inoculants, silage

W105 Effect of new mixtures of silage additives in grass and maize on fermentation quality and aerobic stability. J. Jatkauskas[1], V. Vrotniakiene[1], C. Ohlsson[2], and B. Lund*[2], *[1]Institute of Animal Sci-*

ence of Lithuanian University of Health Sciences, Baisogala, Lithuania, [2]Chr Hansen A/S, Hoersholm, Denmark.

The aim was to evaluate the effect of five new silage additives (A - E) containing lactic acid bacteria on fermentation characteristics and especially aerobic stability. The additives were compared to a positive and negative control in laboratory-scale experiments. The treatments were different combinations of inoculants containing *Lactobacillus plantarum* DSM16568 (B,C,D,E), *Enterococcus faecium* DSM 22502 (B,C,D,E), *Lactobacillus buchneri* DSM 22501 (A,B), *Lactococcus lactis* DSM 11037 (E) and NCIMB 30117 (B,C) at 150,000 cfu/g forage and one treatment was supplemented with sodium benzoate at 400 g/ton forage (C). The positive control was an inoculant of *Lactobacillus plantarum* at 100,000 cfu/g. The 3-liter mini-silos were filled with chopped ryegrass-timothy (DM 26.5%, WSC 2.7% of fresh matter (FM)) or whole-crop maize (DM 27.5%, WSC 2.7% of FM) with 5 replications per treatment and crop. Silos were stored at 20°C for 90 days before measuring the following parameters: pH, dry matter (DM) losses, fatty acids, ethanol, N-NH_3 and aerobic stability. Data were statistically analyzed as a randomized complete block by using the GLM procedure of SAS. In both grass and maize, additives A - E and the positive control resulted in significantly reduced ($P < 0.05$) DM loss, pH, acetic acid, butyric acid, propionic acid, alcohols and/or N- NH_3while lactic acid increased compared with untreated silage ($P < 0.05$). Additives A, B and C designed for improved aerobic stability, had lower temperatures ($P < 0.05$) at the end of the 7-day period of air exposure compared with the negative and positive controls in both silages. Untreated grass silages were stable for 4 days, the positive control 7 days, whereas additives A, B, C, D and E were stable for >13, 10, 7.5, 7 and 7 days, respectively. Untreated maize silage was stable for 2 days, the positive control 3 days, whereas A, B, C, D and E were stable for 6, 5.5, 6, 3 and 4 days, respectively. Additives A - E significantly improved fermentation quality and additives A, B and C significantly improved aerobic stability when compared to the positive control in both silages.

Key words: inoculant, silage additive, aerobic stability

W106 Identification and characterization of spoilage yeasts from high moisture corn and corn silages. M. C. Santos*[1], C. Golt[1], R. D. Joerger[1], G. D. Mechor[2], and L. Kung[1], *[1]University of Delaware, Newark, [2]Elanco Animal Health, Greenfield, IN.*

The objectives of this study were to identify and characterize yeasts associated with aerobic spoilage of high moisture corn (HMC) and corn silage (CS) and to compare 3 methods of yeast identification. Silages were sampled from 21 US dairy farms and shipped to the University of Delaware for analysis. Water extracts were prepared by homogenizing 25 g of silage with 225 mL of quarter-strength ringer's solution for 1 min. Silage pH was measured and yeasts were enumerated by pour plating in malt extract agar and incubated at 32°C for 48 h. Colonies were randomly picked from plates with the highest serial dilutions and taxonomically identified by fatty acid methyl ester (FAME) analysis (MIDI Inc., Newark, DE). An isolate of each species with the highest FAME similarity index was also characterized by DNA sequencing and biochemical tests (ID 32 C system, bioMerieux, Marcy l'Etoile, France). Average pH was 4.3 (ranging from 3.9 to 4.8) and 3.7 (ranging from 3.5 to 4.1) and average yeast counts were 6.3 $\log_{10}$ cfu/g (ranging from 4.3 to 7.9) and 5.4 (ranging from 4.2 to 7.0) for HMC and CS, respectively. Of 266 colonies isolated, 87.3% were identified by FAME in 24 known species and 12.8% were unknown. *Candida valida* (33.1% of total isolates), *Saccharomyces cerevisiae* (10.2%), *C. holmii* (7.1%), *Zygosaccharomyces bisporus* (7.1%) and *C. milleri* (4.1%) were the most prevalent species. The remaining 25.7% of isolates belonged to 19 other species. *C. valida* and *Z. bisporus* were lactate utilizers whereas *S. cerevisiae*, *C. holmii* and *C. milleri* were able to metabolize glucose and sucrose, but not lactate. *C. valida* was the most common species isolated from HMC and CS (35.1 and 30.5%, respectively). *S. cerevisiae* (12.8%) and *C. holmii* (13.6%) were the second most common isolates from HMC and CS, respectively. Yeast diversity was higher in HMC than in CS (21 species vs. 11 for CS) but the later had a higher percentage of unknown species (22.9% vs. 4.7%). Identification of yeasts using DNA analysis generally corresponded with identification using biochemical tests; however, FAME analysis did not generally agree with these 2 methods.

Key words: *Candida valida*, silage, spoilage

W107 Ruminal parameters of cattle fed corn silage inoculated with microbial additive. P. A. R. Salvo*, F. C. Basso, F. H. Kamada, J. V. Yamaguchi, V. V. Naves, and R. A. Reis, *Animal Science Department, College Agricultural and Veterinary Sciences, São Paulo State University, Jaboticabal, São Paulo, Brazil.*

Microbial inoculants containing heterofermentative bacteria are used in corn silage to improve the aerobic stability, however few studies are reported about the effect of microbial inoculants on cattle ruminal parameters. The aim this study was to evaluate the effect of *Lactobacillus buchneri* and *Lactobacillus buchneri* associated with *Lactobacillus plantarum* in corn silage on ruminal parameters of cattle. Therefore, six rumen cannulated beef steers (470 kg) were used. The steers were fed with 80% of corn silage and 20% of commercial concentrate (8% of soybean meal, 87% of ground corn and 5% of mineral salt). The treatments were the corn silages inoculated with *L. buchneri* NCIMB 40788 (1×10^5 cfu/g of fresh forage, CSB); corn silage inoculated with *L. buchneri* NCIMB 40788 (1×10^5 cfu/g) in combination with *L. plantarum* MA18/5U (1×10^5 cfu/g, CSBP) and untreated corn silage (CS). Average daily dry matter intake (DMI) was measured. Rumen fluid samples were collected 0, 3, 6, 9, and 12 hours after feeding. The pH values were evaluated with a pH meter. Approximately 1mL of H_2SO_4 (1:1) was added to the suspensions to stop the microbial activity. Samples were frozen and subsequently, ammonia concentrations were measured by the Kjeldahl method using KOH (2N). The experimental design was a Latin square (3×3) duplicated in time. Data were subjected to analysis of variance and means compared by the Tukey test at a significance level of 5%. Each experimental period consisted of 7 days of adaptation and 3 days of data collection. Average daily DMI, ruminal pH and ruminal ammonia were not affecting by the microbial inoculants in corn silage ($P > 0.05$). Average DMI was 6.99, 6.92 and 6.78; ruminal values of pH were 6.12, 6.09 and 5.99 and the ruminal ammonia levels were 10.61; 9.91 and 9.73 mg/dL, respectively in the CS, CSB, and CSBP silages. Ruminal parameters evaluated were normal. In conclusion, the microbial inoculant treatment of corn silage did not affect the ruminal pH and ammonia concentrations of cattle.

Key words: ammonia, *Lactobacillus buchneri*, *Lactobacillus plantarum*

W108 Investigation of microbial additives on fermentation quality of alfalfa silage. F. Kazemi, M. Dehghan-Banadaky*, A. Zali, and K. Rezayazdi, *Animal Science Department, Campus of Agricul-*

tural and Natural Resources, University of Tehran, Karaj, Tehran, Iran.

The objective of present study was to investigate the effects of microbial additives on physical and chemical characteristics of alfalfa silages. In this experiment treatments included: 1-untreated corn silage (control), 2-treated with Ecosyl (EC) (0.125mg/kg), 3-Lacticil Maize (LM) (0.2 mg/kg), and 4- combination of both them Ecosyl (0.063 mg/kg), Lacticil Maize (0.1 mg/kg) were added to pilot silages. Silages were opened on days 10, 20, 30 and 40 after ensiling. Silage quality was assessed using pH, ammonia nitrogen and VFAs concentrations, Flieg point (ratio between dry matter concentration and pH), crude protein, dry matter, neutral detergent fiber and organic matter concentrations. Treatment 3 had the lowest pH and highest Flieg point compared with the others ($P < 0.05$). While treatment 2 had the highest pH and lowest flieg point. Concentration of Ammonia nitrogen in treatment 4 was higher than the other treatments ($P < 0.05$). Also treatment 2 had the lowest dry matter percentage. The results indicated that among those tested, Lacticil Maize is the preferred microbial additive for alfalfa silage due to improving fermentation quality.

Key words: microbial additives, alfalfa silage, fermentation quality

W109 Volatile organic compounds emissions from different silages and cattle feed. I. L. Malkina[1], R. B. Franco*[1], A. Kumar[2], P. G. Green[3], and F. M. Mitloehner[1], *[1]Department of Animal Science, University of California-Davis, [2]Crocker Nuclear Laboratory, University of California-Davis, Davis, [3]Department of Civil and Environmental Engineering, University of California-Davis, Davis.*

The San Joaquin Valley (SJV) in Central California exhibits high ground-level ozone pollution that may affect human, animal, and plant health. Silage and other feedstuffs were identified as one of the major sources of volatile organic compounds (VOCs), which in reaction with nitrogen oxides (NOx) contribute to ozone formation in this area. For reference, urban concentrations in the SJV represent 125 ppb of VOCs, while the rural concentrations in the SJV represent 62.5 ppb of VOCs. Detailed characterization of VOCs is relevant to ozone formation potential because the impact of different VOCs on ozone formation varies significantly. This study identified and quantified the VOCs emitted from silages and other feedstuffs in environmental chamber experiments conducted under controlled conditions. Approximately 80 VOCs were identified and quantified from corn (*Zea mays* L., alfalfa (*Medicago sativa* L.), cereal (wheat [*Triticum aestivum* L.] and oat [*Avena sativa* L.] grains) silages, total mixed ration (TMR), almond (*Amygdalus communis* L.) shells and hulls using gas chromatography-mass spectrometry (GC/MS) and high performance liquid chromatography (HPLC). Four air samples of silages and TMR, and 2 air samples of almond hulls and almond shells were collected using 6-L SUMMA canisters and DNPH cartridges. High concentrations of emitted alcohols, predominantly ethanol (1615.5 ± 188.6 nL/Lfrom cereal silage and 1043.7 ± 184.9 nL/L from corn silage) and other oxygenated compounds were measured. Highly reactive alkenes and aldehydes, were also detected but in lower concentrations. Further studies in quantification and monitoring of these emissions are critical for assessment of and response to the specific needs of the air quality in the SJV.

Key words: volatile organic compounds, silage, ethanol emissions

W110 Production and quality of corn silage cultivated on integrated crop-livestock-forest system in a Cerrado region of Minas Gerais, Brazil. M. C. M. Viana*[1], W. Botelho[1], P. A. Viana[2], D. S. Queiroz[1], E. A. Silva[1], M. S. Viana[4], and C. G. Guimarães[3], *[1]EPAMIG - Minas Gerais Agricultural Research Corporation, Belo Horizonte, Minas Gerais, Brazil, [2]Embrapa Maize and Sorghum, Sete Lagoas, Minas Gerais, Brazil, [3]UFVJM University, Diamantina, Minas Gerais, Brazil, [4]FEAD University, Belo Horizonte, Minas Gerais, Brazil.*

The trial was carried out at Santa Rita Experimental Farm (19°28′ S, 45°15′W, 732 m) on *Brachiaria decumbens* degraded pasture to evaluate the interference of different eucalyptus structural arrangements and clones on the production and chemical composition of maize silage cultivated in an agroforestry system (iCLF). The experimental design was a randomized complete block in a split plot, with 3 replications. Eucalyptus arrangements: double rows (3 × 2) × 20 m; (2 × 2) × 9 m and single rows (9 × 2m) were distributed in the main plots, with 20 and 9 m between rows and 2 m between tree spacing. Eucalyptus clones: VM 58, GG100 and I144 were tested in the subplots. The corn (hybrid BRS3060) was intercropped with eucalyptus clones. The maize cultivar used was BRS 3060. The maize silage yield, DM, ADF, NDF, lignin and cellulose contents were evaluated. Termites, white grub, wireworm, diplodes and corn rootworm larvae were the main soil pest observed in the experimental area. No difference was observed for maize productivity in relation to structural arrangements and eucalyptus clones in the first year of crop establishment. Also, the DM, ADF, NDF, lignin and cellulose were not influenced by the clones and the various structural arrangements of eucalyptus. The clones and the structural arrangements of eucalyptus did not influence the production and chemical composition of silage corn in the first year of crop establishment in the iCLF system in the Cerrado region of Minas Gerais State. (Research supported by FAPEMIG/CNPq)

Table 1. Dry matter (DM) yield (t/ha) and chemical composition of corn intercropped with eucalyptus in the first year of integrated crop-livestock-forest (iCLF) system

Arrangements	DM Yield (t/ha)	DM (%)	CP (%)	ADF (%)	NDF (%)	Lignin (%)	Cellulose (%)
(3 × 2)+20 m	10.24 [a]	37.27 [a]	4.73 [a]	31.1 [a]	58.55 [a]	4.79 [a]	25.73 [a]
(2 × 2)+9 m	6.03 [a]	36.03 [a]	4.86 [a]	31.26 [a]	59.07 [a]	4.86 [a]	25.72 [a]
(9 × 2) m	10.75 [a]	35.58 [a]	5.02 [a]	31.96 [a]	59.40 [a]	5.46 [a]	25.89 [a]

Same letters in the same column do not differ by Tukey test ($P \geq 0.05$).

Key words: degraded pasture, nutritive value, agroforestry

W111 Effect of molasses, starch and enzyme enrichment of sorghum and corn silage on chemical composition and rumen degradability. M. Dehghan-Banadaky*, M. Ghiasvand, and S. Sadeghi, *Animal Science Department, Campus of Agricultural and Natural Resources, University of Tehran, Karaj, Tehran, Iran.*

The present study investigated the effects of enzyme (1 g Natuzyme per kg DM) and carbohydrate (molasses and barley, 5 g per kg DM) enrichment in sorghum silage and comparison with corn silage. Sorghum and corn were harvested at maturity stage with 25% dry matter. Forage chopped to 3-5 cm length and ensiled. After 60 days, silages were opened and evaluated for odor, color, material tissue, the amount of mold and pH (5 replicates for each treatment). Chemical composition was measured including dry matter digestibility, dry matter (DM), crude protein (CP), neutral detergent fiber (NDF), non fibrous carbohydrate (NFC), acid detergent fiber (ADF), and fermentation products such as ammonia nitrogen and volatile fatty acids. Three rumen fistulated Holstein cows were used for degradability experiment at 0, 6, 12, 24, 48, 72 and 96 h incubation. Corn silage dry matter was signifi-

cantly greater than sorghum silage (28 vs. 25, $P < 0.05$). Silage with barley flour and molasses enrichment had more dry matter. NDF and ADF concentration in sorghum silage with barley flour and molasses additive were significantly lower than sorghum silage without additive and corn silage ($P < 0.05$). Dry matter digestibility, digestible energy and total digestible nutrients in sorghum silage with barely flour and molasses significantly greater than other silages. Results of sensory evaluation showed that sorghum silage without additive had the lowest score and sorghum silage with molasses, barley flour and corn silage had very good quality. The in situ wash fraction was increased in sorghum silage with molasses and barley flour additive equal to corn silage. The potentially degradable fraction significantly increased in sorghum and corn silage with enzyme additives. The degradation rate and effective degradation at passage rates of 2, 5 and 8 percent per hour increased in corn and sorghum silage with barley flour and molasses. Sorghum silage enriched with molasses and barley flour in most parameters did not differ significantly with corn silage. We conclude that the quality of sorghum silage can be improved by adding molasses or barley flour.

Key words: sorghum silage, molasses, corn silage

W112 Effect of processed and unprocessed canola straw on growth performance, feeding behavior and rumen metabolites in Holstein feedlot calves. M. Ghiasvand, M. Dehghan-Banadaky*, and K. Rezayazdi, *Animal Science Department, Campus of Agricultural and Natural Resources, University of Tehran, Karaj, Tehran, Iran.*

Studies on the nutritional value of canola straw are very limited, therefore this forage is unknown to farmers and often is not used in ruminant nutrition. This experiment used 24 Iranian Holstein male calves with 266 ± 64 kg live weight. The study had a randomized complete design with three experimental diets with 25 to 75, forage: concentrate ratio. Diet 1 contained 10% corn silage and 15% alfalfa hay, diet 2 and 3, alfalfa was substituted with unprocessed and processed canola straw respectively. Energy density and protein content of the diets were similar. Canola straw was processed with NaOH (5% of dry matter). Calf live weight was recorded monthly. Calf feeding behavior was recorded for 24 h. Rumen fluid was collected 4 h after morning feeding at the end of experiment. Calves fed diet 2 had significantly less individual DMI than other groups. Final BW and average daily gain were not different between diets (p>0.05). Feed conversion ratio for calves fed diet 2 was significantly less than calves fed diet 1 (5.75 vs. 6.72, $P < 0.05$). Digestibility of DM and OM in calves' fed diet1 were significantly lower than diet 2 and 3. Protein and cell wall digestibility in diets 2 were more than diet 1 and there was no significant difference between diets 2 and 3. Ruminal pH in calves fed diet 3 was significantly greater than calves fed diet 1 and 2 (6.05, 5.90, and 6.27 for treatments 1-3 respectively). There was no significant difference among the calves fed different diets ($P > 0.05$) in rumen total volatile fatty acids and NH3-N concentration. Total ruminating time was greatest in calves fed diet 2. Ruminating time per kg of dry matter, per kilogram of NDF and per kilogram of forage NDF (fNDF) in calves fed diets containing unprocessed canola straw was significantly greater than calves fed diets 1 and 3 . Results indicate that unprocessed canola straw can be used as a roughage source in feedlot calf diets.

Key words: canola straw, Holstein male calves, feeding behavior

W113 Kinetics of solid-state fermentation of waste peach (*Prunus persica*) to be used as animal feed. Y. Castillo[1], O. Ruiz*[2], J. C. Gomez[1], E. Peru[1], H. Gonzalez[3], A. Orozco[3], C. Angulo[2], I. Ramos[3], and M. R. Murphy[4], *[1]División multidisciplinaria, UACJ, Nuevo Casas Grandes, Chihuahua, Mexico, [2]Facultad de Zootecnia y Ecologia, UACH, Chihuahua, Chih., Mexico, [3]Instituto de Ciencia Biológicas, UACJ, Ciudad Juárez, Chihuahua, Mexico, [4]Animal Science Department, University of Illinois, Urbana.*

Feed produced by solid state fermentation (SSF) has been added to ruminant diets to improve the nutritional value, including the true protein content. The aim of the present study was to determine the effect of incubation duration on the fermentation profile and chemical content of fermented peach residues collected after processing in a mill. Peach waste was ground and mixed with 1.5% urea, 0.2% ammonium sulfate, 0.9% calcium carbonate, and 0.5% of a mineral salt mixture. These ingredients were mixed and then 200 g portions were distributed to separate sterile 250 ml flasks for solid-state fermentation (SSF). Each flask was plugged with cotton and incubated under static conditions at 32°C for 0, 24, 48, and 72 h. At each sampling time, four flasks were withdrawn from the incubator. A completely randomized design was used with 4 replications at each time of incubation and data was analyzed with the GLM procedure of the SAS. Results showed that pH decreased ($P \leq 0.0001$) progressively over time (5.80, 4.81, 4.72 and 4.54 for 0, 24, 48 and 72 hours, respectively). Counts of yeast colonies (log cells/ ml) increased ($P \leq 0.0001$) over time. Dry matter (DM) was constant during the first 48 hours and then decreased ($P \leq 0.03$). Neutral and acid detergent fiber (NDF and ADF) increased in the first 24 hours and decreased subsequently ($P \leq 0.001$ and $P \leq 0.003$), respectively). Hemicellulose (HEM) developed in the same way ($P \leq 0.0001$), but showed no changes after 24 h. Crude protein showed no statistical differences during incubation. True protein content did not improve in the first 24 h, but it increased at 48 h ($P < 0.05$), with no changes subsequently (4.62, 5.04, 5.42 and 5.18% for 0, 24, 48 and 72 h, respectively). According to these results, it can be concluded that a fermentation time of 48 h is enough to accomplish an improvement of the nutritional value of residues of the peach industry.

Key words: fermentation, peach, chemical

W114 Chemical additives on sugarcane ensilage: Fermentation parameters, digestibility and intake by sheep. A. F. Pedroso*[1], S. N. Esteves[1], W. Barioni[1], G. B. Souza[1], C. Carbello[2], and G. G. Chiquitin[2], *[1]Brazilian Agricultural Research Corporation - Embrapa, São Carlos, SP, Brazil, [2]Fund. Educacional de Andradina, Andradina, SP, Brazil.*

The objective was to determine the apparent digestibility and intake by sheep of sugarcane silages produced with and without chemical additives, and to evaluate the effectiveness of additives at controlling alcoholic fermentation in the silages. Mature sugarcane (22 ºBrix) was ensiled in 200 L metal drums without treatment (control) or treated with (fresh forage basis): urea (5 g/kg) + sodium benzoate (0.5 g/kg); sodium propionate (4 g/kg); calcium hydroxide (10 g/kg). Silos were opened 80 d after ensiling and silages were fed to 16 wethers (averaging 45 kg live body weight - LW) housed in metabolic cages. Animals were distributed among treatments (four diets based on the different silages) in a complete randomized design with four replicates. Soybean meal and a mineral supplement were used to respectively balance protein content and minerals in diets. Silage DM digestibility and intake were calculated by difference since soybean digestibility was known. All silages had adequate pH (<4.2; Table 1). All additives reduced alcoholic fermentation in the silages but calcium hydroxide had the greatest effect (83% less ethanol relative to control). Urea +

benzoate and calcium hydroxide improved silage digestibility similarly (18% higher) but did not affect silage intake (relative to LW) compared to the untreated silage. Treatment with sodium propionate had no effect on silage digestibility and intake compared to control.

Table 1. Fermentation parameters, apparent digestibility and intake by sheep of sugarcane silages produced with and without additives

Silage	pH	Ethanol (g/kg DM)	Digestibility (% DM)	DM Intake (% LW)
Control	3.55^{c}	96.6^{a}	37.2^{b}	1.8^{ab}
Urea + benzoate	3.77^{b}	67.3^{b}	43.7^{a}	1.7^{ab}
Sodium propionate	3.72^{b}	76.8^{b}	38.2^{b}	1.3^{b}
Calcium hydroxide	4.08^{a}	11.6^{c}	44.3^{a}	2.0^{a}
SE	0.045	6.94	3.03	0.37

^{abc}Means in rows with unlike superscript differ by the *t* test ($P < 0.05$); LW = live body weight.

Key words: alcoholic fermentation, calcium hydroxide, sodium propionate

W115 Effects of the form of applying virgin lime and the treatments duration on the temperature and pH of sugarcane. E. Z. Ramos*, M. D. S. Oliveira, A. C. Rego, M. P. R. Sforcini, and V. B. Ferrari, *UNESP, Jaboticabal, São Paulo, Brazil.*

This study aimed to evaluate the effects of the form of applying virgin lime (powder or solution) and the treatment duration (0, 3 and 6 h) on hydrolysis of sugarcane with particle sizes of 4 or 10 mm. Control samples were untreated at time 0. Each treatment had four replications, and the treatment arrangement was a 2 × 2 × 3 factorial. Virgin lime was applied at the rate of 0.5% (fresh weight basis) to sugarcane. Treatment effects on the cell wall were monitored using Scanning Micrographs (SEM), and effects on temperature and pH were also recorded. The experimental data were analyzed using AgroEstat software and means were compared with the Tukey test at the 5% probability level. Table 1 shows that temperature increased with the treatment duration such that the lowest temperatures occurred at 0 h (24.1°C), and the highest values at 6 h (27.2°C). There was an interactions of treatment duration and temperature and of particle size and duration. Treatment with the powder resulted in higher temperatures (26.1°C) than the solution (25.7°C). Lime-treated samples had higher pH, regardless of the treatment duration, such that values were (5.7) for the control, and (10.3) and (9.8) after lime application for 3 and 6 h, respectively. In conclusion, the application of lime powder proved more efficient than in solution, but the particle size did not affect the results. Treatments duration increased sample temperature, but had no influence on pH values. The SEM images revealed that, regardless of other treatments, application of lime degraded the cell wall and potentially released cell contents that could be utilized by animals.

Table 1. Temperature and pH values

	Virgin lime		Particle size (mm)		Treatment duration (h)		
	Powder	Solution	4	10	0	3	6
Temperature (°C)	26.1^{a}	25.8^{b}	26.0^{a}	25.9^{a}	24.1^{c}	26.5^{b}	27.2^{a}
pH	8.7^{a}	8.6^{a}	8.5^{a}	8.7^{a}	5.7^{b}	10.3^{a}	9.8^{a}

Key words: sugarcane, hydrolysis, microscopy

W116 Effect of calcium chloride fertilization on the dietary cation-anion difference of forage crops in northern New York. E. O. Young[1], C. S. Ballard*[1], and S. Mishra[2], *[1]William H. Miner Agricultural Research Institute, Chazy, NY, [2]TETRA Technologies, Inc., The Woodlands, TX.*

Maintaining forage with an ideal dietary cation-anion difference (DCAD) for non-lactating cows can be challenging. The objective of this experiment was to determine if the application of liquid calcium chloride could increase chloride content and reduce DCAD of grass and mixed alfalfa-grass stands. In June 2010, three replicate plots were established on grass and alfalfa-grass fields at each of four sites at Miner Institute in Chazy, NY. Within plot, treatment was randomly assigned to subplot (with or without calcium chloride). Treatment subplots received 80 kg/ha of chloride as liquid calcium chloride applied one week after first cutting. Plots were harvested near the third week of June 2010 (second cut), and a second harvest was taken at the end of July (third cut). Analysis of variance was used to determine treatment effects on yield, DCAD, and forage nutrient content for each harvest. Results showed that calcium chloride application nearly doubled the chloride content of both forages at each harvest ($P \leq 0.001$) and significantly reduced DCAD ($P \leq 0.001$). For alfalfa-grass, calcium chloride fertilization reduced DCAD from 317 to 179 mEq/kg for the first harvest ($P \leq 0.001$), and 432 to 326 mEq/kg for the second harvest ($P \leq 0.05$). Grass DCAD was reduced from 115 to −108 mEq/kg with calcium chloride fertilization ($P \leq 0.001$) for first harvest and 293 to 91 mEq/kg for second harvest ($P \leq 0.001$). There was no impact on yield from chloride addition ($P \geq 0.58$) and no apparent impacts on forage nutritive value ($P \geq 0.15$) besides chloride content. Fertilizing alfalfa-grass or grass stands with liquid calcium chloride appears to be a viable approach to reduce DCAD in forages fed to non-lactating dairy cattle in Northern NY. Future work will compare the cost- effectiveness of chloride fertilization of forages versus addition of supplements to animal rations to reduce DCAD.

Key words: forage quality, nonlactating cows, dietary cation-anion difference

W117 In vitro ruminal fermentation of dairy cows diets with eight yeast strains isolated from apple byproducts. D. Díaz-Plascencia*[1], C. Rodríguez-Muela[1], P. Mancillas-Flores[1], F. Salvador-Torres[1], C. Arzola[1], L. Durán[1], J. Jiménez[1], and S. Mena[2], *[1]Universidad Autónoma de Chihuahua, Chihuahua, México, [2]Universidad de Guadalajara, Jalisco, México.*

In order to evaluate the effect of the inclusion of eight strains of yeasts isolated from apple byproducts on the in vitro fermentation of dairy cows diets samples, were developed eight yeast inoculums with the following strains (strains 2, 9, 11 and 13 of *Kluyveromyces lactis* (Kl), 3 and 8 of *Issatchenkia orientalis* (Io), 4 and 6 of *Saccharomyces cerevisiae* (Sc) to be assessed by the in vitro gas production technique. Exactly 0.2 g sample, 10 ml rumen fluid, 20 ml artificial saliva and 1 ml of yeast inoculum were evaluated in 72 glass bottles in triplicate for 12, 24, and 48 h at 39° C. Variables evaluated were ammonia nitrogen (AN), lactic acid (LA) and yeast count (YC). The data were evaluated with a completely random design with a split plot in time. Results of the LA variable are showed in Table 1. There were strain and fermentation time effect on AN, LA and YC ($P < 0.01$). Lowest values of AN were obtained with Kl2 ($P<0.01$) and highest with Io3, Io8 and Sc6 (22.5, 24.8, 24.8 and 24.1 mM/L at 48h, respectively). Highest values of YC were obtained with Kl2, Kl9, Kl11, Kl13 and Sc6 with values of 1.9, 1.3, 1.2, 1.1 and 1.0E+07 cells/ml respectively at 48h ($P < 0.01$).

We conclude that *K. lactis* yeast showed to be the most effective on the in vitro rumen fermentation, with better performance on yeast count and lactic acid reduction.

Table 1. Lactic acid values (mM/L) on the in vitro rumen fermentation of dairy cow diets with eight different strains of yeast

	Time (h)		
Strain	12	24	48
Kl 2	21.75^{e}	7.51^{e}	2.47^{e}
Kl 9	27.54^{ed}	10.11^{e}	2.82^{e}
Kl 11	34.77^{a}	10.47^{e}	2.37^{e}
Kl 13	28.14^{cd}	15.82^{cd}	2.39^{e}
Io 3	45.78^{a}	34.48^{a}	17.61^{a}
Io 8	32.80^{ab}	21.95^{b}	15.34^{ab}
Sc 4	26.35^{bcd}	17.72^{bcd}	8.81^{cd}
Sc 6	36.11^{bc}	18.27^{bc}	9.95^{c}

^{abcde}Different letters within columns indicate statistical difference between strains (P <0.01). Rows standard error: ± 0.31.

Key words: yeast, fermentation, lactic acid

W118 Effect of exogenous fibrolytic enzymes on in vitro ruminal fermentation kinetics and energy utilization of three Mexican tree fodder species. D. López[1], R. Rojo*[1], A. Z. M. Salem[1], J. Cedillo-Monrroy[1], B. Albarrán[1], A. González[2], J. L. Martínez-Benites[1], J. Morales-Diaz[1], and J. Tinoco-Jaramillo[1], *[1]Centro Universitario UAEM-Temascaltepec, Universidad Autónoma del Estado de México, Temascaltepec, Estado de México, México, [2]Universidad Autónoma de Tamaulipas, Cd. Victoria, Tamaulipas México.*

A factorial experimental treatment structure (3 x 3) was used to evaluate the effect of exogenous fibrolytic enzymes (EFE) on in vitro ruminal fermentation kinetics and energy utilization of three browse tree foliages (*Pithecellobium dulce*, *Heliocarpus velutinus* and *Guazuma ulmifolia*). A commercial exogenous fibrolytic enzyme (EFE) mixture (Fibrozyme, Alltech Inc., Nicholasville, KY) was added to browse species leaves at three levels: 0 (control), 3.5 and 7.0 mg/g. Browses species were harvested during dry season (April/May 2009) and incubated with goat ruminal inoculum. Chemical composition, plant secondary metabolites [total phenolics (TP), saponins (SAP), aqueous fraction (AF)] as well as in vitro ruminal gas production kinetics were determined using a general compartment model. Short chain fatty acids (SCFA) and metabolizable energy (ME) were estimated. Seven replicates of each treatment were used and data were analyzed using a randomized complete design. Differences among means were determined using a least squares means test. Addition of EFE improved the fermentation kinetics of the browse tree leaves. The CP content of *P. dulce* was higher ($P < 0.05$) than those of the remaining tree species. The NDF and SAP concentration of *G. ulmifolia* was higher ($P < 0.05$) than those of the other species. *P. dulce* and *G. ulmifolia* had high ($P < 0.05$) contents of TP. Gas production at 24 (h) (GP24) of *P. dulce* at the high EFE level (i.e., 7 mg EFE /g DM) showed a higher ($P < 0.01$) ruminal fermentation after 24 h of incubation than that of *G. ulmifolia*. The asymptotic gas production (b) (ml/g DM) and rate of gas production (c) (/h), were affected ($P < 0.01$) by enzyme treatment while the lag phase was not affected. The lower ($P < 0.01$) extent of gas production occurred in *G. ulmifolia* at 0 mg EFE /g DM as well as the c and b values. *P. dulce* with high levels of EFE (7.0 mg/g DM) showed the highest ($P < 0.05$) values for ME and SCFA while the *G. ulmifolia* without EFE showed the lowest values for ME and SCFA. Addition of EFE improved the fermentation kinetics of the browse tree leaves.

Key words: browse species, exogenous fibrolytic enzyme, plant secondary metabolites

W119 Effects of pH and temperature on fibrolytic enzyme activities of various commercial exogenous enzyme preparations. K. G. Arriola*, J. J. Romero Gomez, and A. T. Adesogan, *Department of Animal Sciences, Institute of Food and Agricultural Sciences, University of Florida, Gainesville.*

The objective of this study was to evaluate how the enzyme activity of commercial fibrolytic enzymes differed with the prevailing pH and temperature. Eighteen commercial fibrolytic enzymes from 5 companies were assayed in triplicate for xylanase and endoglucanase activity at pH 4.0, 5.0, 6.0, 7.0 and 8.0 at 39°C (Experiment 1) and at 20, 30, 40, and 50°C at pH 6.0 (Experiment 2). Xylanase was assayed in a 15-mL test tube containing 1.0 mL of 1.0% (wt/vol) oat spelts xylan as substrate and 0.9 mL of citrate-phosphate buffer (pH 6.0). After preincubation for 10 min., 0.1 mL of diluted enzyme was added to initiate the reaction and the suspension was incubated for 5 min. The reaction was terminated by adding 3 mL of dinitrosalicylic acid reagent. Endoglucanase was assayed as described above using 1.0% (wt/vol) carboxymethyl cellulose as substrate. The unit of enzyme was the amount of enzyme required to release 1 μmol of reducing sugars as xylose (xylanase) or glucose (endoglucanase) equivalents min-1 mg-1. Treatments were arranged in an 18 (enzymes) x 5 (pH) or 4 (temperatures) factorial layout and data analyzed with a model including these terms and the interaction using Proc Mixed of SAS. Xylanase activity was optimal at 20, 30, 40 and 50°C for 0, 11, 6, and 83% of the enzymes; whereas endoglucanase activity was optimal for 11, 0, 11, and 78% of enzymes at the respective temperatures. Xylanase activity was optimal at pH 4, 5, 6, 7, and 8 for 17, 44, 17, 5, and 17% of the enzymes, whereas, endoglucanase activity was optimal for 44, 33, 17, 6 and 0% of the enzymes at the respective pH. Xylanase and endoglucanase activities of most enzymes were optimal at 50°C and at pH 4 - 5. Therefore, few (<25%) of the 18 enzymes exhibited optimal activity under ruminal conditions (pH 6–7, 39°C).

Key words: xylanase, endoglucanase, exogenous enzymes

W120 Fiber digestibility of cool-season grasses. T. W. Downing*, *Oregon State University, Corvallis.*

Forage grass production is an important component of profitable dairying along the Pacific Northwest coast. Neutral detergent fiber digestibility (NDFD) is increasingly being used in ration formulation and forage benchmarking. However, data on differences in NDFD between and within cool-season grass species is limited. The objective of this study was to determine if NDFD differs between species and varieties. Eighteen cool-season grass varieties were replicated 3 times each in 6-m^2 randomized field plots. Included were 6 varieties each of perennial ryegrass (*Lolium perenne*), orchardgrass (*Dactylis glomerata*), and tall fescue (*Lolium arundinaceum*). Plots were mechanically harvested six times at approximately 28 d intervals beginning in March each year and harvested over a two year period. Forty eight-hour in vitro neutral detergent fiber (NDF) digestibility was determined using 0.3 g of sample in F57 bags in a DaisyII Incubator (Ankom Technology, Fairport, NY). Neutral detergent fiber was less ($P < 0.001$) for ryegrass (49.5±1.58) compared to both orchardgrass (57.5±3.64) or tall fescues (53.5±1.4). Neutral detergent fiber digestibility was greater

for ryegrass compared to orchardgrass and tall fescue (79.4±1.3, 76.2±1.4, and 76.5±1.1% of NDF respectively; $P < 0.01$). The fescues and orchard grasses were similar in NDF and NDFD. Neutral detergent fiber increased and NDFD decreased ($P < 0.05$) as the growing season progressed. These results indicate ryegrasses when managed intensively were significantly different from orchard grass and fescues.

Key words: neutral detergent fiber digestibility, cool-season grass, in vitro digestibility

W121 Comparison of chemical composition and digestibility among wheat straws treated with *Pleurotus djamur*. O. D. Montañez-Valdez*[1], J. A. Reyes-Gutierrez[1], J. A. Martínez-Ibarra[1], G. Rocha-Chavez[1], J. M. Tapia-Gonzalez[1], C. E. Guerra-Medina[2], J. J. Martínez-Tinajero[3], and J. H. Avellaneda-Cevallos[4], *[1]Centro Universitario del Sur, Ciudad Guzmán, Jalisco, México, [2]Centro Universiario de la Costa Sur, Autlán de la Grana, Jalisco, México, [3]Facultad de Ciencias Agrícolas, Universidad Autónoma de Chiapas, México, [4]Universidad Técnica de Estatal de Quevedo, Quevedo, Los Rios, Ecuador.*

A study was conducted to evaluate the effect of *Pleurotus djamur*, on chemical composition of maize stover. Maize stover treated and untreated with *Pleurotus djamur*, 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 djamur*. 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, OM, CP, C, and L; however, treated maize stover ($P \leq 0.02$) showed higher percentages of ADF, as well as a lower NDF and HC value. We do not found change on in situ digestibility of DM ($P \geq 0.05$; Table 1). The growth of *Pleurotus djamur*, on maize stover changes its chemical composition by decreasing hemicellulose content and modifying cell wall components, this did not improve the nutritional quality of agricultural byproducts. This suggests that *Pleurotus djamur*-treated maize stover is not an ideal forage for ruminants.

Table 1. Chemical composition and in situ digestibility of maize stover treated with and without *Pleurotus djamur* (%)

Component	NC[1]	TMS[2]
DM	92.03[a]	92.56[a]
OM	82.45[a]	82.59[a]
CP	4.78[a]	4.42[a]
ADF	22.67[b]	27.20[a]
NDF	55.91[a]	47.56[b]
C	33.70[a]	32.40[a]
HC	33.24[a]	20.36[b]
L	12.22[a]	11.89[a]
Coefficients of digestibility *in situ* of DM		
48	24.77[a]	25.57[a]
24	30.96[a]	31.13[a]
12	44.46[a]	44.46[a]

[a,b] Superscript letters indicating differences ($P \leq 0.05$).

[1]Negative control.

[2]Treated maize stover.

Key words: byproducts, *Pleurotus djamur*, ruminant

W122 Effect of crude protein content on intake and digestion of coastal bermudagrass hays by horses. C. L. Spurgin, J. A. Coverdale, K. N. Winsco*, and T. A. Wickersham, *Texas A&M University, College Station.*

Forage is an essential component of the equine diet; however, relatively little information is currently available regarding the effects of CP content of bermudagrass (*Cynodon dactylon*) hay on intake and digestion in horses. Therefore, this study was conducted to determine the effect of forage CP content on intake and digestion of bermudagrass hay by horses. Four cecally fistulated geldings (BW 548 ± 23 kg) were used in a 4 × 4 Latin square. Geldings were provided ad libitum access to bermudagrass hay of 4 CP levels (6.9, 9.8, 12.7, and 15.6% CP; L, ML, MH, and H, respectively). Hay was offered daily in 2 equal feedings at 0600 and 1800 each day. Experimental periods were 15 d long, with 9 d of adaptation to treatment. Forage intake was determined from d 10 through d 13 to correspond with total fecal collections from d 11 through d 14. On d 15 cecal fluid samples were collected before feeding (0 h) and 4, 8, and 12 h, after the 0600 feeding. Forage OM intake was not significantly ($P > 0.21$) affected by CP content and was 8.97, 8.60, 9.53, and 10.98 kg/d for L, ML, MH, and H, respectively. In contrast, digestible OM intake increased linearly ($P = 0.04$) with increasing CP content and ranged from 3.70 to 5.35 kg/d for L and H, accordingly. Digestion of OM increased quadratically ($P = 0.03$). This response was largely driven by the increase between L and ML hays from 41.1 to 55.0%, followed by a leveling off at 48.8 and 48.5% for MH and H, respectively. Cecal pH responded in a cubic manner ($P < 0.01$) to CP content of the hays; however, all values were in the acceptable range for promoting fiber digestion. Plasma glucose concentrations increased linearly ($P = 0.04$) with increasing CP content and ranged from 68.8 for L to 73.7 mg/dL for H. Forage intake did not increase in response to increasing CP content; however, utilization, measured as the combination of intake and digestion, was sensitive to increasing CP content, suggesting nutritive value determinations of bermudagrass hay are justified when purchasing bermudagrass hay for horses.

Key words: horses, bermudagrass, intake

W123 The effect of silage nutrient variations on milk prediction outcomes of the Cornell Net Carbohydrate and Protein System. C. T. Hill*[1], M. J. Tetreault[1], and H. M. Dann[2], *[1]Poulin Grain Inc., Newport, VT, [2]William H. Miner Agricultural Institute, Chazy, NY.*

Variability in forages and forage samples is inevitable and measurable. The objective of this study was to determine the amount of variation of key nutrients in typical corn silage and haylage bunkers and how it may affect milk production. Samples were taken from 6 bunker silos [3 corn silage (CS) and 3 haylage (H)] on 24 of 28 consecutive days on 3 Vermont dairy farms. Samples were taken daily at 7, 30-cm intervals up to 2.1 m high, mixed, and sent for NIR analysis. Means were calculated for NIR results of nutrient parameters for each bunk and used to enter each forage into CNCPS (version 6.1.36). A base diet was created for each CS utilizing an alfalfa silage from the CNCPS library. The H base diets utilized a library CS. Forage ratios were 64.1% for the CS diets and 58.5% for the H diets. The ratio of CS to H was approximately 2:1 on a DM basis for all diets. Standard deviations were calculated (Microsoft Excel, 2007) within bunks for DM, CP, NDF, starch, and K_d. Diets of plus or minus one SD for each nutrient were created

for comparison to the base diets. Mean nutrient values and SD for each bunk are shown in Table 1. Variations in DM resulted in a predicted AF difference up to 2.6 kg. There was a 1.2 kg and 1.7 kg increase in ME and MP milk respectively for plus one versus minus 1 SD for CS1 K_d. Minus one SD resulted in approximately 1.0 kg of increased ME and MP milk for all CS NDF. All other variations resulted in less than 1.0 kg difference in ME and MP predicted milk. Although silages may appear uniform throughout a silo, frequent sampling may reduce variation in diets and improve the accuracy of model predictions.

Table 1. Silage mean nutrient values and standard deviations

	Forage					
Nutrient	CS1	CS2	CS3	H1	H2	H3
DM	36.8	36.4	36.4	36.1	43.0	33.5
DMSD	1.6	1.1	1.4	1.5	3.2	2.2
CP	7.0	7.3	7.6	15.7	19.4	18.3
CPSD	0.5	0.4	0.6	0.9	0.8	0.5
NDF	34.7	36.8	37.0	59.3	43.7	41.6
NDFSD	2.1	2.2	1.9	2.2	1.6	2.1
Starch	40.5	37.0	33.6	1.3	2.2	1.4
StarchSD	2.6	2.5	6.9	0.5	1.0	0.5
Kd	5.0	5.0	5.9	5.2	5.9	5.1
KdSD	0.2	1.0	0.4	0.3	0.4	0.2

Key words: silage variation, CNCPS, forage sampling

W124 Partially replacing alfalfa and corn silages with fescue silages maintained fat corrected milk production. W. D. Verbeten*, D. K. Combs, and D. J. Undersander, *University of Wisconsin Madison, Madison.*

Meadow fescue or tall fescue silage was fed in combination with alfalfa and corn silage to evaluate the effects on milk production in early lactation dairy cows. Four treatment diets were fed to 52 early lactation (60.7 DIM ± 46.4 DIM) Holstein dairy cows (39 multiparous, 13 primiparous) producing 46.4 kg ± 11.7 kg of milk per day at the University of Wisconsin-Arlington research station. The feeding trial was a continuous lactation trial with a covariate period (2 weeks) before 6 treatment periods (2 weeks each). The cows were randomly assigned in pairs to electronic feeding gates, with 1 of the 4 treatment diets randomly assigned to each gate. Each gate was an experimental unit. The 4 diets varied in forage composition: the meadow fescue diet contained 4.6 kg DM of meadow fescue silage, 4.6 kg DM alfalfa silage, and 4.6 kg DM corn silage; the tall fescue diet contained 4.6 kg DM of tall fescue silage, 4.6 kg DM alfalfa silage, and 4.6 kg DM corn silage; the positive control diet contained 5.6 kg DM of alfalfa silage, 5.6 kg DM of corn silage, and 2.2 kg DM of wheat straw; the negative control diet contained 6.8 kg DM of corn silage and 6.8 kg DM alfalfa silage. All diets contained between 11 and 12 kg DM of concentrate feeds. The meadow fescue, tall fescue, and positive control diets were formulated to 30% NDF, while the negative control diet was formulated to 27% NDF. Total covariate adjusted 84 d, 3.5% FCM yields were analyzed in a mixed effects model, where the gate was the random effect and the diet was the fixed effect. The milk yields for the meadow fescue, tall fescue, positive control, and negative control diets were not statistically different at $P > 0.05$ (7219.94 kg/gate, 7110.19 kg/gate, 7352.60 kg/gate, and 7197.18 kg/gate, respectively). This data indicates that high quality meadow and tall fescue silages can be fed to high producing dairy cows without a decrease in fat corrected milk production.

Key words: meadow fescue, tall fescue, wheat straw

W125 Processed and unprocessed canola straw in Holstein male calves diets changed blood parameters and carcass characteristics. M. Ghiasvand, K. Rezayazdi, and M. Dehghan-Banadaky*, *Animal Science Department, Campus of Agricultural and Natural Resources, University of Tehran, Karaj, Tehran, Iran.*

Canola has been vastly cultivated for edible oil production. After harvesting, the canola straw remains in the field and is burnt. This research used 24 Iranian Holstein male calves with 266 ± 64 kg live weight in an experiment with a completely randomized design with three diets. Diet 1, included 10% corn silage and 15% alfalfa hay and in diet 2 and 3, alfalfa substitute with unprocessed and processed canola straw. Energy value and protein content of the diets were similar. The animals were housed in individual concrete-floor tie stalls and individually fed. The experimental period lasted 90 days and at the end of experiment, four hours after the morning meal, blood samples were taken. After slaughter some carcass characteristics were measured and beef quality was evaluated by a sensory panel. Blood glucose level was significantly decreased in calves fed diet 2 ($P < 0.05$) and cholesterol level was significantly lower in calves fed diets 2 and 3 ($P < 0.05$). Effect of diet 3 on T3 (tri-iodoothyronine) hormone was significant, calves fed this diet had higher levels of T3 ($P < 0.05$) but values in calves fed diets 2 and 1 did not significantly differ. Hormone levels of T4 (thyroxine) and thyroid weight had no significant difference among calves. Hot carcass weight, visceral fat weight, back fat thickness, carcass length and muscle cross section were not affected by diets. But the effect of different diets on dressing % was significant ($P < 0.05$). Calves fed diet 2 had the highest dressing % and calves fed diet 3 the lowest ($P < 0.05$). The results indicated that chemical composition and sensory quality of meat did not differ among treatments. Canola straw can be used in the diet of male calves for fattening particularly under drought conditions and or when there is a shortage of other forage sources.

Key words: canola straw, Holstein male calves, carcass characteristics

W126 Chromium acetate induces adipogenesis of bovine intramuscular adipocytes through reduced phosphorylation of adenosine monophosphate–activated protein kinase α. K. Y. Chung*, R. T. Tokach, and B. J. Johnson, *Texas Tech University, Lubbock.*

Chromium sources have positive effects on glucose uptake in both cattle and pigs. Chromium aids in insulin signaling in insulin-sensitive cells such as adipocytes. Adenosine monophosphate-activated protein kinase α (AMPKα) can affect lipid metabolism in the bovine intramuscular (i.m.) and subcutaneous (s.c.) adipocytes. We hypothesized that chromium acetate (CrAc) may affect AMPKα phosphorylation state in bovine i.m. and s.c. adipocytes. Bovine i.m. and s.c. preadipocytes were incubated with similar differentiation factors such as 10 μM insulin, 10 μM ciglitizone, 1 μM dexamethasone, and 100 μM oleic acid. Multilocular lipid droplets accumulated in the cultured i.m. adipocytes, but unilocular lipid droplets accumulated in the s.c. adipocytes after 96 h of CrAc treatment. Data were analyzed as a completely randomized design using the MIXED model, each treatment performed in triplicate. Difference between control and treatments were determined using the LSD procedure. Quantity of mRNA was measured by agarose gel electrophoresis and OD calculation. Western blot analysis revealed that CrAc reduced ($P < 0.05$) phospho-AMPKα to AMPKα in i.m. adipocytes but had no effect in s.c. adipocytes. Relative PPARγ mRNA concentrations were greater ($P < 0.05$) in i.m. adipocytes with CrAc treatments compared with the control cultures. Treatment with 10 μM sodium acetate compared with CrAc did not differ ($P > 0.05$) from control for PPARγ, glucose transporter 4 (GLUT4), and GPR43 mRNA concentrations. Total amount of PPARγ mRNA was 5 times greater in s.c. than in i.m. adipocytes ($P < 0.05$). Although GLUT4 level was not different in i.m. adipocytes, there was a dose-dependent effect of CrAc in the s.c. adipocytes. The mRNA concentrations of GPR43, a short-chain fatty acid receptor, tended to be increased ($P = 0.08$) in i.m. adipocyte cultures. Chromium acetate can induce adipogenic development in the i.m. preadipocytes potentially by reducing phosphorylation of AMPKα, and the GPR43 membrane protein may be involved in this process.

Key words: chromium acetate, adenosine monophosphate–activated protein kinase α, adipocyte

W127 Palmitoleic acid regulation of lipid metabolism in primary bovine adipocytes could involve genes associated with fatty acid oxidation. A. K. G. Kadegowda*, T. A. Burns, S. L. Pratt, and S. K. Duckett, *Clemson University, Clemson, SC.*

Palmitoleic acid (C16:1n7) is a proposed lipokine that regulates systemic metabolism. The objective was to determine the effect of C16:1 on fatty acid metabolism gene expression in adipocytes. Bovine primary preadipocyte cultures were isolated from intermuscular fat from rib sections of 18-mo old Angus crossbred heifers (n = 3) fed a concentrate diet. Preadipocytes were differentiated (D0) in differentiation media [DMEM containing 10% fetal calf serum, 2.5 μg/mL insulin, 0.25 μ*M* dexamethasone (DEX), 20 μ*M* troglitasone (TRO), 0.5 m*M* isobutylmethylxanthine (IBMX), and 10 m*M* acetate] for 2 d. Cells were further differentiated from D2 to D12 in differentiation media [with out DEX and IBMX] containing 1 of 4 levels of C16:1 (0, 50, 150, or 300 μ*M*). Cells were harvested on D6 and D12 for fatty acid analysis using GLC and mRNA expression by RT-qPCR. We measured the expression of *Acyl-Coenzyme A oxidase 2 (ACOX2), Acyl-CoA dehydrogenase, long chain (ACADL), Phytanoyl-CoA 2-hydroxylase (PHYH), Caveolin1 (CAV1)* and *Adipose differentiation-related protein (ADFP)*. The geometric mean of *Eukaryotic translation initiation factor 3, subunit k* (*EIF3K*) and *Ubiquitously expressed transcript* (*UXT*) was used for normalization. Increasing the concentration of C16:1 in the media increased the cellular concentration of C16:1 ($P < 0.05$) and C18:1cis11 ($P < 0.05$), a C16:1 elongation product but decreased ($P < 0.05$) the cellular levels of C16:0, C18:0, C18:1c9. Of the measured genes related to fatty acid oxidation, *ACADL* increased by 2.36 fold ($P < 0.07$) while *PHYH* increased by 95.5 fold ($P < 0.01$) compared with controls on D6 suggesting potential increase in mitochondrial β-oxidation and peroxisomal α-oxidation, respectively. The increase in the mRNA expression of lipid droplet associated proteins *CAV1* (1.47 fold, $P < 0.07$) and *ADFP* (3.4 fold, $P < 0.01$), could be a consequence of increase in lipid droplet content due to increase in C16:1 level. The results from the study shows that C16:1 regulates lipid metabolism in the adipose tissue and could potentially involve mechanisms related to fatty acid oxidation.

Key words: palmitoleic acid, adipocyte, fatty acid oxidation

W128 Effect of anabolic implant and quality grade on lipogenic gene expression in subcutaneous adipose tissue. S. K. Duckett*, S. L. Pratt, and J. W. Long, *Clemson University, Clemson, SC.*

Angus-cross steers (n = 24; 488 kg) were randomly allotted to either non-implant (CON) or implant (IMP) treatments to explore the effects of anabolic implants on lipogenic gene expression in subcutaneous adipose depots by quality grade. Steers allocated to IMP received a single Revalor-S (24 mg estradiol, 124 mg trenbolone acetate) on d 0. All steers were individually fed a high-concentrate diet for 72 d and slaughtered. At slaughter, adipose tissue samples were collected from subcutaneous adipose depots, flash-frozen, and stored at −80°C for subsequent RNA extraction. Carcass weight and skeletal maturity were greater ($P < 0.05$) for IMP than CON. Other carcass variables including marbling score, quality grade and yield grade did not differ among treatments. For qPCR, a sub-sample (n = 8) was selected from each treatment based on quality grade, LOW (Select-) vs. HI (Choice-). Data were analyzed with implant treatment, quality grade, and 2-way interaction in the model. Total RNA yield from subcutaneous adipose tissues averaged 36.2 μg/g and was not affected by treatment or quality grade. All 2-way interactions were significant ($P < 0.05$) for the lipogenic genes evaluated. Stearoyl-CoA desaturase (SCD) is the rate-limiting enzyme in the conversion of saturated fatty acids to monounsaturated fatty acids. The SCD mRNA expression was downregulated ($P < 0.05$) by 11.3-fold in IMP-LOW subcutaneous adipose tissues compared with CON-LOW. Expression of SCD did not differ ($P > 0.05$) for CON-HI or IMP-HI compared with CON-LOW. Fatty acid synthase (FASN) is 1 of 2 enzymes regulating de novo fatty acid synthesis. The mRNA expression of FASN was downregulated ($P < 0.05$) in IMP-LOW by 11.6-fold and IMP-HI by 1.9-fold compared with CON-LOW. Fatty acid elongase (ELOVL6) is the enzyme responsible for the elongation of fatty acids. ELOVL6 mRNA expression was downregulated ($P < 0.05$) in IMP-LOW by 6-fold compared with CON-LOW. ELOVL6 mRNA expression did not differ ($P > 0.05$) in IMP-HI or CON-HI compared with CON-LOW. Lipogenic gene expression was downregulated in subcutaneous fat from implanted steers with low quality grades.

Key words: beef, implant, gene expression

W129 Signaling pathways mediating the effects of insulin-like growth factor-I on proliferation, protein synthesis, and protein degradation in bovine satellite cells. X. Ge and H. Jiang*, *Department of Animal and Poultry Sciences, Virginia Tech, Blacksburg.*

The objective of this work was to identify the signaling pathways mediating the effects of IGF-I on proliferation, fusion, protein synthesis, and protein degradation in bovine muscle cells. Satellite cells were isolated from adult cattle skeletal muscle and were allowed to activate and proliferate or were induced to form myotubes following standard protocols. Cell proliferation was determined by measuring the numbers of viable cells at different times. Protein synthesis and degradation were determined by measuring the accumulation of 3H-phenylalanine in cellular protein and the release of 3H-phenylalanine to the medium, respectively. The signaling pathway involved was identified by including in the medium rapamycin, LY294002, or PD98095, which are specific inhibitors of the IGF-I receptor signaling molecules mTOR, AKT (PKB), and ERK (MAPK), respectively. Western blotting confirmed that IGF-I action caused phosphorylations of p70S6K (a signaling molecule immediately downstream of mTOR), AKT, and ERK, and that these phosphorylations were completely or near completely blocked by their corresponding inhibitors. Proliferation of bovine myoblasts was stimulated by 500 ng/mL IGF-I ($P < 0.01$), and this stimulation was partially blocked by PD98059 ($P < 0.05$), and was completely blocked by rapamycin or LY294002 ($P < 0.01$). Protein degradation in myotubes was inhibited by approximately 20% by 500 ng/mL IGF-I ($P < 0.05$), and this inhibition was completely relieved by LY294002 ($P < 0.01$), but not at all by rapamycin or PD98095. Protein synthesis in myotubes was increased by 30% by 500 ng/mL IGF-I ($P < 0.01$), and this increase was completely blocked by rapamycin, LY294002, or PD98059 ($P < 0.01$). Addition of IGF-I to the culture medium had no effect on fusion of myoblasts into myotubes. These data suggest that IGF-I stimulates proliferation of bovine myoblasts and protein synthesis in bovine myotubes through both the PI3K/AKT and the MAPK signaling pathways, and that IGF-I inhibits protein degradation in bovine myotubes through the PI3K/AKT pathway only from the IGF-I receptor.

Key words: IGF-I, muscle, signaling

W130 Effects of energy intake and age on the expression of adipogenic genes in subcutaneous and intramuscular fat in bovine Spanish Pirenaica breed. B. Soret*, P. Tiberio, A. Arana, JA Mendizabal, and L. Alfonso, *Universidad Publica de Navarra, Pamplona, Navarra, Spain.*

An improved understanding of the molecular mechanisms that drive adipose tissue development in livestock may allow for new strategies to modify adipose tissue distribution to improve meat quality by enhancing intramuscular fat (IMF). The objective of this study was to investigate the effects of dietary energy and age on the expression of key adipogenic genes in Pirenaica, a very low fattening breed widely used in cattle production systems in Navarra, Spain. Sixteen half-sibling young Pirenaica bulls were distributed into 4 groups (n = 4) and slaughtered at 6, 12, and 18 mo of age; the later assigned to 2 groups differing in energy density in the ration (ME 3.29 and 2.87 Mcal/kg DM). Subcutaneous fat (SCF) and IMF were harvested at slaughter for mRNA isolation. Gene expression was measured by reverse transcription and quantitative PCR. Relative gene expression (Ct method) was calculated by normalizing against β-actin using the 6-mo-old group as calibrator. Backfat thickness (BFT), IMF chemical fat content, and adipocyte diameter were measured. Statistical analysis was performed by ANOVA. No differences in gene expression for *PPARγ*, sterol regulatory element binding protein (*SREBP*), fatty acid binding protein (*FABP*), lipoprotein lipase, and acetyl-CoA carboxylase (*ACC*) were found in IMF, maybe related to the low state of development of that depot in these animals which only had 2.4% chemical fat. Energy content of the diet did not affect SCF expression of any of the genes evaluated. In contrast *FABP* ($P < 0.01$) and *ACC* ($P < 0.001$) were affected by age, showing the higher values at 12 mo. Also BFT and the diameter of the SCF adipocytes showed the higher increase between 6 and 12 mo ($P < 0.05$); thus, some genes involved in lipogenesis changed with age accordingly to changes in cell size in a depot-dependent manner. Differences between depots in expression of *FABP*, *PPARγ*, and *SREBP*($P < 0.001$) were found. This, together with changes with age for SCF only, may suggest depot-specific patterns of gene expression during fattening.

Key words: adipogenic gene, intramuscular fat, bovine

W131 Age post weaning but not birth weight and sex affects the small intestinal glutathione redox status of piglets. J. Michiels*[1,2], E. Claeys[2], A. Ovyn[2], and S. De Smet[2], *[1]Faculty of Biosciences and Landscape Architecture, University College Ghent, Ghent, Belgium, [2]Laboratory for Animal Nutrition and Animal Product Quality, Department of Animal Production, Ghent University, Melle, Belgium.*

Glutathione (GSH) serves as the major endogenous antioxidant in gut tissue and cells keep it predominantly in the reduced state, i.e., a low oxidized to reduced glutathione (GSSG/GSH) ratio. The aim of the study was to assess the effect of birth weight, sex, and age post weaning on small intestinal mucosal glutathione redox status of piglets. Newborns from 17 Danbred hybrid sows were weighed and tagged. At weaning (18.8 ± 0.44d) pairs of intra-uterine growth-retarded (IUGR) and normal birth weight sex-matched littermates were selected and fed a starter ad libitum until 1h before sampling at 0, 2, 5, 12, and 28d post weaning. An IUGR pig was defined as having a birth weight <1 kg and < mean litter birth weight – 1.5 SD. Mucosa was collected from 2 small intestinal sites; at 5% (≈end of duodenum) and at 75% of total length. GSH and GSSG were determined by HPLC using γ-Glu-Glu as internal standard following the reaction of thiols with iodoacetic acid to form S-carboxymethyl compounds and derivatization with 2,4-dinitrofluorobenzene. Data were analyzed by linear models with birth weight, sex, and age post weaning as fixed factors and presented as adjusted means. Birth weight and sex showed no significant effects. A temporal decline in GSH content at d2 and increase in the GSSG/GSH ratio at d5 in the proximal small intestinal mucosa indicates that oxidative stress occurred in that time window (Table 1). At 75% of length of the small intestine there was a gradual decrease of the GSSG/GSH ratio with time. The higher GSH content and GSSG/GSH ratio in the proximal small intestine might illustrate the higher need for antioxidant action against dietary pro–oxidants at that site.

Table 1. Effect of age post weaning (d) on glutathione redox status of small intestinal mucosa in piglets (n = 16)

	Age post-weaning (d)						
	0	2	5	12	28	SEM	*P*-value
5% of length							
GSH (μmol/g)	1.94[c]	1.79[c]	2.11[c]	2.65[b]	3.27[a]	0.075	<0.001
GSSG/GSH	0.042[b]	0.043[b]	0.089[a]	0.044[b]	0.046[b]	0.0040	<0.001
75% of length							
GSH (μmol/g)	1.23[b]	1.44[b]	1.79[a]	1.89[a]	1.90[a]	0.062	0.001
GSSG/GSH	0.036[a]	0.038[a]	0.031[ab]	0.030[ab]	0.027[b]	0.0036	0.055

[a-c]Values with different superscripts within a row are significantly different at $P < 0.05$; LSD-test.

Key words: pig, glutathione, gut health

W132 Feed restriction alters reactivity of body fat after catabolic stimulation in growing pigs. B. U. Metzler-Zebeli, S. Görs, K. Giggel, R. Krüger, H. M. Hammon, and C. C. Metges*, *Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany.*

Birth weight (BIRTH) and feed restriction (FR) may affect later body composition due to persistent alterations in catabolic and anabolic processes. Therefore, we investigated the effect of BIRTH and FR on the reactivity of body fat after stimulation of catabolic processes by pST-Clenbuterol (ST+C). Two female littermate pigs from 20 sows each with low (≤1.1 kg) or normal birth (1.4 to 1.6 kg) weight were used. Half of the pigs were fed ad libitum whereas the other half was restrictively fed (50% ad libitum) between ages d 78 and 98. Subsequently, all pigs were (re)fed ad libitum. At d 84 of age, 20 pigs were fitted with catheters in A. carotis and V. jugularis. After intravenous ST+C administration, plasma lipids, glycerol, and glucose concentrations were determined over 12 h at ages d 96, 104, and 118. Body fat content was determined using DXA measurement at ages d 75 and 96. The statistical model included BIRTH, feeding type, time, litter size group, interactions, and random factor sow. Mobilization of body fat and glycogen due to ST+C was confirmed by increased ($P < 0.01$) plasma triglycerides (TG; 1 to 8 h after ST+C), glycerol (1 to 6 h after ST+C) and glucose (0.5 to 6.5h after ST+C) concentrations at d 96. Plasma TG, glycerol, and glucose were not affected by BIRTH and FR. In contrast, plasma NEFA were greater ($P < 0.01$) in restrictively compared with ad libitum-fed pigs after ST+C at d 96 indicating increased lipolysis. The enhanced catabolic status in restrictively-fed pigs was confirmed by their lower body fat as compared with ad libitum-fed pigs at age d 96 ($P < 0.05$). Although TG increased after ST+C stimulation at ages d 104 and 118, NEFA release did not differ among pigs at age d 104. Interestingly, after ST+C stimulation at d 118 plasma NEFA were again greater in pigs that were restrictively fed between d 78 and 98 of age ($P < 0.05$), but were not affected by BIRTH. In conclusion, FR causes alterations in the catabolic reactivity of body fat not only during the immediate FR period but also at 3 wk of refeeding. However, BIRTH did not affect body fat mobilization after catabolic stimulation. Supported by BMBF (VISION EPIFOOD).

Key words: lipolysis, body fat, NEFA

W133 The effect of different methods of using zilpaterol hydrochloride on growth performance in Japanese quail. M. Mohammadi*, A. Towhidi, H. Moravej, and A. Zareh Shahne, *Department of Animal Science, University of Tehran, Karaj, Alborz, Iran.*

Zilpaterol hydrochloride is a β2-adrenergic agonist which has been shown to increase lean muscle and decrease fat deposition. It seems that the chronic supplementation of β-agonists diminishes the response because of desensitizing of the receptors. This study was designed to compare 2 methods of using zilpaterol hydrochloride including once a day and skip 2 d on growth performance in Japanese quail. Ninety-six quail of 33 d of age were assigned to 3 groups with 4 replications. Treatments were defined as: T1 as control, T2 received zilpaterol skip 2 d, and T3 received zilpaterol once a day. Diets were based on corn and soybean meal in the finisher period (24% CP and 2.9 Mcal/kg of ME) and the birds orally received 0.225 mg/kg of live weight/d zilpaterol for 14 d and slaughtered at 50 d of age. The complete randomized design in GLM procedure was used to analyze the data. Results showed zilpaterol supplementation improved weight gain ($P < 0.0001$) and feed conversion ratio ($P < 0.001$) in both treatments compared with control, but did not affect feed intake at d 33 to 40 ($P = 0.10$), whereas at d 40 to 47, zilpaterol did not have a significant effect on growth performance ($P > 0.05$). Furthermore, there were no significant differences in weight gain ($P = 0.15$), feed conversion ratio ($P = 0.21$), or feed intake ($P = 0.31$) between the 2 treatments that received zilpaterol at 40 to 47 d. The feed conversion ratio ($P = 0.23$) and weight gain ($P = 0.13$) were negatively affected in the period of 40 to 47 d in all groups. It seems that maturity and hormonal modification had considerable effects on growth performance. It was concluded that zilpaterol hydrochloride could improve growth performance when used by either method for the 33 to 40 d of quail rearing. However, considering the economics, the skip 2 d was better than once-a-day consumption and will have less cost.

Key words: zilpaterol hydrochloride, Japanese quail, growth performance

W134 Effects of dietary supplementation of sodium stearoyl-2-lactylate in a low-energy density diet on growth performance, blood profiles, and relative organ weight in broilers. S. M. Hong*, J. P. Wang, and I. H. Kim, *Dankook University, Cheonan, Choongnam, South Korea.*

The aim of this study was to investigate the effects of supplementation of a dietary emulsifier sodium stearoyl-2-lactylate (SSL) in a low-energy density diet on growth performance, blood profiles, and relative organ weight in broilers. A total of 260 male and female ROSS 308 broiler chicks (2-d old, average BW = 45 ± 1.0 g) were randomly allotted to 1 of 5 treatments with 4 replications per treatment and 13 chicks per pen. The diets were fed during the experiment in 2 phases consisting of a starter phase from d 0 to 21 and a finisher phase from d 22 to 35. A corn-soybean meal-based diet was formulated as a control diet and dietary treatments were as follows: 1) NC (negative control; −200kcal ME/kg energy down spec diet), 2) PC (positive control; 3,150kcal ME/kg), 3) P1 (−50 kcal ME/kg energy down spec diet + 0.05% SSL), 4) P2 (−150kcal ME/kg energy down spec diet + 0.05% SSL), and 5) P3 (NC + 0.1% enzyme and 0.05% SSL). Body weight gain (BWG) was greater in PC, P1, and P3 treatments than in NC treatment ($P < 0.05$) and feed intake (FI) was lesser ($P < 0.05$) in P2 treatment than in P3 treatment throughout the whole experiment. The PC and P1 treatments had greater ($P < 0.05$) FCR than NC and P3 treatments overall during the experiment. Lymphocyte percentages in NC and PC treatments were greater ($P < 0.05$) than that in P1 treatment. Birds fed PC, P1, and P3 diets resulted in an increased triglyceride level compared with birds fed NC diet ($P < 0.05$). The relative spleen weight was decreased ($P < 0.05$) in P3 treatment compared with CON treatment. The bursa of Fabricius was heavier in P3 treatment than

that in PC, P1, and P2 treatments. In conclusion, SSL administration partially improved BG, FCR, and triglyceride level.

Key words: broiler, emulsifier, growth performance

W135 Insulin-like growth factor-I (IGFI), IGF binding proteins (IGFBP), and growth hormone receptor (GHR) mRNA concentration in fetal liver and duodenum in response to variable maternal nutrition during gestation. M. Field*, R. Anthony, T. Engle, S. Archibeque, and H. Han, *Colorado State University, Fort Collins.*

Undernutrition during gestation is known to influence fetal development and predispose offspring to the metabolic syndrome. We investigated the mRNA concentration of IGFI, IGFBP-2 and −3, and GHR in liver and duodenum from twin fetal lambs. Multiparous whiteface ewes were randomly assigned to 1 of 3 treatments at 21 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). Fetal liver (L) and duodenum (D) were collected at 135 dGA. Concentration of each mRNA was corrected by ribosomal protein S15 mRNA concentration. Concentration of IGFI mRNA did not differ in fetal liver ($P = 0.54$) and duodenum ($P = 0.32$), but was numerically greater in 50–100 (L = 0.90 ± 0.02, D = 0.58 ± 0.05) than Control (L = 0.87 ± 0.02, D = 0.54 ± 0.04) and 50–50 (L = 0.87 ± 0.02, D = 0.64 ± 0.04) fetuses. There were no differences in expression of IGFBP3 mRNA between treatments in either liver or duodenum. Liver expression of IGFBP2 mRNA did not differ and concentrations were low or undetectable in duodenum. Liver GHR mRNA was numerically greater ($P = 0.15$) in 50–100 fetuses (0.92 ± 0.02), than Control (0.90 ± 0.02) and 50–50 (0.87 ± 0.02) fetuses. Duodenal GHR mRNA did not differ (Control 0.78 ± 0.03; 50–100 0.72 ± 0.04; 50–50 0.81 ± 0.03; $P = 0.266$). Natural intrauterine growth restriction in twin pregnancy may contribute to lower IGFI and GHR concentrations while realimentation from mid-gestation may induce elevated GHR and IGFI expression, which contributes to compensatory fetal growth during late gestation in twin pregnancy. This project was supported by National Research Initiative Competitive Grant no. 2009–35206–05273 from the USDA National Institute of Food and Agriculture.

Key words: sheep, insulin-like growth factor I, growth hormone

W136 Effects of variable maternal undernutrition on uterine and umbilical IGF-I, insulin, and ghrelin concentrations in near-term sheep twin pregnancies. M. Field*, R. Anthony, T. Engle, S. Archibeque, and H. Han, *Colorado State University, Fort Collins.*

Maternal undernutrition during gestation alters the developmental environment of a fetus and predisposes the offspring to the metabolic syndrome in later life. We investigated the impact of maternal undernutrition on IGF-I, insulin, and ghrelin concentrations in uterine and umbilical blood in near-term twin pregnant sheep. Multiparous whiteface ewes were randomly assigned to 1 of 3 treatments and acclimation to individual pens (7 d) begun at 21 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). During cesarean section uterine and umbilical blood was collected while the fetus was viable. Blood hormone concentrations were determined by RIA and analyzed using the PROC MIXED model of SAS. Uterine artery IGF-I and insulin concentrations were not different between treatments. Umbilical vein (UV) IGF-I was greater ($P = 0.02$) in 50–100 (74.4 ± 6.7 ng/mL) than Control (50.9 ± 5.9 ng/mL) and 50–50 (46.7 ± 5.6 ng/mL). Umbilical artery (UA) IGF-I exhibited a similar trend ($P = 0.10$) where 50–100 (91.4 ± 9.0 ng/mL) was greater than Control (67.9 ± 8.1 ng/mL) and 50–50 (66.6 ± 7.5 ng/mL). Insulin in UA was greater ($P = 0.08$) in 50–100 (0.70 ± 0.15 ng/mL) than Control (0.30 ± 0.14 ng/mL) and 50–50 (0.24 ± 0.13 ng/mL). The UV and UA ghrelin concentrations were not different between treatments, although UV and UA ghrelin were numerically greater in 50–50 (UA = 44.5 ± 10.3, UV = 31.8 ± 7.5 pg/mL) than both Control (UA = 29.6 ± 11.1, UV = 25.3 ± 8.0 pg/mL) and 50–100 (UA = 24.5 ± 12.5, UV = 23.0 ± 8.8 pg/mL). The IGF-I and insulin concentrations in 50–100 umbilical V and A indicate a shift in IGF-I and accelerated fetal growth as a result of nutrient deprivation followed by realimentation.

Key words: undernutrition, IGF-I, blood

W137 Transfer of omega-3 fatty acids from dams to calves in dairy cows. M. Zachut*[1,2], A. Romanenco[1,2], H. Lehrer[1], A. Arieli[2], and U. Moallem[1], *[1]Agriculture Research Organization, Bet Dagan, Israel, [2]Faculty of Agriculture, Hebrew University, Rehovot, Israel.*

In many species fatty acid (FA) composition of the maternal diet during pregnancy can affect the FA composition of the fetus. Omega-3 FA have a crucial role in neonatal brain development, yet the transfer of long chain FA through the placenta in ruminants is very limited. The objectives were to examine 1) the plasma FA composition in newborn calves, and 2) the transfer of various omega-3 FA from dams into calves' plasma. Twenty 7 multiparous Israeli-Holstein dry cows (256 d pregnant) were assigned to 3 groups and supplemented with 300 g/d per cow of encapsulated fat that contained: (i) control - saturated FA; (ii) FLX - 51.3 g/d per cow 18:3n-3 (ALA) from flaxseed oil, and (iii) FO - 3.6 C22:5n-3 (DPA) and 3.0 g/d per cow C22:6n-3 (DHA) from fish oil. Blood samples were collected from cows twice a week and from calves immediately after calving, before colostrum offering. FA composition was determined in dams in the last sample before parturition. Data were analyzed using the GLM model of SAS. Across treatments analysis revealed that the proportions of saturated and mono-unsaturated FA in plasma were greater in calves than in cows (49.8 vs. 42.5% and 30.0 vs. 12.7%, respectively), while the proportion of polyunsaturated FA (PUFA) was 2-fold greater in dams than in calves (44.8 vs. 20.1%, respectively). The proportion of ALA in plasma of FLX cows was elevated to 5.2% as compared with 2% in the control; however, this FA was not transferred into calves' blood. Greater plasma proportions of DPA (0.32 vs. 0.16%) and DHA (0.30 vs. 0.02%) were found in the FO cows than in the controls, respectively, and the proportion of DHA was nearly doubled in the FO calves' blood as compared with controls (0.47 vs. 0.26%, respectively). Furthermore, the FO calves had greater proportions of total PUFA in plasma as compared with both other groups (23.9 vs. 18.5%, respectively). In summary, the low permeability of the placenta to FA resulted in a very different plasma FA composition in newborn calves as compared with dams. Furthermore, dietary DHA, but not ALA, passages from dam to fetus in cows, perhaps in an active transfer due to the essentiality of this FA to fetal development.

Key words: omega-3, calf, fatty acid composition

W138 Temporal changes in the proteome of the uterine histotroph in cattle. M. P. Mullen*[1], A. C. O. Evans[2], G. Elia[3], M.

Hilliard[3], N. Forde[2], M. H. Parr[1], M. G. Diskin[1], and M. A. Crowe[2], *[1]Animal and Bioscience Research Department, Animal and Grassland Research and Innovation Centre, Teagasc, Athenry, Co. Galway, Ireland, [2]School of Agriculture, Food Science and Veterinary Medicine, University College Dublin, Belfield, Dublin 4, Ireland, [3]Conway Mass Spectrometry Resource, University College Dublin, Belfield, Dublin 4, Ireland.*

The composition of the uterine fluid (or histotroph) that bathes the early embryo is critical for its growth and development as it is the sole supply of nutrients. The objective of this study was to characterize the proteome of the bovine histotroph during key stages of the estrous cycle. The uterine horn ipsilateral to the corpus luteum of Holstein-Friesian heifers on Day 7 (n = 6) and Day 13 (n = 6) of separate estrous cycles was non-surgically flushed with 50 mL of 100 mM Tris pH 7.2. Global protein abundance was analyzed using a label-free shot gun proteomics approach encompassing SCX fractionation coupled with reversed phase LC–MS/MS analysis. Thresholds for defining proteins more abundant on either day included (i) an average spectral count value ≥ 2, (ii) signal in at least 3 animals and (iii) spectral count ratio of ≥ 5 between days. This led to the classification of 20 proteins more abundant on Day 7 vs. Day 13 including serpins, immune related complement proteins, structural cytokeratins, and hypothetical proteins. In addition, 35 proteins were more abundant on Day 13 vs. Day 7 and included novel bovine histotroph proteins such as members of the Cathespin family B, D, Z, and L2; previously reported bovine histotroph protease modulators Legumain (LGN), Metalloproteinase inhibitor 2 (TIMP2), Tripartite motif-containing protein 25 (TRIM25); metabolic proteins Actin and Lysosomal α-mannosidase (MAN2B1) and growth factor binding proteins IGFBP-1 and −5. Furthermore, uncharacterized and structural proteins were only identified on Day 7 while proteins involved in stressful microenvironment management were more abundant on Day 13. Lowering the spectral count ratio threshold to include proteins with a ratio of 2 to 4 resulted in an additional 28 proteins more abundant on Day 7 vs. Day 13 and 46 proteins more abundant on Day 13 vs. Day 7. Because temporal changes in uterine gene expression between Day 7 and Day 13 are associated with embryo development, we propose that the abundance of these proteins is similarly supportive of embryo development and required for the establishment of pregnancy in cattle. Funded by Science Foundation Ireland 07/SRC/B1156.

Key words: uterus, histotroph, global proteomics

W139 Effect of maternal diet on the ontogenetic development of the hepatic proteome in intrauterine growth-restricted porcine offspring. M. Peters, B. Kuhla, I. S. Lang, E. P. Rudolph, and C. C. Metges*, *Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany.*

We determined the effect of intrauterine growth restriction (IUGR) caused by excess and low-protein gestation diets (Rehfeldt et al. J Anim Sci 89:329, 2011) on development of hepatic proteome of pre- and postnatal porcine offspring. Gilts (n = 58; 241 d, 150.6 kg) were randomly assigned to 3 diet groups. The isocaloric diets contained adequate (AP, 12.1%), high (HP, 30%) or low (LP, 6.5%) protein levels at the expense of carbohydrates. Pigs were killed and liver samples of light (L) and heavy (H) offspring at d 94 post conception (dpc), d 1, 28, and 188 post natum (dpn) were analyzed by 2D-SDS-PAGE and MALDI-TOF MS. The model (SAS PROC MIXED) included maternal diet, offspring BW class (94 dpc, 1 dpn), sex, all interactions, and Tukey-Kramer test ($P \leq 0.05$). In HP fetuses and LP neonates the same number of proteins related to glycolysis (GL) and glycogen synthesis (GS) were diet dependently affected, whereas proteins of gluconeogenesis (GNG) were increased in HP and L neonates and L offspring at 28 dpn (Table 1). The LP fetuses had an increased expression of GL-related enzymes and a reduced expression of proteins related to GS. Proteins related to TCA cycle were upregulated in HP, LP, and L fetuses, as well as in LP and L offspring at 28 dpn, but downregulated in HP, LP, and L neonates and HP offspring at 28 dpn, whereas they could not be detected at 188 dpn. Validation of 6 selected proteins at 1 dpn via Western blot confirmed the expression pattern obtained from 2D analysis. In conclusion, maternal LP and HP diets persistently changed the offspring proteome profile of major metabolic pathways. Different diet-dependent profiles indicate different intrauterine regulatory mechanisms leading to offspring IUGR. Supported by DFG (ME 1420/8-1) and BMBF (Fugatoplus-FEPROeXPRESS)

Table 1. Effect of maternal gestation diet and BW class on offspring hepatic protein expression ratios related to glucose metabolism

Effect	94 dpc	1 dpn	28 dpn	188 dpn
HP vs. AP	GS = GL = 0.94	GNG = 1.04	GL = 0.87	GL = 1.13
LP vs. AP	GL > GS = 1.18	GS = GL = 1.13	GL = 0.95	GL = 1.32
L vs. H	GL = 1.11	GL, GNG = 1.11	GNG = 1.45	GL = 1.18

Key words: proteomics, fetal growth retardation, pig

W140 Changes in plasma amino acid concentrations in preterm and term born calves. J. Steinhoff-Wagner*, S. Görs, J. Flor, C. C. Metges, and H. M. Hammon, *Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany.*

Neonatal development is characterized by ontogenic maturation and high nitrogen (N) turnover. Adequate amino acid (AA) availability is important for protein and nucleic acid synthesis, but might be impaired in immature calves. The objective of the present study was to investigate dependency of plasma AA changes on ontogenic development and colostrum feeding in neonatal calves. Calves were delivered by Cesarean section 9 d before term (preterm; PT) or were born at term (T). Calves of PT and T were not fed during first 24 h of life. Calves of TC were born at term and were fed colostrum at 8% of BW during first 24 h of life (n = 7/group). Blood samples were taken at 2 to 3 h and 24 h after birth and before feed intake (TC) for determination of total protein (TP), urea, and free AA plasma concentrations. Data were analyzed by Mixed Model of SAS with ontogenic stage and postnatal feeding as fixed effects. Plasma concentrations of TP increased ($P < 0.05$) during 24 h only in TC due to immunoglobulin absorption. Plasma urea concentrations were greatest ($P < 0.05$) at birth and 24 h after birth in PT. At birth, plasma concentrations of Phe, Val, Leu, Ile, Glu, and Tyr were greater ($P < 0.05$) in PT than T and TC, whereas after 24 h plasma concentrations of Lys, Thr, Glu, Asp, Asn, Ala, Cys, Ser, Orn, and Pro were greater ($P < 0.05$) in PT than T. Colostrum feeding resulted in greater ($P < 0.05$) plasma concentrations of Leu, Val, Ile, Trp, His, and Tyr in TC than in T and PT, and greater ($P < 0.05$) plasma concentrations of Asp and Pro than in T. Plasma concentrations of Thr, Gly, Ala, Cys, Ser, and Orn were greater ($P < 0.05$) in PT than in TC. Plasma concentrations of Glu increased ($P < 0.05$) in TC and were greatest ($P < 0.05$) 24 h after birth in TC, whereas Gln increased in PT, but decreased in TC and were lowest ($P < 0.05$) 24 h after birth in TC. Greater essential AA (EAA) in PT than in T and greater non-EAA and urea plasma concentrations in PT than in T and TC suggested enhanced protein breakdown and AA degradation in PT. Colostrum

feeding leads to an improved EAA status and less AA degradation, but indicates enhanced N use for anabolic metabolism.

Key words: calf, preterm, amino acid

W141 Placental and fetal plasma amino acid uptake and release in mid and late pregnancy of gilts fed limited- and excess-protein diets associated with intrauterine growth retardation (IUGR). C. C. Metges*, S. Görs, I. S. Lang, K.-P. Brüssow, G. Nürnberg, C. Rehfeldt, W. Otten, and B. U. Metzler-Zebeli, *Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany.*

Low- and high-protein diets fed to pregnant gilts lead to IUGR (Rehfeldt et al. 2011, J Anim Sci). To explore underlying mechanisms, maternal, umbilical, and fetal amino acid (AA) concentrations were analyzed. Eighteen gilts each were fed isoenergetic diets with low (6.5%, LP), adequate (12.1%, AP), or high (30%, HP) protein levels, starting at insemination. Gilts and fetuses were examined at d 64 and 94 of pregnancy. Blood was collected during Caesarian section from maternal V. jugularis, umbilical vein (V) and artery (A), and fetal V. cava cranialis (4 fetuses/gilt). Fetal weight was recorded. Plasma AA concentration was analyzed by HPLC. Placental and fetal AA uptake (UPT) and release (REL) were calculated by V-A differences. Effects were evaluated by ANOVA with diet, fetal litter size, sex and weight class, interactions and random factor gilt. In HP, fetal weight was lower than in AP at d 94 but not at d 64 ($P < 0.05$). In LP maternal plasma, Leu, Phe, Tyr, Thr, and Trp were lesser and Ala was greater at d 64, whereas at d 94 Leu, Trp, Val, Cys, and Tyr were lesser and Ala and Gly were greater than in AP ($P < 0.05$). In HP gilts at d 64, Ile, Thr, and Val concentrations were greater and Ala and Gly were lesser than in AP gilts whereas at d 94, Ile, Lys, and Val were greater and Ala, Gly, and Glu were lesser ($P < 0.05$). At d 64 and d 94, placental UPT of Ile, Leu, Trp, and Val was greater in HP than in LP. Placental Lys REL did not differ at d 64 but was lower in HP and LP than in AP at d 94 ($P < 0.05$). At d 64, Thr was taken up by the placenta in HP while it was released in LP; at d 94, placental Thr REL was greater in LP and AP than in HP ($P < 0.05$). At d 64, fetal AA UPT did not differ among diets, whereas at d 94 Leu and Lys UPT was lower in LP and HP than in AP ($P < 0.05$). Thus, placental AA metabolism largely compensated the imbalanced maternal AA patterns. In LP, but also in HP, fetal utilization of Leu and Lys was limited, which relates to lower birth weights in both groups.

Key words: amino acid, high protein, intrauterine growth retardation

W142 Hormonal regulation of suspected components of bovine IgG1 transcytosis mechanism in primary bovine mammary cells in vitro. A. Stark[1], E. Vaschkova[2], O. Wellnitz*[1], R. M. Bruckmaier[1], and C. R. Baumrucker[3], *[1]Veterinary Physiology, Vetsuisse Faculty, University of Bern, Switzerland, [2]Trakia University, Stara Zagora, Bulgaria, [3]Penn State University, State College.*

Colostrogenesis is distinguished by the specific transfer of IgG1 from the blood to mammary secretions. It occurs during the last 2–3 weeks of pregnancy when steroid concentrations of estradiol (E2) and progesterone (P4) are high. Rodent intestinal uptake of immunoglobulin G has indicated this transcytosis process is mediated by a receptor termed Fc fragment of IgG, Receptor, Transporter, α (FcGRT) and supported by light chain β2 Microglobulin (β2M). The bFcGRT has been cloned by others and mRNA exists in the mammary tissue and intestines of ruminant species. We hypothesized that steroid hormone treatments E2 and P4 of bovine mammary cells in vitro would induce changes in mRNA expression indicating which components are involved in IgG1 transcytosis. Two different cultures (passage 6 to 14) of primary bovine mammary cells were evaluated by qPCR. Cells on plastic and rat tail collagen were treated with hormonal combinations (steroids/lactogenic). Evaluated components were bFcGRT, bβ2M, and various bRab GTPases; the latter components direct endosomal transcytosis movements in other eukaryotic cells. All tested components showed strong expression of mRNA in the cells. Plastic experiments showed that FcGRT, Rab11b, Rab25, were significantly regulated ($P < 0.05$) by steroid hormones while Rab11A and β2M were not changed. Experiments on collagen gels showed that lactogenic hormones increased expression of bLf mRNA (8X; $P < 0.0001$) in both mammary cells. Less increased expression of FcGRT was principally stimulated by steroids (E2), while the Rab25 was increased by lactogenic and steroid treatments. These results indicate that some suspected components of IgG1 transcytosis have their mRNA altered by hormones in vitro. However the 2 different primary cultures of bovine mammary cells show different expression patterns, perhaps reflecting animal to animal variation that is experienced by in vivo experiments. Mammary cell bFcGRT, and bRab25 are candidates that are hormonally altered for the colostrogenesis period.

Key words: colostrum, IgG, cattle

W143 Reducing metabolic stress of dairy cows during the transition period by partial milking or nursing. É. Carbonneau*[1], A.-M. De Passillé[2], J. Rushen[2], B. G. Talbot[1], and P. Lacasse[3], *[1]Université de Sherbrooke, Sherbrooke, QC, Canada, [2]AAFC-Pacific Agri-Food Research Centre, Agassiz, BC, Canada, [3]AAFC-Dairy and Swine Research and Development Centre, Sherbrooke, QC, Canada.*

During the transition from pregnancy to lactation, the sudden increase in nutrient demand for milk production causes metabolic perturbations and high incidences of metabolic diseases in high yielding cows. We previously showed that limiting milk yield by milking once a day during the first wk of lactation improved metabolic status but reduced milk production during the following weeks. In this study, we examined if limiting milk harvest postpartum while maintaining milking-induced endocrine stimulus could improve the metabolic status of cows without reducing overall milk production. Forty-seven Holsteins cows were allocated to 3 treatments, balanced for parity and milk production: 1) cows were milked completely twice a day from calving (control); 2) cows were partially milked twice a day until d5 after calving (partial); 3) cows were left with the calf to suckle from the dam until d5 and were milked once a day from d3 to d5 (nursing). All cows were milked twice a day from d6 to the end of the experiment (d63). During the treatment period (d1 to d5), milk production averaged 27.3 and 9.7 kg/d for control and partial, respectively. There was no residual effect ($P = 0.7$) of treatments on milk production which averaged 47.5, 45.9 and 46.4 kg/d for the control, partial and, nursing, respectively, between wk2 and 9. The DMI of the cows were similar during and after treatment ($P > 0.2$). From wk2 to 9, milk protein and lactose content were not affected by treatments, but milk fat content tended ($P = 0.06$) to be higher in control cows than in cows where milk harvest was limited (partial + nursing). Blood concentrations of glucose ($P < 0.001$) and phosphorus ($P < 0.05$) were lower and the concentrations of NEFA ($P < 0.05$) and BHBA ($P < 0.0001$) were higher in control cows than in the other cows during the treatment period. The positive effects on glucose and BHBA remained significant ($P < 0.05$) up to d28. There was no effect of treatments on blood urea, calcium and haptoglobin. These results suggest that reducing milk harvest postpartum while maintaining milking stimuli reduces metabolic stress without compromising productivity of high yielding dairy cows.

Key words: milking management

W144 Analysis of the bovine milk transcriptome by RNA sequencing. S. Wickramasinghe, G. Rincon, A. Islas-Trejo, and J. F. Medrano*, *Dept. of Animal Science, University of California-Davis, Davis.*

Even though the chemical and physical properties of cow milk are well characterized, very limited research has been done on characterizing the milk transcriptome. The objective of this project was to perform a comprehensive expression profiling of genes expressed in milk somatic cells in Holstein cows. Milk samples were collected from 6 Holstein cows at d 15 (transition milk) and 250 (late) of lactation and RNA was extracted from the pelleted milk cells. Expression analysis was performed by RNA sequencing (RNaseq) using the Illumina GAII analyzer. Reads were assembled, annotated and analyzed in CLC Genomics workbench 3.7. Data was normalized by calculating the "reads per kilo base per million mapped reads" (RPKM) for each gene and annotated with Ensemble bovine annotation (24,580 unique genes). *t*-test was performed to identify the genes with significant changes in expression between the 2 stages of lactation. GenMAPP and MAPPFinder applications were used to determine the most significant gene ontology (GO) classifications (permutation $P \leq 0.05$) among these genes. The RPKM value of 0.3 was set as the threshold for detectable gene expression. The transition milk had 11,876 genes and late milk had 12,553 genes above the threshold. Genes encoding milk proteins had the most abundant transcripts in transition milk, and genes involved in immune regulation and cell defense had the most abundant transcripts in late lactation. Transition milk was enriched with gene ontology (GO) terms for Golgi vesicle transport while late milk was enriched with GO terms for DNA replication and signal transduction. ~8,000 genes had ubiquitous expression in milk and most of these genes were localized to intracellular organelles and intrinsic membranes. 4359 genes had significant change in expression ($P \leq 0.05$ and FDR $q \leq 0.2$) between the 2 stages, and these genes were mostly localized in extracellular matrix or vesicles. This is the first study to describe the comprehensive bovine milk transcriptome. Our results revealed that 48–51% of anno-

tated genes are expressed in the bovine milk and provided a valuable insight into the bovine lactome.

Key words: cow milk, gene expression, RNAseq

W146 Residual effects of incomplete udder emptying during milking in dairy cows. J. Guinard-Flament*, A. Albaaj, P.-G. Marnet, and C. Hurtaud, *UMR Production du Lait, INRA/Agrocampus OUest, Saint-Gilles, France.*

Extended milking intervals reduce milk yield with residual effects on following milking intervals, which could depend on the quantity of milk stored in the udder. The aim of this trial was to simulate milk accumulation by decreasing udder emptying (100, 70, 40, and 0%) at one milking to describe the short-term effects on milk yield in relation with mammary morphology and epithelium permeability. Sixteen dairy cows (55 DIM) were assigned to treatments 100, 70, 40, and 0% according to a Latin square design with 4 7-d periods. Cows were milked twice daily at 0700 and 1730. Treatments were applied at the morning milking called M0 and milk yield was recorded on following milking (from M0 to M7). Changes in the udder morphology were assessed 1 and 10 h after M0 milking by estimating the distance between the 4 teat tips and the cisternal surface area using ultrasonography. The permeability of mammary epithelium was estimated using lactose concentrations in blood plasma measured 1 h before M0 and 4, 7, and 10 h after M0. The quantity of milk collected at M1 linearly increased as udder emptying decreased at M0. Nevertheless, because of milk accumulation in the udder, milk yield of M0+M1 curvilinearly decreased with treatments (42.9, 41.1, 36.4, 26.9 kg for 100, 70, 40 and 0%, respectively; SEM = 1.14). Residual effects on milk yield were observed only for 40 and 0% on M2 and M3 milking, and did not differ between 40 and 0% (e.g., 20.8 and 20.4 vs 21.9 kg for 100% at M2; SEM = 0.745). The udder cistern area was maximal just after M0 for 70, 40 and 0% treatments. However, udder continued to distend as shown by measurement of the distance between teats. Before M1, this distance was higher than after M0 and linearly increased as udder emptying decreased at M0. Increase in concentration of lactose in blood plasma occurred only for 40 and 0% and were observed respectively 10 and 4h after M0. In conclusion, dairy cows are poorly sensitive to low amounts of milk forgotten in the udder at one milking. When observed, residual effects on milk yield were associated with loss of the mammary epithelium integrity.

Key words: milk yield, incomplete milking, dairy cow

W147 Effect of prolactin-release inhibition on milk production and mammary gland involution at drying-off. S. Ollier*[1], X. Zhao[2], and P. Lacasse[1], *[1]AAFC-Dairy and Swine Research and Development Centre, Sherbrooke, QC, Canada, [2]Department of Animal Science, McGill University, Sainte-Anne-de-Bellevue, QC, Canada.*

Drying-off is a challenging period for high-yielding cows as they are often dried off while still producing significant quantities of milk and, consequently, are highly susceptible to new intra-mammary infections. Once active involution is completed, the mammary gland becomes much more resistant to infection. Therefore, it is of critical importance to develop strategies to reduce milk production before the drying-off and to accelerate mammary gland involution. In this study, we assessed the effect of an inhibition of the lactogenic signal driven by prolactin (PRL) on milk production and on evolution of involution markers. Sixteen Holstein cows in late lactation were assigned to 2 treatments based on milk yield, somatic cell count and parity. Eight cows received twice daily i.m. injection of quinagolide (2 mg per injection), a specific inhibitor of PRL-release, from 4 d before drying-off to 3 d after (Quin). The 8 others received injections of the solvent (water, Control). Blood and milk (mammary secretion) samples were collected on the last 5 d before and 1, 3, 5, 7, 10, and 14 d after the last milking. On the day preceding the first injection and the following day, several blood samples were also collected around milking time. Quinagolide reduced ($P < 0.01$) basal serum PRL concentrations on all the injection days and PRL released in blood during milking. The PRL inhibitor induced a decrease ($P < 0.05$) in milk production before drying-off, which averaged, over the last 3d of lactation, 19.3 and 15.5 kg/d for the control and the Quin groups, respectively. Quinagolide had no significant effect on milk citrate:lactoferrin and Na:K ratios, which decreased and increased respectively ($P < 0.001$) during the first 2 wk of the dry period. Nevertheless, the increases ($P < 0.001$) in somatic cells and bovine serum albumin in milk during early involution were greater ($P < 0.01$) in the Quin than the control cows. This experiment shows that inhibition of PRL-release induces a decrease in milk production of cows in late lactation. Changes in mammary secretion composition suggest that this approach is also hastening mammary gland involution.

Key words: quinagolide, dry period

W149 Putative stem/progenitor cell markers in lactating and re-developing bovine mammary glands. E. Brijs*, K. Singh, and A. Molenaar, *AgResearch Ltd., Ruakura Research Centre, Hamilton, New Zealand.*

The study of stem and progenitor cells in the bovine mammary gland is still developing, especially in the area of stem cell regenerative capacity during lactation. The objective of this study was to investigate whether the putative stem/progenitor cell markers integrin β 3 (CD61), keratin 5 (K5) and integrin β 1 (CD29) used in murine and human studies are expressed in the bovine mammary gland. Mammary gland biopsies were collected from 16 multiparous cows at near-peak (66 ± 3 DIM) and late lactation (226 ± 6 DIM), and at 30 (29 ± 10) and 10 (11 ± 6) days prepartum to the next lactation season. Qualitative immunohistochemistry (IHC) analysis demonstrated the presence of CD61 positively labeled cells in the basal epithelium, intra-alveolar cells and stromal cells at all 4 time points; however the tissue sections from late lactation and 30 d prepartum appeared to have a greater number of positively stained cells. The putative bipotent marker K5 had intense cytoplasmic labeling in the majority of the basal epithelium during the prepartum period in comparison to near-peak lactating tissue. Positive cells were also found in a luminal position. IHC analysis indicated that as alveolar become more differentiated in prepartum tissue there was a decrease in K5 expression. Real-time RT-PCR confirmed this expression pattern showing a 4.4- and 3.3-fold increase at 30 ($P < 0.001$) and 10 ($P < 0.001$) days prepartum, respectively, in comparison to near-peak lactation. Preliminary IHC analysis of CD29 indicated diffuse staining in the majority of basal epithelium at all 4 time points. However, RT-PCR showed a similar expression pattern to K5, with a 1.8-fold increase at 30 d prepartum ($P < 0.001$) and 1.5-fold increase at 10 d prepartum ($P < 0.01$) in comparison to post-peak lactation. Collectively these preliminary data show that these cell markers can be used to study stem/progenitor cells in bovine mammary tissue and suggest that stem cell activity is upregulated during mammary gland re-development.

Key words: stem cell markers, mammary gland, dairy cows

W150 Responses to steroidal doses and growth hormone treatment of nulliparous dairy ewes induced to lactate. M. Ben Khedim, G. Caja, A. K. K. Salama, A. Schalageter, E. Albanell, and M. Rovai*, *G2R, Universitat Autònoma de Barcelona, Bellaterra, Barcelona, Spain.*

With the aim of improving the response to lactation induction protocols in dairy ewes, 2 treatments based on s.c. injections of estradiol and progesterone (d 1 to 7) at reduced doses (half dose: HD, 0.25 and 0.63 mg/kg BW, respectively; one third dose: TD, 0.17 and 0.42 mg/kg BW, respectively) and hydrocortisone (d 18 to 20; 50 mg/d), compared with a previously-tested protocol (Ramírez et al., 2008, J. Dairy Sci. 91), were applied in 47 ewes of 9 mo of age (Manchega, n = 24; Lacaune, n = 23). Ewes were penned in 8 groups and fed ad libitum a TMR. Machine milking (twice daily) started on d 21 and lactation success (Manchega, > 0.2 L/d; Lacaune > 0.4 L/d) was evaluated on d 35. Ewes under these thresholds were dried-off. Lactating ewes were treated with growth hormone (bST, 250 mg) on d 48 and 62 of lactation. Group intake was recorded daily during the experiment (4 wk before and 10 wk after milking started) with individual estimations during lactation by using polyethylene glycol 6000 (50 g/d for 14 d). Treatments decreased DM intake according to the steroidal dose used (HD, –28%; TD, –18%; $P < 0.05$) but recovered thereafter. Lactation success was in the range of the standard protocol (55% on average) and did not vary by steroidal dose or breed. Onset of lactation increased DM intake 16% in both breeds ($P < 0.01$). Lacaune ewes produced nearly 2 times more milk than Manchega on d 14 of lactation and this varied with treatment (HD, 817 mL/d; TD, 458 mL/d; $P < 0.01$), whereas milk yield in Manchega did not vary with treatment (351 mL/d). No differences in milk composition were detected according to breed or treatment during the first 14 d of lactation. Milk yield increased with exogenous bST (Manchega, 114%; Lacaune, 90%; $P < 0.01$), but only a decrease in milk protein content ($P < 0.01$) and a numerically greater DM intake ($P = 0.16$) were detected when bST and control lactating ewe-lambs were compared. In conclusion, lactation induction success did not vary with treatment, but a breed × treatment effect was observed in ewes induced to milk, and this was related to the hormonal environment and milk potential of each breed.

Key words: lactation induction, bST, sheep

W151 Traceability of animal byproducts in quail (*Coturnix coturnix japonica*) tissues using carbon-13 and nitrogen-15 stable isotopes. C. Mori*[2], E. A. Garcia[1], C. Ducatti[1], J. C. Denadai[1], and K. Pelicia[1], *[1]São Paulo State University, Botucatu, São Paulo, Brazil, [2]São Paulo State University, Registro, São Paulo, Brazil.*

Consistent information on meat products consumed by the public is essential. The technique of stable isotopes is a powerful tool to recover consumer confidence, as it allows the detection of animal byproduct residues, particularly in quail meat. This study aimed at checking the presence of poultry byproduct mixtures in quail diets by applying the technique of carbon ($^{13}C/^{12}C$) an nitrogen ($^{15}N/^{14}N$) stable isotopes in quail breast muscle, keel, and tibia. Sixty 4 one-day-old male quails were obtained from commercial farm. Birds were randomly distributed into 8 experimental treatments, and fed diets containing poultry offal meal (POM), bovine meat and bone meal (MBM) or poultry feather meal (PFM), or their mixtures. Four birds per treatment were slaughtered at 42 d of age, and breast (Pectoralis major), keel, and tibia were collected for analyses. Isotopic analyses of feed ingredients, feeds, and tissues were carried out at the Center of Stable Environmental Isotopes of the Biosciences Institute (CIE/IB), UNESP, Botucatu campus. Isotopic carbon (13C/12C) and nitrogen (15N/14N) ratios were determined in a isotopic ratio mass spectrometer (IRMS) type DELTA S (Finnigan Mat) coupled to an Elementary Analyzer (EA 1108 CHN) The obtained isotopic results were submitted to multivariate analysis of variance (MANOVA) using GLM (General Linear Model) procedures of SAS statistical software. Data were generated by error matrices for each tissue, which were later graphically distributed in regions (ellipses) with 95% confidence of observing possible differences between experimental treatment means and control treatment means. The inclusion of animal byproducts in quail diets was detected by $^{13}C/^{15}N$ analyses in the tissues of the birds; however, it was not possible to specify which byproducts were used. It was concluded that quail meat can be certified by the technique of stable isotopes.

Key words: animal byproducts, meat quails, stable isotopes

W152 Meat quality of Pelibuey sheep finished with different levels of alfalfa. V. Resendiz-Cruz[1], O. Hernadez-Mendo[1], J. Gallegos-Sanchez[1], I. Guerrero-Legarreta[2], P. A. Martinez-Hernandez[3], and G. Aranda-Osorio*[3], *[1]Colegio de Postgraduados, Montecillos, Estado de Mexico, Mexico, [2]Universidad Autonoma Metropolitana-Iztapalapa, Mexico D.F., Mexico, [3]Universidad Autonoma Chapingo, Chapingo, Estado de Mexico, Mexico.*

The objective of this study was to evaluate the effect of feeding different levels of alfalfa to sheep on meat quality and fatty acid profile. For this purpose, 36 Pelibuey male sheep with initial live weight mean of 22.3 ± 0.3 kg were finished for 11 weeks. They were distributed homogeneously into 4 groups of 3 each, with 3 replicates per group, and then randomly assigned to each of the following treatments: 0, 20, 30 and 40% alfalfa (dry basis). Meat chemical composition, color, shear force in raw and cooked meat, water activity (Aw), water holding capacity (WHC) and fatty acid profile (FAP), were evaluated. A completely random design under Proc GLM of SAS was used, and a mean comparison with Tukey test was done. Results about ether extract are stated later and includes discussions of fatty acid content. The red index (a) of meat was more intense ($P \leq 0.05$) for the control animals diet than for the alfalfa treatments. The resistance to the cut of raw and cooked meat, and the WHC, did not show differences ($P \geq 0.05$) between treatments, averaging 1.4 and 2.5 kg/cm^2, and 18.5 mL/100 g of meat, respectively. The Aw was higher when animals were fed with no alfalfa in the diet ($P \leq 0.05$). Within the fatty acid profile, only myristic, palmitic, palmitoleic, stearic and oleic acids, were higher ($P \leq 0.05$), 49.6, 553.8, 47.9, 326.6, and 1075.4 mg/100g, respectively, when sheep received no alfalfa, followed by those with 20, 30 and 40% alfalfa. CLAc9 was higher (18.8 mg/100g) ($P \leq 0.05$) when included 20% alfalfa in the diet, followed by those with 40, 30 and 0% alfalfa, with values of 15.0, 14.7, and 12.0 mg/100g, respectively. Meat from animals fed with alfalfa in the diet, had lower ($P \leq 0.05$) amounts of fatty acids, with higher proportion of unsaturated fatty acids, compared with those with the control diet. These results suggest that including alfalfa in the diet of finishing sheep, improves fatty acid profile and, it is proposed as a viable alternative to meet current demand of healthier food.

Key words: lambs, alfalfa, meat characteristics

W153 Meat quality of lambs fed fresh or dehydrated spineless cactus (*Opuntia ficus-indica*). M. I. Aguilar-Yañez[1], O. Hernadez-Mendo[1], G. Aranda-Osorio*[2], J. E. Ramirez-Bribiesca[1], I. Guerrero-Legarreta[3], and M. M. Crosby-Galvan[1], *[1]Colegio de Postgraduados, Montecillos, Estado de Mexico, Mexico, [2]Universidad Autonoma Chapingo, Chapingo, Estado de Mexico, Mexico, [3]Universidad Autonoma Metropolitana-Iztapalapa, Mexico D.F., Mexico.*

The objective of this study was to evaluate meat quality and fatty acid profile of lambs supplemented with fresh or dehydrated spineless cactus (*Opuntia ficus-indica*). Twenty-seven crossbred male lambs with initial live weight mean of 21.4 ± 2.18 kg were finished for 11 weeks of different treatment diets. They were distributed homogeneously into 3 groups of 9 each, and then randomly assigned to each of the following treatments: (T1) control diet, (T2) diet with 17% (dry basis) of dehydrated cactus, and (T3) diet with 17% (dry basis) of fresh cactus. Color, texture of raw and cooked meat, water activity (Aw), water holding capacity (WHC) and fatty acid profile were evaluated. A completely random design under Proc GLM of SAS was used, and when statistical differences were observed, a mean comparison was done using the Tukey test. Meat chemical analysis, color and texture, were not different ($P \geq 0.05$) between treatments, neither were the percentage of total fatty acids, saturated, monounsaturated or polyunsaturated. The only difference was found on WHC ($P \leq 0.001$), which was greater when feeding fresh and dehydrated cactus, than that with no cactus, with values of 32.13, 30.50, and 25.58 mL/100g of meat, respectively. These results suggest that the inclusion of cactus into the finishing lamb diets, had similar benefits on meat quality than that of the commercial one, which makes cactus a viable feeding strategy.

Key words: cactus, sheep, meat characteristics

W154 Qualitative characteristics of meat from lambs fed with sunflower seeds and vitamin E. F. A. Almeida*, A. G. Silva Sobrinho, G. M. Manzi, N. L. L. Lima, N. M. B. L. Zeola, V. Endo, and J. C. Barbosa, *Universidade Estadual Paulista - Unesp/ Campus de Jaboticabal, Jaboticabal, São Paulo, Brasil.*

Health professionals recommend diets low in saturated fatty acids. It is possible to obtain learner carcasses or to increase levels polyunsaturated acids in meat from cattle and sheep by feed them with sun-

flower seeds. Supplementation of diets with vitamin E increases the Î ± -tocopherol concentration of muscle and improves color stability of beef and lamb meat. The objective of this study was to evaluate the qualitative characteristics pH, color, water holding capacity, cooking loss and tenderness of the Longissimus dorsi muscle from Ile de France lambs fed with diets that contain sunflower seeds and vitamin E. Thirty 2 lambs were used with an average body weight of 15 kg, which were housed in individual stalls. The work consisted of 4 treatments as it follows: D1 - sugarcane + concentrate without sunflower seeds; D2 - sugarcane + concentrate with sunflower seeds; D3 - sugarcane + concentrate without sunflower seeds and 1000 mg vitamin E/kg of dry matter (DM) from the diet; D4 - sugarcane + concentrate with sunflower seeds and 1000 mg vitamin E/kg of DM from the diet. The experimental design was completely randomized, with a factorial scheme 2x2 (2 diets (with or without the inclusion of sunflower seeds) x 2 levels of vitamin E (0 and 1000mg/kg DM diet)). The qualitative characteristics were not influenced by the sunflower seeds and vitamin E with the exception of the variable b * (yellowness) was higher in meat of the lambs fed with diets that contain sunflower seeds and vitamin E (3.74), sunflower seeds without vitamin E (2.47) and vitamin E without sunflower seeds (2.20), than in meat of the lambs fed with diets without sunflower seeds and vitamin E (−0.12). The meat pH ranged from 5.47 to 5,57, L* (lightness) from 39.42 to 40.85, a* (redness) from 12.70 to 13.79, water holding capacity from 60.96 to 64.87, cooking loss from 36,16 to 38.01 and tenderness from 2.35 to 2.64. Finally, it could be concluded that the values found for the qualitative characteristics studied are consistent with the guidelines for lamb meat. Sunflower seeds and vitamin E may be used to feed lambs without harming the quality of meat.

Key words: qualitative characteristics, lamb meat, nutrition

W155 Effects of nutritional plane and selenium supply during gestation in primiparous ewes on offspring skeletal muscle development. C. A. Schwartz*, W. L. Keller, T. L. Neville, L. P. Reynolds, D. A. Redmer, A. M. Meyer, C. J. Hammer, K. A. Vonnahme, J. S. Caton, and K. R. Maddock-Carlin, *Department of Animal Sciences, North Dakota State University, Fargo.*

To investigate the effects of nutritional plane and selenium (Se) supply during gestation, serviced ewes were stratified by BW and randomized to receive diets formulated to contain either adequate Se (ASe; 3.5 μg Se•kg BW^{-1}•d^{-1}) or high Se (HSe; 65 μg Se•kg BW^{-1}•d^{-1}). On d 40 of gestation 42 ewes from each Se treatments were assigned randomly to 1 of 3 nutritional planes supplying 60% (RES), 100% (CON), or 140% (HI) of NRC requirements. At birth, lambs were given artificial colostrum for the first 20 h and then ad libitum access to feed and milk replacer. On d 21, lambs were stunned and exsanguinated. LM, semimembranosus (SM), and psoas major (PM) muscles were harvested and snap frozen for later analyses of μ-calpain autolysis by Western blotting, cellularity, myosin heavy chain types 1 and 2 by SDS-PAGE, and μ-calpain and calpastatin mRNA expression by RT-PCR. Autolysis of μ-calpain in the PM was greater ($P = 0.01$) in lambs from HSe supplemented ewes as compared with ASe ewes. The LM DM percentage in lambs from HI ewes was greater ($P = 0.02$) than that in lambs from RES ewes. Protein in the SM from HI lambs was greater ($P = 0.03$) than that from RES lambs. The RNA and RNA:DNA in the LM were greater ($P < 0.02$, $P < 0.04$, respectively) in the ASe RES lambs than in the ASe HI lambs. HSe RES lambs had lower LM protein than that from ASe HI. The RNA:DNA in the LM HSe HI was greater ($P < 0.03$) than that in the HSe RES. Overall, the protein:DNA was greater in the PM than in LM and SM while the RNA:DNA was greater in SM than in PM and LM. μ-Calpain autolysis was less ($P < 0.01$) in the PM of HSe RES lambs than in the PM of HSe HI lambs while autolysis in the LM of the ASe CON tended ($P < 0.07$) to be greater than all other treatment groups. Of all muscles, the LM had less ($P < 0.04$) μ-calpain autolysis than both the SM and PM muscles. Maternal Se supply and nutritional plane appeared to have an influence on offspring skeletal muscle protein expression and cellularity. We can conclude that the interaction of maternal Se and nutritional supplementation may affect fetal skeletal muscle growth and development.

Key words: skeletal muscle, selenium, calpain

W156 Maternal dietary protein affects transcriptional regulation of myostatin gene distinctively at weaning and finishing stages in skeletal muscle of Meishan pigs. X. Liu, J. Wang, R. Li, X. Yang, Q. Sun, and R. Zhao*, *Nanjing Agricultural University, Nanjing, P. R. China.*

Skeletal muscle is susceptible to nutritional programming and myostatin is identified as a potential mediator of offspring phenotype. In this study, we determined the effects of maternal dietary protein on transcriptional regulation of myostatin in skeletal muscle of pig offspring. Sixteen Meishan sows were fed either low-protein (LP) or standard-protein (SP) diets throughout gestation and lactation, and myostatin expression in the longissimus dorsi muscle were determined both at weaning and finishing stages. Myostatin mRNA abundance was downregulated at weaning, but upregulated at finishing in LP pigs, indicating stage-specific transcriptional regulation of myostatin. At weaning, CCAAT enhancer binding protein (C/EBPβ) expression in nuclear lysate was decreased in LP piglets, associated with diminished binding of C/EBPβ to all the 3 putative binding sites at myostatin promoter. None of the histone modification marks showed differences between SP and LP piglets. Among 12 microRNAs predicted to target myostatin, none was differently expressed between 2 groups. At finishing stage, C/EBPβ expression remained unchanged, but the binding of C/EBPβ to 1 of the 3 putative binding sites increased in LP pigs. H3Ac and H3K27Me3 modifications on myostatin promoter were increased, while H3K9Me1 decreased in LP pigs. Moreover, ssc-miR-136 and ssc-miR-500 expression reduced significantly. These results indicate that maternal dietary protein affects myostatin expression through distinct transcriptional regulation mechanisms at different stages. The immediate effect at weaning is mediated by C/EBPβ binding without epigenetic modifications, whereas the long-term effect at finishing stage involves both C/EBPβ binding and epigenetic regulations including histone modification and microRNA expression.

Key words: Meishan pig, maternal dietary protein, skeletal muscle

W157 Linear mixed models built with the stepAIC function in the R environment for evaluation of TPA and WBSF. A. Dufek*[1,2], J. Subrt[3], and J. Simeonovova[3], *[1]Research Institute for Cattle Breeding, Ltd., Vikyrovice, Czech Republic, [2]Agriresearch Rapotin Ltd., Vikyrovice, Czech Republic, [3]Mendel University in Brno, Brno, Czech Republic.*

The first aim of this work was to test the significance of selected fixed and random effects on Warner-Bratzler Shear Force (WBSF [N]) and Texture Profile Analysis (TPA [$N.cm^{-2}$]). The second aim was to determine the efficiency of the R software for quick fitting linear mixed models using a new combination of 2 functions: the lme function in the package nlme to test significance of random effects and the stepAIC function in the MASS package to test the significance of fixed effects.

Random effects were put into the models at nested levels – animals within a sire. Further, the stepAIC selected automatically from the fixed effects: aging time, sex and age of animal, carcass mass, length of quarters, weight and proportion of longissimus muscle (LM), and others. Log-transformed and centered data were used in the case of aging time in relation to the WBSF decline. The LM (n = 70) was divided into 4 samples, vacuum packed, stored at 2–4°C and analyzed 48 h, 16, 30 and 44 d post-mortem. In both cases (WBSF and TPA) the random effects analyses showed that only the subject affected dependent variables. In the case of model for WBSF, the stepAIC selected 5 significant fixed effects (AIC declined from 2786.8, model with no fixed effect, to 2347.8 for the final model): the estimates of parameters of the final model revealed that higher values for aging time, weight of fat and weight of LM resulted in lower values of WBSF (reg. coef. −24.2,-2.7,-3.7, resp.). Higher values for age of animals resulted in higher WBSF (reg. coef. 0.1). Steers had lower WBSF (74 N) than heifers (81 N) or bulls (84 N). In the case of model for TPA the stepAIC selected 5 significant fixed effects (AIC declined from 3313.7 to 3303.8): the parameters of the final model revealed that higher values for proportion of separable fat and length of quarters resulted in lower values of TPA (reg. coef. −9.9,-2.1, resp.). Higher values for aging time, weight of bones and age of animals resulted in higher values of TPA (reg. coef. 1.2,4.0,0.2, resp.). Data indicate that the lme and stepAIC functions are useful for fitting of mixed models when hypotheses on more fixed effects are tested.

Key words: AIC, mixed, meat

W158 Effect of kidney matrix on the detection of β-lactam and tetracycline residues by UPLC-MS/MS. M. P. Almeida[1,2], M. O. Leite*[2], S. V. Cançado[2], M. R. Souza[2], and M. M. O. P. Cerqueira[2], *[1]Lanagro-MG/Ministério da Agricultura, Pecuária e Abastecimento, [2]Escola de Veterinária - Universidade Federal de Minas Gerais.*

Antimicrobials are widely used in veterinary medicine, mostly in livestock as therapeutic, prophylactic, and growth promoters. The indiscriminate use of them may lead to the presence of their residues in foods. Most methods recommended for β-lactam and tetracycline detection use ultra performance liquid chromatograph (UPLC) connected to a mass spectrometer, commonly referred to as UPLC/MS/MS system. Biological matrices are very complex and interfere on the analytes compromising their quantification. The aim of this work was to study the influence of the kidney matrix on the detection and quantification of β-lactam and tetracycline residues by UPLC-MS/MS. The following drugs were studied: β–lactam - ampicillin, cefazolin, penicillin G, nafcilin, cloxacillin, dicloxacillin, oxacillin, penicillin V, and penicillin G deuterated (N-etilpiperidin) as internal standard, and tetracyclines – chlortetracycline, oxytetracycline, and tetracycline. Pure standard calibration curves and matrix curves were prepared at the concentrations of 0.50, 0.75, 1.00, 1.25, and 1.50xLMR7 in 3 different days. The matrix curve was prepared from the extraction of swine kidney blank samples (2g) with water/acetonitrile (8:2), followed by purification in hexane, and Bond Elut C18 dispersive phase. The curves were simultaneously injected and compared by F test and Student′s t- test, point to point, at 95% significance level. The slopes and intercepts were also compared by *t*-test using the same aforementioned significance level. Significant effect of matrix on the studied analytes was observed even with the use of β-lactam internal standard. Tests of slope and intercept at 95% significance level indicated a significant effect of the matrix in search of the tetracyclines. Penicillin G was the only substance that had no effect on all tests. As significant influence of the kidney matrix on the detection and quantification of β-lactam and tetracycline residues by UPLC-MS/MS was observed, kidney samples should be carried out using the matrix curve.

Key words: antimicrobial residues, matrix effect, mass spectrometry

W159 Extent of μ-calpain autolysis differs depending on the extent of destructered tissue in the ham. M. Müller[2], C. Biolley[1], P. Silacci[1], and G. Bee*[1], *[1]Agroscope Liebefeld Posieux Research Station (ALP), Posieux, Switzerland, [2]Swiss College of Agriculture, SHL, Zollikofen, Switzerland.*

Destructured zones in cooked hams cause great economic losses to the Swiss meat industry. In previous studies it has been reported that these zones can be observed already at 24 h postmortem (pm) in the outer portion of the semimembranosus muscle (SM). These observations suggested that pm processes might be causally linked to these problems. Thus the objective of the study was to determine the relationship between the extent of tissue destruction, muscle pH decline, μ-calpain autolysis and desmin degradation in the SM. To achieve these objectives, 12 pigs were selected the day after slaughter and their SM were classified into 1 of 3 classes: 1 = none; 2 = mild and 3 = strong tissue destruction in the outer portion of the SM. Using a cylindrical cutting device, muscle samples from the outer (O), middle (M) and deeper (D) portion of each muscle were obtained. The samples were prepared for immunoblotting with antibodies against μ-calpain 80-kDa subunit and desmin. The class 1 SM originated from lighter (7.7 vs. 8.2 and 8.2 kg; $P < 0.10$) hams than those from class 2 and 3. Compared with class 3, the SM in class 1 tended (5.7 vs. 5.4; $P < 0.10$) to have higher 3 h pm pH with intermediate values for those in class 2 (5.5). No ($P > 0.10$) pH differences among classes were observed at 45 min and 24 h pm. In the M- and I-portion but not the O-portion, marked class effects were observed for the relative abundance of the unautolyzed (80 kDa) μ-calpain subunit and its autolysis products (78 and 76 kDa) at 24 h pm. Compared with the classes 2 and 3, the 80-kDa band was less ($P < 0.10$) abundant and the 76-kDa band was more ($P < 0.10$) abundant in the M- and I-portion of class 1 samples. In the I-portion the abundance of intact desmin was lower ($P = 0.05$) in class 1 than class 2 with intermediate values for class 3. In accordance, the abundance of a degradation product was numerically higher ($P = 0.14$) in class 1 samples. These data indicate that extent of visible tissue destruction may affect autolysis of μ-calpain also in the deeper portion of the muscle.

Key words: μ-calpain autolysis, proteolysis, ham

W160 Early adaptation of sarcoplasmic reticulum Ca^{2+} pump in bovine myofiber under chronic low-frequency electrical stimulation. T. Sakurada*[1], E. Kitagawa[1], M. Miyake[1,2], S. Ohwada[1], H. Aso[1], and K. Watanabe[1], *[1]Tohoku University, Sendai, Japan, [2]The University of Tokushima, Tokushima, Japan.*

SERCA (Sarcoplasmic reticulum Ca^{2+} pump, Ca^{2+}-ATPase) is one of crucial regulators of muscular contraction, which is involved in transferring of cytosolic Ca^{2+} into sarcoplasmic reticulum (SR). SERCA is classified into 2 isoformes: fast-type SERCA1a in fast myofiber and slow-type SERCA2a in slow myofiber. Chronic low-frequency electrical stimulation (CLFS) changes myofiber type from fast to slow. The fast-to-slow transformation of myofiber by CLFS exhibits drastic turnover of myofilaments and finally remodeling of whole myofiber, however, in bovine, no information of CLFS effect on muscle has been reported. In this study, we investigated mechanism of adaptation for CLFS in the bovine longissiumus lumborum (LL) muscle, especially

focused on expression of SERCA. Six Holstein male calves were used: 3 calves were CLFS group (5 Hz, 24 h/day) and 3 calves were control group. After 30 d of CLFS, calves were slaughtered and the LL muscles were removed. Muscle samples were quickly frozen by a mixture of dry ice and acetone. Serial frozen sections (10 μm thick) were cut on a cryostat. Then the serial sections were stained immunohistochemically with anti-myosin heavy chain (MyHC: fast and slow) and anti-SERCA (1a and 2a) antibodies. Myofiber types were classified into fast, slow, and hybrid (fast and slow co-expressed) myofibers by MyHC staining pattern. Expressions of MyHC and SERCA in myofiber types were measured by a microscopic densitometry using image analyzing software (Scion Image). Thirty days of CLFS increased percentages of slow and hybrid myofibers in the bovine LL muscle ($P = 0.051$). This change of myofiber types indicated functional adaptation for endurance muscle contraction by CLFS. Expression of SERCA2a in CLFS myofibers were higher in order of slow, hybrid and fast myofibers ($P < 0.01$). In CLFS hybrid myofibers, expression of slow MyHC increased in advance, and expression of SERCA2a rose subsequently. This fast-to-slow transition pattern suggests that the CLFS induced transformation of SERCA may need preceding upregulation of slow MyHC in the early phase of bovine myofiber type adaptation.

Key words: myofiber types, SERCA, CLFS

W161 Effects of temperament classification on carcass characteristics, tenderness and value in Angus-based composite steers. J. W. Behrens*[1], R. K. Miller[1], D. S. Hale[1], J. T. Walter[1], J. C. Bailey[1], A. N. Hafla[1], T. Machado[2], L. O. Tedeschi[1], and G. E. Carstens[1], *[1]Texas A&M University, College Station, [2]Texas A&M University at Kingsville, Kingsville.*

Angus-based composite steers (n = 508; initial BW = 310 ± 56 kg) obtained over 3 years from Rex Ranch were used in this study. Steers were fed a high-grain diet (ME = 3.08 Mcal/kg DM) and feed intakes measured using a GrowSafe system for 70 d. Thereafter, steers were fed in group pens and harvested at an average backfat thickness of 1.2 cm in 2 groups. Exit velocity (EV), measured as the rate of distance traveled (m/s) while exiting from a squeeze chute, was used as an objective measure of temperament. Within year, steers were classified into calm, moderate and excitable temperament groups based on ± 0.50 SD from the mean EV. Steers were commercially harvested and USDA Yield and Quality grade characteristics determined. Carcass weights tended ($P = 0.13$) to be lighter in excitable than calm steers (312.7 vs 306.7 ± 3.37 kg). Warner-Bratzler (WBSF) and Slice shear force (SSF) values were measured on top loin steaks after 1, 7, and 14 d of vacuum-packaged storage at 2°C. Carcasses from calm and moderate steers had lower ($P = 0.005$) d 7 SSF values (9.29 and 9.09 vs 9.99 ± 2.58 kg) and tended to have lower ($P = 0.06$) d 7 WBSF values (2.08 and 2.02 vs 2.14 ± 0.053 kg) than excitable steers, respectively. One and 14 d WBSF and SSF values and carcass Yield and Quality grades were not affected ($P > 0.10$) by temperament classification. Carcass value ($/kg) was determined using a grid formula based on premiums for Quality grade (Prime = +0.11), and discounts for carcass weight (<250 kg = −0.37; > 454 kg = −0.44), Quality grade (Select = −0.18; Standard = −0.44), Yield grade (>5 = −0.40; > 4 and <5 = −0.24) and tenderness assessment (WBSF >3.9 kg = −0.44). Carcass value tended ($P = 0.09$) to be lower for steers with excitable temperaments compared with steers with calm temperaments (1038.11 vs 1013.93 ± 11.89 $/carcass, respectively). Temperament classification did not affect carcass characteristics, but tended to affect carcass value of Angus-based steers. Steers with excitable temperaments had higher 7 d SSF values, suggesting that temperament classification of steers may influence carcass tenderness.

Key words: temperament, tenderness

W162 Rump measurements as related to others carcass traits. M. N. Bonin*[1], S. L. Silva[1], J. B. S. Ferraz[1], D. P. D. Lanna[2], F. Manicardi[1], R. C. Gomes[1], M. H. A. Santana[1], V. N. Barbosa[1], F. Novais[1], J. H. A. Campo[1], and F. Syuffi[1], *[1]University of Sao Paulo, College of Animal Science and Food Engineering, Pirassununga, Sao Paulo, Brazil, [2]University of Sao Paulo, College of Agricultural Sciences, Piracicaba, Sao Paulo, Brazil.*

Ultrasound carcass traits, such as ribeye area (UREA), backfat thickness (UBFT) and rump fat thickness (RFT) are used to estimate carcass composition in beef cattle. Additionally, others traits obtained on the rump may also be correlated to traditional carcass traits and contribute to predict retail product yield in beef cattle. Therefore, the aim of this study was to evaluate the correlations between rump measurements and carcass traits evaluated by ultrasound. A total of 410 Nellore bulls, with 18 mo of age, grass fed and reared in the Paraná State, Brazil, were evaluated by ultrasound scanning. A first image was collected of Longissimus dorsi muscle at 12th and 13th ribs for measures of UREA and BFT. A second image was obtained from Gluteus medius muscle to measure RFT and Gluteus medius depth (GDT). Images were collected utilizing an Aloka 500V equipment with a 3.5–Mhz, 17.2–cm linear array transducer. Other traits obtained were the rump width (RWD) and length (RLG), defined as the distance between the tuber coxae extremities and between the hip and the pin bone, respectively. The traits were correlated by simple Pearson correlations analyses using the statistical procedure PROC CORR of SAS. Positive correlations were found between UREA and GDT (r = 0.50; $P < 0.0001$), RWD (r = 0.39; $P < 0.0001$), RLG (r = 0.38; $P = 0.0001$), UBFT (r = 0.09; $P = 0.08$) and RFT (r = 0.16; $P = 0.002$). The high correlation between UREA and GDT indicates that these measures could be adequate indicatives of rump primal cuts yield. High correlations were found between UBFT and RFT (r = 0.53; $P < 0.0001$) and a low correlation between BFT and GDT (r = 0.08; $P = 0.12$) and between RFT and GDT (r = 0.10; $P = 0.04$), indicating that GDT measurements could not explain large variations in the rump fat depth. The GDT presented medium correlation with RWD (r = 0.28; $P < 0.0001$) and RLG (r = 0.26; $P < 0.0001$). Results suggest that measurements obtained on the rump can be used as auxiliary in vivo measures to predict carcass composition and rump primal cuts yield in beef cattle.

Key words: *Bos indicus*, gluteus medius, ultrasound

W163 Effect of finishing heifers on tall fescue, tall fescue with grain, or alfalfa on: I. carcass and LM quality. S. K. Duckett*[1], M. C. Miller[1], T. A. Burns[1], and M. L. Wahlberg[2], *[1]Clemson University, Clemson, SC, [2]Virginia Tech University, Blacksburg.*

Angus heifers (n = 40) were used to evaluate the effect of finishing on endophyte-free tall fescue (TF), TF with grain (TF+G), or alfalfa (AL) on carcass and LM quality. Heifers were finished on TF or AL to 2 time endpoints, which corresponded to 161 or 189 d of grazing. The TF+G heifers also grazed TF for 161 or 189 d and after adaptation were offered corn grain ad libitum for a total of 56 or 84 d before slaughter. Carcasses were graded at 24 h postmortem and one rib obtained. Two steaks were removed from the posterior end of the rib for Warner-Bratzler shear force (WBS) and proximate composition. Hot carcass weight was greater ($P < 0.05$) for AL than TF and TF+G.

Fat thickness, KPH, marbling score and quality grade were higher ($P < 0.05$) for AL than TF and TF+G. There was a 10% incidence of dark cutters; however, no effect of dietary treatment or slaughter time was observed. Longissimus muscle pH and objective color scores (L*, a*, b*) did not differ ($P > 0.05$) by dietary treatments or slaughter time. Supplementation of corn grain during the grazing period did not alter ($P > 0.05$) WBS in ribeye steaks aged 14 d. Warner-Bratzler shear force averaged 2.89 kg across all treatments. Total lipid content of the ribeye steaks was higher ($P < 0.05$) for AL than TF or TF+G. Total saturated fatty acid concentration was higher ($P < 0.05$) for AL and TF compared with TF+G. Monounsaturated fatty acid concentration was higher ($P < 0.05$) for TF+G than TF. Omega-6 polyunsaturated fatty acid (PUFA) concentration was highest ($P < 0.05$) for TF+G-84d and lowest ($P < 0.05$) for TF-189d. The ratio of omega-6 to omega-3 PUFA was higher ($P < 0.05$) for TF+G-84d than for TF+G-56d, which were both higher ($P < 0.05$) than AL or TF. Concentration of conjugated linoleic acid (CLA), cis-9 trans-11 isomer, was highest ($P < 0.05$) for TF+G-56d and TF-189d. Extending time of grain supplementation on TF lowered ($P < 0.05$) CLA levels compared with TF+G-56d and TF-189d. Finishing heifers on alfalfa increased carcass weight, fat thickness and marbling score. Corn grain feeding on TF increased linoleic acid and the ratio of omega-6 to omega-3 PUFA.

Key words: beef, forages, fatty acids

W164 Effect of finishing heifers on tall fescue, tall fescue with grain, or alfalfa on: II. fatty acid composition and lipid oxidation in ground beef. S. K. Duckett*[1], M. C. Miller[1], T. A. Burns[1], and M. L. Wahlberg[2], *[1]Clemson University, Clemson, SC, [2]Virginia Tech University, Blacksburg.*

Angus heifers (n = 40) were used to evaluate the effect of finishing on endophyte-free tall fescue (TF), endophyte-free tall fescue with grain (TF+G), or alfalfa (AL) on fatty acids and lipid oxidation in ground beef. Heifers were finished on TF or AL to 2 time endpoints, which corresponded to 161 or 189 d of grazing. The TF+G heifers also grazed TF for 161 or 189 d and after adaptation were offered corn grain ad libitum for a total of 56 or 84 d before slaughter. Carcasses were graded at 24 h postmortem and one rib obtained from each. The rib (6–11th rib) was trimmed to a similar fat thickness and ground. Ground beef patties were held at 2°C under lights for 0, 2, 5, 7, 9, and 11 d for lipid oxidation (TBARS) and objective color (L*, a*, b*) measurements. Ground beef samples were also packaged in vacuum packages or chubs for frozen storage and measurement of lipid oxidation over time (0, 30, 60, 90, 180, and 360 d). Hydrophilic and lipophilic ORAC values did not differ ($P > 0.05$) by finishing treatment or slaughter time. Total lipid content was higher ($P < 0.05$) for AL than TF and TF+G. Total saturated fatty acid percentage was greater ($P < 0.05$) for TF and AL than TF+G. Total MUFA concentration was highest ($P < 0.05$) for TF+G and lowest ($P < 0.05$) for TF. Omega-3 polyunsaturated fatty acid concentration (PUFA) was highest ($P < 0.05$) for AL and lowest ($P < 0.05$) for TF+G. Trans-11 vaccenic acid (TVA) concentration was higher ($P < 0.05$) for TF and TF+G than AL in the first slaughter time but TVA decreased in TF+G with increased time of grain feeding. Length of grain feeding increased ($P < 0.05$) linoleic acid and omega-6 PUFA concentration in TF+G. Lipid oxidation on a total lipid basis (mg TBARS/kg lipid) in fresh ground beef was higher ($P < 0.05$) for TF+G than TF or AL at 9 and 11 d of retail display. In frozen ground beef samples, AL had higher ($P < 0.05$) TBARS values than TF and TF+G in chub packages but TBARS did not differ ($P > 0.05$) among treatments in vacuum packages. Finishing heifers on TF with grain increased omega-6 PUFA levels and lipid oxidation rates in fresh ground beef.

Key words: beef, forages, lipid oxidation

W165 Gene expression profile of M. longissimus in Japanese Black, Holstein, and Charolais steers fed a high-energy diet. E. Albrecht*[1], S. Ponsuksili[1], K. Wimmers[1], T. Gotoh[2], and S. Maak[1], *[1]Leibniz Institute for Farm Animal Biology, Dummerstorf, Germany, [2]Kyushu University, Kuju Agricultural Research Center, Kujucho, Oita, Japan.*

Cattle breeds differ largely in their capability for intramuscular fat (IMF) deposition. In an experiment comprising each 3 Japanese Black (JB), Holstein (HS), and Charolais (CH) steers, the animals received a high-energy diet typical for the production of highly marbled beef in Japan. The animals were slaughtered at 26 mo of age. The breeds differed significantly in marbling, measured via image analysis as fat area percentage (JB > HS > CH; $P = 0.001$) and in the average diameter of the adipocytes (JB > HS > CH; $P = 0.04$) in M. longissimus (LM). Total RNA was isolated from LM and RT-qPCR was conducted for selected candidate genes for marbling. There were neither significant differences in the expression of adipogenic transcription factors (CEBPB, CEBPA, PPARG) nor in downstream targets (PLIN1, ADIPOQ). A subsequent genome wide expression analysis confirmed these results (Affymetrix GeneChip Bovine Genome Array). However, pathway analyses revealed, among others, differential regulation of genes involved in calcium signaling. Beside muscle specific genes significantly upregulated in CH compared with JB and HS (RYR1, ATP2A1), we found significant differences in mRNA abundance for members of the S100 calcium binding protein family (S100A1, S100A16, S100B). Genes of this family have been linked only recently to adipogenesis and obesity in cell cultures and human, respectively. Separate analyses of their expression in dissected IMF from JB and HS revealed a more than 2.3-fold upregulation of S100B in JB ($P = 0.005$). In contrast, no differences were found in IMF between both breeds for S100A1 and S100A16, indicating that the observed differential expression in LM is linked to muscle cells rather than to adipocytes. Our results demonstrate that the mRNA abundance of S100 calcium binding protein B is related to IMF content in LM of intensively fed cattle. These results underline the necessity of separate expression analyses of LM (usually containing IMF) and dissected IMF to identify markers for differences in IMF deposition between breeds.

Key words: cattle, gene expression, intramuscular fat

W166 Effect of genotype on fatty acid composition of bovine muscles fattened with maize silage and flaxseed supplemented concentrate. G. Hollo*[1], T. Somogyi[1], K. Loki[1], I. Anton[2], and I. Hollo[1], *[1]Kaposvár University, [2]Research Institute for Animal Breeding and Nutrition.*

The aim of this study was to determine the intramuscular fat level (IM) and fatty acid composition in longissimus dorsi, (LD) semitendinosus (ST)and psoas major (PM) muscles of young bulls kept under the same condition and fed with flaxssed supplemented concentrate in the finishing period. Sixty-two growing bulls from Angus (A), Charolais (CH), Holstein (H), Hungarian Grey (HG), Hungarian Simmental (HS), Charolais x Hungarian Grey (CHxHG) were used. The diet consisted of maize silage ad lib., grass hay 2 kg/day, and 2-4 kg concentrate. After 450 kg live weight the concentrate contained 25% linseed supplementation. The average slaughter weight was 598.89+25.11 kg.

Muscle samples were taken after 24 hours chilling from the right half carcass. The effect of genotype and muscle was evaluated with multivariate analysis of variance GLM III (SPSS 10.0). The differences were evaluated with Tukey's test (P <0.05). A bulls had the highest IM level (3.76), particularly in PM (4.74), followed by HG (3.40), CHxHG (3.05), CH (2.33), HS (2.21), with the lowest level for H (2.11). IM for LD (2.87) and ST (1.77) were significantly lower than PM (3.60). SFA was significantly higher for the PM, due to the high level of IM. ST contained the highest PUFA (12.99), followed by LD (10.30) and PM (10.19). The n-6 fatty acids were affected either by breed, or by muscle type. The linoleic acid was the highest in H bulls except for PM, whilst the lowest was in all cases in A bulls. The same tendency can be seen for long chain n-6 fatty acids. The n-3 fatty acids differed among genotypes from 1.36 to 1.80%. Significant differences were shown only for PM. The n-3 long chain fatty acids were the highest level in ST of H, in LD of CH and in PM of HS bulls. The n-6/n-3 ratio was ranged from 4.48 to 6.22 and significantly higher in H than in A bulls. The highest CLA level was detected in all cases in HG bulls. The results demonstrate the clear effect of genotype on intramuscular fat content and fatty acid composition of beef despite the same housing and feeding conditions.

Key words: cattle, beef, fatty acid composition

W167 Quality characteristics of dried meat laver made from different beef muscle types. G. D. Kim*[1], E. Y. Jung[1], H. U. Seo[1], J. Y. Jeong[2], S. J. Hur[3,1], H. S. Yang[1], and S. T. Joo[1], *[1]Division of Applied Life Science (BK21 Program), Gyeongsang National University, Jinju, Republic of Korea, [2]Swine Scientic and Technology Center, Gyeongnam National University of Science and Technology, Jinju, Republic of Korea, [3]College of Biomedical and Health Science, Department of Applied Biochemistry, Konkuk University, Chungju, Republic of Korea.*

The aim of this study is to find adequate muscle type for making dried meat laver which can be used for making rice rolls. In general, a dried laver from seaweed is used for making steamed rice roll (Kimbab). However, a meat laver was made from beef meat instead of seaweed and investigated the quality characteristics of meat laver. Four types of meat lavers were made from different beef muscles: Semimembranosus m. (SM), Semitendinosus m. (ST), Gracilis m. (GR) and Extensor carpi radialis m. (EC). A homogenate made of 20 g of meat and 180 g of water was spread on the fabric (0.2x0.2 mm). The homogenate was dried for 7 h in the oven (DS-80–1, Dasol Sci. Co., Ltd., Korea) of 60°C. The quality traits of meat laver such as yield (%), proximate composition (%), surface color (CIE L*a*b*) and textural properties (folding test, cutting strength) were investigated. Fat content was significantly higher in meat lavers made from SM (26.62%) and EC (26.75%) muscle than in those of ST (24.28%) or GR (24.99%) muscle ($P < 0.05$). However, moisture, crude protein and crude ash content were not significantly different among the meat lavers ($P > 0.05$). Yield of meat laver range from 40.57% to 41.85%, but there were no significant differences between meat lavers ($P > 0.05$). The meat laver made from EC muscle had the highest CIE a* value (45.76) of surface color among meat lavers ($P < 0.05$), however, CIE L* or CIE b* value were not significantly different among meat lavers ($P > 0.05$). The meat laver made from SM muscle had the lowest value of folding test (2.30 cm) and cutting strength (1780.00 g/cm2), however, there were no significant differences in cutting strength and folding test of meat lavers between ST muscle (2605.00 g/cm^2 and 3.07 cm, respectively) and EC muscle (2835.00 g/cm^2, 3.33 cm, respectively) ($P > 0.05$). Therefore, the results of folding test (2.30 cm) and cutting strength (1780.00 g/cm2), which are the lowest values among the meat lavers, indicate that meat laver made from SM muscle is neither flexible nor useful for making rice rolls. In conclusion, EC muscle or ST muscle could be used for making a more flexible and red meat laver.

Key words: laver, beef, muscle type

W168 Carcass characteristics of bullocks of different genotype finished under feedlot conditions. O. V. Vazquez-Mendoza, G. Aranda-Osorio*, M. Huerta-Bravo, E. J. Maldonado-Siman, and J. C. Garcia-Ortiz, *Universidad Autonoma Chapingo, Chapingo, Estado de Mexico, Mexico.*

The objective of this study was to evaluate the effect of breed type on carcass characteristics of young bulls finished in feedlot. There were 90 tropical bullocks fattened in a temperate region of Mexico with the following distribution: Zebu (Z) n = 5 (initial liveweight 385.6 ± 24.7 kg); European Brown Swiss (EBS) n = 8 (365.1 ± 112.4 kg); Holstein (H) n = 9 (401.6 ± 63.4 kg); Z × European Brown Swiss (Z × EBS) n = 28 (423.4 ± 46.4 kg); Z × American Brown Swiss (Z × ABS) n = 19 (399.6 ± 49.9 kg); and Z × H (Z × H) n = 21 (428.7 ± 32.6 kg). The cattle were fed with a diet based on: ground corn (43%), bakery waste (24%), corn stalks (20%), soybean meal (8%), mineral premix (1.5%), bypass fat (Enervit®, Zuavit; 1%), buffer (18.2% Na and 8.4% Mg; 0.5%) and zilpaterol hydrochloride (Zilmax®, Intervet; 6.7 mg kg^{-1}) to fulfill the requirements for this type of livestock. Variables evaluated for feedlot performance were: average daily gain (ADG) and final liveweight (FLW). Variables evaluated for carcass attributes were: hot carcass weight (HCW), hot carcass yield (HCY), backfat depth (BFD), ribeye area (REA), physiological age (PA), fat percentage on kidney, pelvis and heart (KPH), marbling score (M), carcass conformation (CONF), and carcass fatness (CF). Data were analyzed using the GLM procedure of SAS, taking days of finishing, type of breed × days of finishing and initial and final liveweight as covariates. The Z × ABS presented the highest ($P = 0.001$) ADG. The greatest ($P = 0.017$) FLW was for Z × ABS ≥ EBS ≥ H. The genotype did not affect ($P = 0.161$, 0.143, 0.218) HCW, HCY or BFD, but the REA was larger ($P = 0.012$) for the EBS. The H and EBS bullocks exhibited the lowest ($P = 0.001$) PA; although the H cattle had greater ($P = 0.006$) KPH. The best ($P = 0.014$) CONF was obtained by the Z × ABS and Z × EBS genotypes. The greatest amount of M ($P = 0.001$) was found for the H breed. There were not differences ($P \geq 0.05$) on CF among genotypes. The crossbred genotypes showed better feedlot performance and carcass characteristics, and it seems that Holstein breed could have a potential from the marbling score point of view.

Key words: beef cattle, finishing, carcass attributes

W169 Relationship between meat quality and the expression of related genes in the muscle of two different genetic groups of cattle. J. Giusti[1], E. P. Castan[1], S. R. Baldin[2], M. D. B. Arrigoni[2], M. Dal Pai-Silva[2], and H. N. Oliveira*[1], *[1]State University of Sao Paulo, Jaboticabal, Sao Paulo, Brazil, [2]State University of Sao Paulo, Botucatu, Sao Paulo, Brazil.*

All body functions and traits of living beings are controlled by specific genes, and for meat quality is not different. In this paper we correlate μ-calpain, m-calpain, Thyroglobulin (TG), diacylglycerol acyltransferase 1 (DGTA1) and leptin (LEP) gene expression to meat quality of longissimus dorsi in 2 beef cattle genetic groups: Nellore and Canchim. We analyzed 15 young bulls of each breed. The animals were kept at the experimental feedlot facilities of the College of Veterinary

Medicine and Animal Science of UNESP, Botucatu. They were fed with the same diet and kept under the same management conditions. Animals were slaughtered at minimum weight of 470 kg and 4 mm of fat thickness accessed by ultra–sound. Samples of longissimus dorsi were collected for meat traits analysis (marbling), total lipids contents (TL), shear force (SF) and myofibrillar fragmentation index (MFI) at zero and 7 d postmortem and gene expression analysis, using qRT-PCR technique. Among the meat quality traits, MFI and TL contents were different between groups ($P < 0.01$ and $P < 0.03$, respectively). The calpains did not show differential gene expression or correlations with meat traits between groups. Among genes involved in metabolism of fat, DGTA1 did not show difference between groups ($P < 0.87$). However, a positive correlation was observed between DGTA1 and SF ($r = 0.51$, $P < 0.05$) and negative correlation between DGTA1 and MFI ($r = -0.52$, $P < 0.05$) at 7 d postmortem. In Nellore breed, in contrast, the correlation was negative to SF at the d 7 ($r = -0.75$, $P < 0.01$). The TG gene expression did not differ between groups ($P < 0.15$), however it has been negatively correlated in both breeds to the MFI on day zero ($r = -0.52$, $P < 0.05$). With the results, we conclude that the tender meat phenotype is not obtained only by the action of genes related to it, but by the handling of carcasses in the postmortem. Therefore, more studies should be conducted joining these parameters to understand the processes between gene expression and phenotype, enabling the development of breeds adapted to produce quality beef.

W170 Measurement of loin muscle in the carcass of Nellore breed on *Brachiaria brizantha* 'Marandu' with two levels of concentrate supplementation. S. L. S. Cabral Filho*[1], R. V. Oliveira[1], J. M. S. Diogo[1,2], R. A. Mandarino[1], C. F. Lobo[1], F. A. Oliveira[1], and G. S. Firmino[1], *[1]Universidade de Brasília, Brasilia, Distrito Federal, Brasil, [2]Fazenda Experimental Agua Limpa, Brasilia, Distrito Federal, Brasil.*

The objective of this study was to measured loin muscle area in the carcass of Nelore cattle grazing in *Brachiaria brizantha* 'Marandu', with 2 levels of concentrate supplementation. A total of 30 Nellore bulls at 22 mo of age with average weight of 330.42kg and final slaughter weight of 477.94 kg were used. The supplement consisted of corn, sunflower meal, soybean hulls, urea and minerals, and the treatments were SCONF1 - average daily intake of supplement of 0.91% of body weight in dry matter (DM) and SCONF2 - average intake of daily supplement of 1.42% of live weight, DM basis. The statistical design was randomized blocks with 2 treatments and 3 replications. Data were subjected to ANOVA the averages were compared by Duncan test at 5% of significance level. After the slaughter the carcass was proceeded to skinning, gutting, separation of the 2 symmetrical halves of the body (right and left), weighed and cooled for 24 h at 3°C. Longissimus dorsi area (AOL) and subcutaneous fat (SF) were measured between the 12th and 13th rib. There was no statistical difference ($P > 0.05$) among treatments for AOL, which showed average values of 74.50 and 70.33 cm2 for SCONF1 and SCONF2, respectively. However, levels of supplementation affected ($P < 0.05$) SF, and the treatment SCONF2 showed higher values (2.70 mm) compared with SCONF1 (2.00 mm). Supplementation did not impact AOL but increased subcutaneous fat with a higher supplementation level.

Key words: *Bos indicus*, supplement, meat quality

W171 Frame size and sex effects on meat quality characteristics of Nellore cattle. S. L. Silva*, R. C. Gomes, A. F. Rosa, M. D. Poleti, M. N. Bonin, T. M. C. Leme, J. L. F. Souza, L. M. Zoppa, and P. R. Leme, *Universidde de São Paulo (FZEA/USP), Pirassununga, SP, Brazil.*

Large frame cattle and intact males produce leaner carcasses which can affect meat tenderness due to cold shortening during the chilling process. Because the beef meat production in Brazil is based on Nellore (*Bos indicus*) intact males, it is necessary to investigate the effects of sex and frame size (FS) on carcass quality in this breed. The aim was to evaluate carcass and meat quality traits of Nellore young bulls and steers from different FS, finished under feedlot conditions. Throughout 2009 and 2010, Nellore bulls (n = 75, 500 ± 4.5 BW, 23-mo old) and steers (n = 80, 474 ± 6.1 BW, 23-mo old) from small (n = 51), medium (n = 53) and large (n = 50) frame size, according to BIF, were finished in feedlots receiving high-grain diets for 50d to 140d. Following slaughter, carcasses were weighed (HCW), chilled for 24h (0–2°C) and then ribbed between 12th/13th ribs for determination of Longissimus muscle (LM) area (LMA) and backfat thickness (BFT). LM samples were removed, vacuum packaged and aged 1d, 7d or 14d postmortem for Warner-Bratzler shear force (WBSF) and cooking loss (CL) determinations. Data analysis included the fixed effects of sex, FS, year and sex x FS interaction. There were no sex x FS interactions for any trait ($P > 0.05$). Intact males had heavier carcasses (154 vs. 142 kg; $P < 0.0001$), greater LMA (73.7 vs. 67.3 cm^2; $P < 0.0001$) and lower BFT (4.8 vs. 5.5 mm; $P = 0.0012$) than castrated males. Sex did not affect WBSF on 1d (9.7 kg) and 14d postmortem (6.7 kg) but WBSF was lower for castrated cattle than for intact males (7.7 vs 8.5 kg; $P < 0.0001$). Large FS cattle showed heavier HCW than small FS animals (151 vs. 145 kg, $P = 0.0028$). There was no effect of FS in LMA (70 cm^2), BFT (5.1 mm) and WBSF (9.3, 7.7 and 6.8 kg for 0, 7 and 14 d of aging, respectively). Meat CL were not affected by sex or frame size. Despite the high WBSF values observed in this work (greater than 4.5 kg), the results indicate that meat quality attributes are not greatly affected by sex or FS in Nellore cattle. It is likely that the fat thickness of carcasses from both intact and castrated males was enough to avoid problems of cold shortening during chilling process.

Key words: beef cattle, carcass, tenderness

W172 Carcass traits obtained at the fifth rib level to predict retail cuts in Nellore (*B. indicus*) cattle. J. L. F. Souza*, S. L. Silva, R. C. Gomes, M. N. Bonim, P. Z. Silva Neto, and P. R. Leme, *Universidade de São Paulo/ Faculdade de Zootecnia e Engenharia de Alimentos, Pirassununga, São Paulo, Brazil.*

Measurements conducted on Longissimus muscle (LM) at the 12th rib level are traditionally associated to lean meat yield. However, in the Brazilian industry, carcasses are sectioned into hindquarter and forequarter at the 5th to 6th ribs, making unfeasible the exposure of LM at the 12th rib in packing plants. Therefore, the objective was to estimate predicting equations of retail product weight (RPW) and percentage (RPP) in relation to cold carcass weight (CW) using traits measured on LM at the 11th/12th (LM12) and 5th/6th (LM5) by video image analysis (VIA) of Nellore bulls carcasses. Seventy-six bulls were feedlot finished and slaughtered (523 ± 34 kg BW, 22-mo old) following humanitarian procedures. The left carcass side was broken into wholesale cuts and digital images were taken of the LM5 and LM12 surfaces. Wholesale cuts were weighed and broken into retail product, bones and trimmings. Retail product was defined as the sum of all cuts trimmed to a fat thickness of 5 mm. The Lince software (M&S Consultoria Ltda. Pirassununga, SP, Brazil) was used to analyze LM images. For the LM5 images, the evaluated traits were rib eye area (REA5), rib thickness (RIBT), intermuscular fat thickness (INTERFAT5) and

subcutaneous fat thickness (SFT5). In LM12 images, the rib eye are (REA12) and subcutaneous fat thickness (SFT12) were obtained. Multiple regression analyses were carried out to estimate predicting equations for RPW and RPP using measurements obtained by VIA as independent variables. Traits that best explained RPW and RPP were selected using stepwise regression and entered into the prediction equation. Using LM12 traits, the best equations for RPW and RPP were RPW (kg) = 10.63502 + 0.06402*REA12 + 0.76071*CW (R^2 = 0.94; SEP = 2.38); and RPP (%) = 67.47563 + 0.06252*REA12; R^2 = 0.09; SEP = 1.56). Using LM5 traits, the best equations were RPW (kg) = 14.78075 + 0.23758*REA5 + 0.28579*BFT5 + 0.79065*CW; (R^2 = 0.94; SEP = 2.38) and RPP (%) = 62.87192 + 0.16159*REA5 – 0.17820*BFT5 + 0.04108*CCW; R^2 = 0.21; SEP = 1.46). Results indicated that LM measurements obtained at the 5th rib level can be used to predict retail product yield in Nellore cattle.

Key words: edible portion, Longissimus muscle, video image

W173 The influence of two levels of supplementation on the yield of hindquarter cuts of Nellore in *Brachiaria brizantha* 'Marandu'. R. V. Oliveira*[1], F. A. Barbosa[2], J. M. S. Diogo[1], G. S. Firmino[1], J. F. A. Oliveira[1], J. F. B. Guedes[1], I. S. Silva[1], and G. A. Carneiro[1], *[1]Faculty of Agronomy and Veterinary Medicine, University of Brasília - UnB, Brasília, DF, Brazil, [2]School of Veterinary Medicine, Federal University of Minas Gerais - UFMG, Belo Horizonte, MG, Brazil.*

This study was conducted to evaluate the yields of cuts from the carcasses from of the young cattle raised under semi-confinement system, grazing Brachiaria brizantha cv Marandu with 2 levels of dietary supplementation (0.91 or 1.42% of BW, dry matter basis). Thirty Nellore bulls were used, with medium age of 22 mo, average of 330.42 kg live weight and 477.94 kg slaughter weight. The dietary supplementation was based on corn, sunflower meal, soybean hull, urea and minerals. The statistical design was randomized blocks design with 2 treatments and 3 replications, and the Duncan test was applied at 5% significance level. After slaughter, the carcasses were cooled during 24 h at 3°C. The right half-carcasses (hindquarter) were separated in the following cuts: eye of rump, cap of rump, flatround, inside, loin, tenderloin, eye of round and knuckle. There was no influence ($P > 0.05$) of the supplementation levels on the weights of the cuts, which had average values of 4.28 kg of eye of rump, 1.60 kg of cap of rump; 6.40 kg of flatround, 10.30 kg of inside; 8.16 kg of loin; 2.47 kg of tenderloin, 2.86 kg of eye of round and 5.58 kg of knuckle. The yields of the cuts were not affected by treatments ($P > 0.05$), obtaining average values of 6.57% of eye of rump, 2.46% of cap of rump, 9.81% of flatround, 15.79% of inside, 12.52% of loin, 3.79% of tenderloin, 4.38% of eye of round and 5.58% of knuckle. The different levels of supplementation resulted in similar weight and yields for all cuts, suggesting the use of the intake level of 0.90% to Nellore without negatively affecting in the carcass quality.

Key words: *Bos indicus*, commercial cuts, concentrated

W174 Influence of two levels of supplements on the characteristics of cuts yields of carcass in Nellore cattle grazing *Brachiaria brizantha* 'Marandu'. R. V. Oliveira*[1], J. F. A. Oliveira[1], F. A. Barbosa[2], F. F. Gouveia[1], G. A. Carneiro[1], J. M. S. Diogo[1], J. F. B. Guedes[1], and R. A. Mandarino[1], *[1]Faculty of Agronomy and Veterinary Medicine, University of Brasília - UnB, Brasília, DF, Brazil, [2]School of Veterinary Medicine, Federal University of Minas Gerais - UFMG, Belo Horizonte, MG, Brazil.*

The objective of this study was to evaluate the yields of carcass cuts of cattle submitted to the semi-confinement system, with 2 different levels of supplement intake during 6 mo, grazing Brachiaria brizantha cv. Marandu. Thirty Nellore bulls 22 mo old were used, with an average body weight (BW) of 330.42 kg and final slaughter weight of 477.94 kg. The supplement consisted of corn, sunflower meal, soybean hulls, urea and minerals. There were 2 treatments: SCONF1 - average daily intake of 0.91% of BW of supplement in the dry matter (DM); and SCONF2 - average daily intake of 1.42% of BW of supplement, in the DM. The statistical design was randomized blocks design with 2 treatments and 3 replications, and the Duncan test was applied at 5% significance level. After the slaughter, the carcass was divided in 2 symmetrical halves, weighed and cooled for 24 h at 3°C. The right half-carcasses were separated in the following cuts: hindquarter (HIND) which covers the posterior region of the carcass separated in the fifth and sixth ribs at a distance of approximately 20 cm from the spine; forequarter (FORE), which includes neck, shoulder, arm and 5 ribs; and spare ribs (SR) which includes the region of the sixth rib over the abdominal muscles. The cuts were weighed individually and their proportion to the cold half-carcass determined. There was no influence of the supplementation level on the cuts weights, which presented values of 60.85 and 66.53 kg for FORE, 64.45 and 65.20 kg for HIND and 15.50 and 15.47 for SR, in treatments SCONF1 and SCONF2, respectively. The yields of FORE, HIND and SR were 44.21, 45.05 and 10.74%, respectively, and did not show statistical difference between treatments ($P > 0.05$). The different supplementation levels provided similar weights and yields of cuts, suggesting that ingestion of 0.91% of BW of animals can be adopted in semi-confinement systems, without losing carcass quality.

Key words: *Bos indicus*, beef cattle, special hindquarter

W175 Effect of different levels of whole raw soybean grain on performance and meat characteristics of feedlot finished Nelore steers. N. R. B. Consolo*, A. S. C. Pereira, J. R. Gandra, R. Gardinal, C. S. Takiya, P. Barros J. Carvalho, F. P. Renno, J. E. Freitas Junior, G. D. Calomeni, and R. D. Mingoti, *Universidade de Sao Paulo, Pirassununga, Sao Paulo, Brasil.*

The aim of this study was to evaluate the performance and carcass quality of steers fed whole raw soybeans at increasing inclusion levels. Fifty-four Nellore with mean weight and age of 350 kg and 24 mo were fed for 84 d with 4 isoproteic diets of 15% crude protein: T0, with 0% of whole raw soybean grain, T8, with 8% whole raw soybean grain, T16, with 16% whole raw soybean grain and T24, with 24% whole raw soybean grain, on dry matter basis. Steers were allotted to 4 pens and assigned to a completely randomized design. Animals were weighed at 28 d intervals after 18 h fasting to evaluate the performance. Animals were slaughtered in the commercial plant, according to proper welfare guidelines, and hot carcass weight, carcass yield, liver weight were evaluated. Twenty-four hours later, *Longissimus* muscle area and backfat thickness was measured at the interface of the 12th and 13th ribs. Longissimus muscle samples were aged 14 d with temperature varied between 0°C and 4°C for Shear force (SF) analysis. SF was obtained with Warner Bratzler equipment. Effects of treatments were evaluated using SAS software. No difference ($P > 0.05$) was observed for the measured variables: performance (1.82 ± 0.09 kg/d), hot carcass weight (284.07 ± 4.65kg), carcass yield (53.45 ± 0.52%), liver weight (5.69 ± 0.19kg), muscle area and backfat thickness (74.61 ±

2.46mm^2 and 2.08 ± 0.26mm). However, shear force characteristics had a quadratic effect ($P > 0.05$) with the highest scores for the treatment with 8% of soybean grain (7.17 kgf), which differed from the T0 (5.61 kgf) treatment but not the other treatments. The inclusion of whole raw soybean grain in beef cattle diets at the trial levels did not affect performance and carcass traits except for a slight increase in shear force at 8% grain inclusion levels.

Key words: protein source, tenderness, ruminants

W176 Genetic group and slaughter weight influence on meat color of feedlot cattle. R. Mello*[1], A. C. de Queiroz[2], F. D. de Resende[3], L. A. de Miranda Gomide[2], P. B. Costa[2], and W. da Silva Cotrim[2], *[1]Universidade Federal de Santa Maria, Santa Maria, Rio Grande do Sul, Brazil, [2]Universidade Federal de Viçosa, Viçosa, Minas Gerais, Brazil, [3]Agência Paulista de Tecnologia dos Agronegócios, Colina, São Paulo, Brazil.*

The purpose of this study was to investigate the genetic group and slaughter weight influence on meat color of the cattle. 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 animals were slaughtered in a commercial slaughter-house. The meat color evaluation was carried out in the Longissimus dorsi muscle at 13th rib. Data were analyzed with SAS® software using initial SBW as a covariate. The table below shows the least squares means of L* (luminosity), a* (redness), b* (yellowness), c* (saturation) and h* (hue). There was no effect ($P > 0.05$) of genetic group on color indexes. The interaction between genetic group and slaughter weight was not significant ($P > 0.05$) for all color traits. As the slaughter weight increased, the hue (h*) increased ($P < 0.05$) and a*/b* ratio decreased ($P < 0.05$). Accordingly, lighter weight animals at slaughter produced meat with better visual appearance of color than animals slaughtered at heavier weights, regardless of breed.

Table 1. Least squares means

	Genetic Group (GG)		Slaughter Weight (SW)				
	½ RA ½ N	½ BA ½ N	480	520	560	CV	SEM
L*	39.73	40.24	39.29	40.46	40.21	4.6	0.30
a*	4.87	5.07	4.89	5.39	4.64	14.9	0.12
b*	6.60	7.32	6.44	7.14	7.30	16.2	0.20
c*	8.24	8.93	8.12	8.97	8.66	13.4	0.20
h*	53.12	55.22	52.02^b	52.95^{ab}	57.53^a	8.9	0.89
a*/b*	0.77	0.70	0.80^a	0.76^{ab}	0.64^b	19.6	0.03

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, *Longissimus dorsi*, young bulls

W177 C18:1,2,3 fatty acid isomers from intramuscular fat influenced by genetic group and slaughter weight. 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, Rio Grande do Sul, Brazil, [2]Universidade Federal de Viçosa, Viçosa, Minas Gerais, Brazil, [3]Agência Paulista de Tecnologia dos Agronegócios, Colina, São Paulo, Brazil, [4]Universidade de São Paulo – Escola Superior de Agricultura 'Luiz de Queiroz', Piracicaba, São Paulo, Brazil.*

The work was carried out to evaluate the effect of genetic group (GG) and slaughter weight (SW) on C18:1, C18:2 and C18:3 fatty acid isomers of intramuscular fat from Longissimus dorsi muscle at 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 because previously to the beginning of the experiment they remained for 2 mo at Brachiaria brizantha pasture under continuous grazing system. 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 rised, being 2.1, 2.7 and 4.4 mm, respectively, for animals slaughtered at 480, 520 and 560 kg. The 1/2 BA 1/2 N young bulls had higher ($P < 0.05$) cis-13 C18:1 and cis-9 trans-11 C18:2 (CLA) levels than 1/2 RA 1/2 N young bulls. As the slaughter weight rised the trans, trans-9, trans-11 and trans-16 C18:1; cis-9 trans-11 and trans-10 cis-12 C18:2 (CLA); and cis-9,12,15 and cis-6,9,12 C18:3 levels decreased ($P < 0.05$); while cis, cis-9 and cis-12 C18:1 levels increased. The interaction between GG and SW was not significant ($P > 0.05$) for all levels of C18:1,2,3 fatty acid isomers. Therefore, crossbred F1 Blonde D′Aquitaine × Nellore young bulls and lighter animals had better profile of C18:1,2,3 fatty acid isomers in the intramuscular fat than F1 Red Angus × Nellore young bulls and heavier animals.

Table 1. Least squares means

	Genetic Group		Slaughter Weight		
	½ RA ½ N	½ BA ½ N	480	520	560
C18:1					
cis-9	32.42	33.49	32.01^b	32.3^{ab}	34.53^a
cis-13	0.26^B	0.31^A	0.27	0.27	0.32
trans-9	0.16	0.17	0.19^a	0.18^a	0.13^b
trans-11	0.85	1.03	1.15^a	1.00^{ab}	0.66^b
C18:2					
cis-9 *trans*-11 (CLA)	0.24^B	0.30^A	0.34^a	0.27^b	0.21^c
trans-10 *cis*-12 (CLA)	0.02	0.01	0.02^{ab}	0.03^a	0.005^b
C18:3					
cis-9,12,15	1.16	1.05	1.35^a	1.13^{ab}	0.84^b
cis-6,9,12	0.10	0.09	0.10^a	0.09^{ab}	0.08^c

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: conjugated linoleic acids, *trans* stereoisomer, young bulls

W178 Fatty acids profile of intramuscular fat from crossbreed young bulls slaughtered at different body 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, Rio Grande do Sul, Brazil, [2]Universidade Federal de Viçosa, Viçosa, Minas Gerais, Brazil, [3]Agência Paulista de Tecnologia dos*

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The aim was to investigate fatty acids profile of intramuscular fat from Longissimus dorsi muscle at 13th rib of crossbred bulls at different body weights. 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 rised, being 2.1, 2.7 and 4.4 mm, respectively, for animals slaughtered at 480, 520 and 560 kg. The 1/2 BA 1/2 N young bulls had higher ($P < 0.05$) monounsaturated fatty acids levels than 1/2 RA 1/2 N young bulls. As the slaughter weight rised the n-3 fatty acids levels decreased ($P < 0.05$). Thus, crossbred F1 Blonde D′Aquitaine × Nellore young bulls and lighter animals had better fatty acids profile in the intramuscular fat than F1 Red Angus × Nellore young bulls and heavier animals.

Table 1. Least squares means

	Genetic Group		Slaughter Weight			
FA	½ RA ½ N	½ BA ½ N	480	520	560	SEM
Short-chain	0.2	0.2	0.2	0.2	0.1	0.01
Medium-chain	33.2	33.2	32.6	33.2	33.8	0.5
Long-chain	60.3	60.2	60.2	60.4	60.3	0.3
Very long-chain	4.0	4.0	4.6	3.9	3.4	0.3
Odd-chain	2.3	2.4	2.4	2.3	2.3	0.1
Saturated	46.7	46.0	45.9	46.9	46.4	0.5
MUFA	42.8^{B}	44.3^{A}	43.4	42.9	44.4	0.4
PUFA	10.4	9.6	10.7	10.2	9.2	0.5
n-3	3.0	3.0	3.6^{a}	3.0^{ab}	2.5^{b}	0.2
n-6	7.7	6.8	7.3	7.5	7.0	0.3

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: breed, feedlot, *Longissimus dorsi*

W179 Effects of modified wet corn distillers grains containing 6.7% fat on beef quality and rib fat composition. J. L. Veracini*[1], P. M. Walker[1], B. R. Wiegand[2], H. L. Evans[2], R. L. Atkinson[3], M. J. Faulkner[1], and L. A. Forster[4], *[1]Illinois State University, Normal, [2]University of Missouri, Columbia, [3]Southern Illinois University, Carbondale, [4]Archer Daniels Midland Co., Decatur, IL.*

As the demand for ethanol increases, the availability of modified wet corn distillers grains (DGS) for inclusion in cattle diets increases. Several studies evaluating the effects of dietary DGS on performance characteristics have been reported. Fewer studies have evaluated high inclusion levels (over 50% diet DM) of DGS in finishing cattle diets on the effects on beef quality and adipose profile. The objective of this study was to compare beef quality characteristics and rib fat profile of steers fed 0, 25, 40 and 70% DGS (DM basis). Following a 48 h chill, rib sections (ribs 10 to 12) were removed, individually tagged, bagged and refrigerated. Rib sections were allowed to age for 7 d at 4°C before they were deboned, sliced into 2.54 cm steaks, and evaluated for Minolta color, cooking loss, shear force, % fat, % moisture and intramuscular fat (IMF) fatty acid composition. There were no differences ($P > 0.05$) in % moisture, % fat, shear force, or cooking loss between treatments. Steers fed 70% DGS diets produced ribeye steaks with significantly lower a* values ($P < 0.05$), and a trend for lower b* ($P < 0.10$) values compared with ribeye steaks from steers fed 0, 25, or 40% DGS. Lower redness scores (a*) can be associated with oxidation of unsaturated fatty acids that can trigger oxidation of myoglobin. Fatty acid analysis showed a linear increase ($P < 0.05$) in SFA (44% vs. 48% for 0% and 70% DGS, respectively) at the expense of MUFA (50% vs. 43% for 0% and 70% DGS, respectively). Linear increases were observed in PUFA/SFA, CLA, and ω6 fats, with increasing DGS level. Citing a decrease in C18:2n6c from 3.51 to 4.50 to 5.23 to 6.69 for 0%, 25%, 40% and 70% DGS, respectively. Since DGS can have 3 to 12% (depending on extraction and blending methods) corn oil and corn oil has a high percentage of linoleic acid, it appears that increasing dietary DGS resulted in increased rumen bypass or incomplete rumen biohydrogenation of corn oil, thus shifting fatty acid profiles of IMF.

Key words: DGS, beef color, fat profile

W180 Diet and genotype effects on the quality index of beef Nellore and F1 Nellore × Brahman produced in feedlot. R. A. Mandarino*[1], F. A. Barbosa[2,1], I. S. Silva[1], S. L. S. Cabral Filho[1], J. L. Vilela[1], and C. F. Lobo[1], *[1]University of Brasília, Brasília, DF, Brazil, [2]Federal University of Minas Gerais, Belo Horizonte, MG, Brazil.*

This experiment evaluated the effect of diet and genetic group on meat tenderness and the initial (pHi) and final pH (pHf) of the carcass after slaughter. The experiment lasted 96 d. The herd was composed of 42 bulls with a average age of 23 mo composed of 21 breed Nellore (NEL) and 21 crossbreed Nellore x Brahman (NBR). Each genetic group was divided into 3 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 randomized scheme in a 2 × 3 factorial, divided as follows: NELSIL, NELPEL, NELGRN, NBRSIL, NBRPEL and NBRGRN. The average initial body weights were 352.36 kg for genetic group NEL and 377 kg for the NBR animals. The final body weight averages were 481.37 kg for NEL and 461.4 kg for the NBR animals. The results of the pH measured 2 h (pHi) after slaughter were higher for NEL compared with NBR, 6.11 and 5.85, respectively ($P < 0.05$). There was a influence by the diet on the pHi with higher value to GRN when compared with PEL and SIL, 6.08, 5.99, 5.86, respectively ($P < 0.05$). The results of pH measured 24 h (pHf) after slaughter were higher for NEL compared with NBR, 5.92 and 5.28, respectively ($P < 0.05$) but were not influenced by the diets ($P > 0.05$). The meat tenderness, measured by shear force, was only numerically higher for NEL with a value of 4.97 and 4.62 kgf for NBR but were not influenced by genetic or by diet ($P > 0.05$). For both genetic groups the meat can be considered as a moderately soft meat and resilient to consumption. The pH can be influenced by genetics or the diet. The results also showed a normal value for pH what is expected to be 2 h and 24 h after slaughter.

Key words: shear force, tenderness, pH

W181 Beef quality parameters of Nellore bulls finished with cottonseed cake as fat source. A. P. Neto*[1,2], R. H. Branco[3], S. F. M. Bonilha[3], T. L. S. Corvino[3], E. N. Andrade[2], and R. de Oliveira

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Cottonseed cake (CSC) is a residue obtained by mechanical extraction of oil seed upon biodiesel manufacturing. This study aimed to evaluate effects on beef quality of CSC inclusion as fat source in finished diets of Nellore bulls. Forty bulls were slaughtered with averages of 21 mo for age and 451 kg for BW, after 102 d under feedlot conditions. CSC inclusion was based on diet ether extract (EE): 3%, 4% and 5%. Other treatments, with 3% and 5% of EE, having soybean (SB) products as fat source were also tested. Beef quality parameters evaluated were: pH 24 h, shear force, beef color objectively by Minolta CR-410 [L* = brightness; a* = red; b* = yellow] and subjectively using score of 1 = extremely light red to 7 = extremely dark red. Means were tested using 4 non-orthogonal contrasts: C1 = 3%SB vs. 3%CSC; C2 = 5%SB vs. 5%CSC; C3 = 3%CSC vs. 5%CSC; and C4 = 3%CSC and 5%CSC vs. 4%CSC. Contrasts were analyzed by Scheffé test. Beef quality parameters evaluated were not influenced by fat source and EE level. Means of 5.71 for pH 24 h, 5.70 kg for shear force, 38.8 for brightness, 16.7 for red color, 4.6 for yellow color and 3.75 for subjective color score were observed. The meat traits evaluated indicated high quality beef. Therefore, CSC did not influence beef traits and can be used as fat source on finishing diets of Nellore bulls.

Table 1. Beef quality parameters of Nellore bulls feed with cottonseed cake (CSC) and soybean (SB)

	SB		CSC			*P*[1]			
	3%	5%	3%	4%	5%	C1	C2	C3	C4
pH 24 h	5.70	5.65	5.59	5.66	5.97	NS	NS	NS	NS
Shear force, kg	6.02	5.93	5.62	6.03	4.91	NS	NS	NS	NS
L*	39.1	39.2	39.6	38.2	37.9	NS	NS	NS	NS
a*	16.5	16.4	17.8	16.3	16.7	NS	NS	NS	NS
b*	4.64	5.13	5.37	4.10	3.82	NS	NS	NS	NS
Color score	3.87	3.37	3.00	3.87	4.62	NS	NS	NS	NS

[1]C1 = 3%SB vs 3%CSC; C2 = 5%SB vs 5%CSC; C3 = 3%CSC vs 5%CSC; and C4 = 3%CSC and 5%CSC vs 4%CSC. NS = no significance ($IYI \geq S$; $\alpha = 0.05$).

Key words: biodiesel, byproducts, feedlot

W182 Meat tenderness of Nellore cattle classified for residual feed intake. T. L. Sobrinho[1], K. Zorzi[2], R. H. Branco[3], S. F. M. Bonilha[3], L. T. Egawa[3], E. Magnani[3], and M. E. Z. Mercadante*[3], *[1]Faculdade de Ciências Agrárias e Veterinárias, Jaboticabal, São Paulo, Brasil, [2]Universidade Federal de Viçosa, Viçosa, Minas Gerais, Brasil, [3]Instituto de Zootecnia, Sertãozinho, São Paulo, Brasil.*

Residual feed intake (RFI), expressed as the difference between DM intakes observed and estimated by regression equation as function of metabolic BW and ADG, is an alternative measure of feed efficiency and can be used as tool to reduce costs of beef production. This study aimed to evaluate Warner-Bratzler shear force (SF) and myofibrillar fragmentation index (MFI) of meat from low (more efficient) and high (less efficient) RFI animals. The experiment was conducted at Instituto de Zootecnia, Sertãozinho/São Paulo/Brazil, with 59 Nellore bulls slaugthered with 447 kg of average BW and 20 mo of age. Carcasses were chilled at 2°C for 24 h and then steak samples of Longissimus dorsi muscle, with 2.5 cm of thickness, were removed from 11th rib for SF and MFI determination. Steaks were aged for 7 and 21 d at 0–2°C and then were frozen, totaling 3 samples for animal, with 1, 8 and 22 d post mortem. Data were analyzed using GLM procedure of SAS, and means were compared using *t*-test. RFI variation was 0.740 kg of DM per d, with averages of −0.330 and 0.410 kg, respectively, for animals more and less efficient. No difference was detected for MFI between RFI levels, being MFI averages 35.8 and 40.6 (d 1; $P = 0.0877$), 49.3 and 50.5 (d 8; $P = 0.800$) and 70.9 and 78.8 (d 22; $P = 0.249$), respectively for low and high RFI levels. Low RFI animals had higher SF than the high RFI ones. SF averages were 4.30 and 3.83 kg (d 1; $P = 0.0424$); 4.00 and 3.47 kg (d 8; $P = 0.0339$); and 3.12 and 2.58 kg (d 22; $P = 0.005$), respectively for low and high RFI levels. MFI increases with aging result from proteolytic enzymes, among them calpains, that act on muscle fibers and promote meat tenderness. However, despite not showing up significant difference for MFI, low RFI animals had higher SF values, indicating less tender meat. According to literature, more efficient animals have stronger action of calpastatin, responsible for inhibiting calpain action, resulting in less tender beef.

Key words: beef quality, efficiency, shear force

W183 Effects of purified zearalenone on serum reproductive hormone, immunoglobulin, antibody titer and spleen pro-inflammatory cytokines mRNA in young gilts. S. Z. Jiang*[1], Z. B. Yang[1], W. R. Yang[1], S. L. Johnston[2], and F. Chi[2], *[1]Department of Animal Sciences and Technology, Shandong Agricultural University, Taian, Shandong, China, [2]Amlan International, Chicago, IL.*

A study was conducted to evaluate the effects of 1 to 3 mg/kg purified dietary zearalenone (ZEA) on reproductive hormones, immune response, and antibody production in young gilts. Seven days postweaning, 20 gilts (LxYxD) (BW = 10.36 ± 1.21 kg) were randomly allotted to 4 treatments, which were 0, 1, 2, or 3 mg/kg additions of purified ZEA to a basal diet fed for 18 d. Data were analyzed using the GLM procedure of SAS with individual pig as the basis for analysis. Difference was determined as $P < 0.05$. Pigs received classical swine fever (CSF) vaccine 1-d before the study. Blood was collected on d-6 and d-12 for CSF antibody titer determination. Fasted pigs were injected with LPS (50 μg/kg BW) 3 h before blood collection and euthanasia on d-18. Blood samples were used for estrogen, progesterone, testosterone, LH, FSH, and prolactin measurements, and for IgA, IgG, IgM, and IL-2 level determination. Lymphocytes from the blood and spleen were used to determine the lymphocyte proliferation rate (LPR). Spleen mRNA of IL-1β, IL-6, IFN-γ, and TNF-α was determined by real time PCR. There was no difference on CSF titer levels on d-6 or 12 but d-18 titers decreased as ZEA increased ($P < 0.001$). A similar result was observed in IgG but there was no effect on IgA or IgM level. Serum testosterone, estradiol, LH, and FSH decreased as ZEA increased. Progesterone tended ($P = 0.058$) to decrease and prolactin increase with increasing ZEA. No effect was found in FSH level ($P > 0.05$). The IL-2 and LPR of blood and spleen cells decreased ($P < 0.05$) as ZEA increased. Spleen mRNA of IL-2 and IL-6 increased as ZEA increased. As ZEA increased IFN-γ mRNA decreased but TNF-α showed no effect. Dietary ZEA at 1 to 3 ppm level negatively affects the pig′s reproductive hormone, immunoglobulin, and antibody production, and may increase the inflammatory response.

Key words: zearalenone, immune response, hormone

W184 Ameliorate effect of Calibrin Z enterosorbent on serum reproductive hormone, immunoglobulin, antibody titer in young pigs fed purified zearalenone. S. Z. Jiang*[1], Z. B. Yang[1], S. L. Johnston[2], and F. Chi[2], *[1]Department of Animal Sciences and Technology, Shandong Agricultural University, Taian, Shandong, China, [2]Amlan International, Chicago, IL.*

Thirty-six pigs (BW = 8.9 ± 0.2 kg) were used to evaluate the effect of Calibrin-Z (CZ) on the effects of zearalenone (ZEA) on immune response in piglets. The pigs were allotted to 6 treatments (TRT). The 6 TRT were: 1) Control (Con); 2) Con + 0.1% CZ; 3) Con + 1 ppm ZEA; 4) Con + 1 ppm ZEA + 0.1% CZ; 5) Con + 1 ppm ZEA + 0.2% CZ; 6) Con + 1 ppm ZEA + 0.4% CZ. Data were analyzed using the GLM procedure of SAS with individual pig as the basis for analysis. Each pig received classical swine fever (CSF) vaccine 1-d before the study, serum samples were collected weekly for CSF antibody titer determination. On d 21, blood and spleen samples were collected for hormone, immunoglobulin, interleukin (IL) cytokine analyses, and lymphocyte proliferation rate (LPR). Gilts fed TRT 3 had lower ($P < 0.05$) progesterone (75% of 1 and 2), and testosterone (74% of 1 and 2) levels than TRT 1 and 2. Adding clay improved serum hormone levels and the elevated hormone was clay dosage dependent. Male pigs fed TRT 3 showed similar results as gilts except serum estrodial was not different. Serum IgA and IgM were not different, IgG level was reduced ($P < 0.01$) in TRT 3 (77% of 1 and 2) compared with TRT 1 and 2. It increased linearly ($P < 0.05$) in TRT 4, 5, and 6 but remained lower ($P < 0.05$) than TRT 1 and 2 (84% of 1 and 2).The LPR from blood and spleen cells followed a trend similar to IgG. Serum IL-2 followed results similar to those of the hormones; pigs fed TRT 3 had the lowest IL-2 but an addition of 0.4% clay restored the levels equal to TRT 1 and 2. There was no difference on d-7 or d-14 on CFS titers. On d-21, pigs fed TRT 2 had the highest titer against CSF and greater ($P < 0.01$) than pigs fed TRT 3, 4, 5, and 6; but not different than TRT 1. Feeding 1 ppm of purified ZEA caused adverse effects on immunity in pigs; which were ameliorated by CZ. Feeding CZ without ZEA had the greatest antibody titer production, implying that the Calibrin-Z adds value to feed with or without a mycotoxin challenge.

Key words: zearalenone, titer, immunoglobulin

W185 Dietary effect of short-chain organic acids on growth performance, mortality, and development of intestinal lymphoid tissues in young non-medicated rabbits. C. Romero*[1], P. G. Rebollar[1], A. Dal Bosco[2], C. Castellini[2], and R. Cardinali[2], *[1]Universidad Politécnica de Madrid, Spain, [2]Università degli Studi di Perugia, Italy.*

This work aimed to test the effect of a dietary inclusion of formic and citric acids (0.4%) on growth performance, mortality, jejunal histology, and development of intestinal lymphoid tissues in growing non-medicated rabbits. For that purpose, a diet including the acids (diet A) was compared with a control diet (diet C). Sixty rabbits weaned at 28 d were submitted to each diet. At 56 and 77 d, 10 rabbits were slaughtered to assess cecal traits, jejunal histology, and follicular development in the caudal ileal Peyer′s patch and in the appendix. In the 56–77 d period, average daily weight gain of rabbits fed diet A was greater than that of control rabbits (48.0 vs. 43.9 g, $P = 0.019$). Mortality rate was not affected by the diet (6.12% on average). Cecal pH was lower at 77 than at 56 d (6.02 vs. 6.19, $P = 0.016$). The concentration of ammonia in the cecal contents increased from 9.62 to 14.2 mmol/l ($P = 0.003$) when rabbits reached 77 d of age. The appendix was heavier (9.75 vs. 4.30 g, $P < 0.001$), longer (13.3 vs. 10.4 cm, $P < 0.001$), and wider (1.74 vs. 1.45 cm, $P = 0.006$) at 77 than at 56 d. Rabbits of 56 d of age fed diet C had shorter villi than the mean value of the other 3 treatments (662 vs. 807 μm, $P < 0.001$). In the Peyer′s patch, the average follicle area was greater at 77 than at 56 d of age (118 vs. 88.4 × 10^3 μm^2, $P < 0.001$) and was also greater in rabbits fed diet C than in those fed diet A (109 vs. 97.5 × 10^3 μm^2, $P = 0.049$). In the appendix, no differences on the average follicle area were found at 56 d of age (115 × 10^3 μm^2) whereas, at 77 d, the area increase was higher for rabbits fed diet C than for those fed diet A (95.5 vs. 50.8%, $P < 0.001$). In conclusion, including formic and citric acids in growing rabbit diets improves weight gain, has a trophic effect on the jejunal mucosa, and controls the development of gut-associated lymphoid tissues.

Key words: gut histology, lymphoid tissue, organic acids

W186 Casein glycomacropeptide and mannan-oligosaccharides reduce the enterotoxigenic *E. coli* (ETEC K88) adhesion to IPEC-J2 cell line. R. G. Hermes*[1], E. G. Manzanilla[1], S. Martin-Orue[1], J.

F. Perez[1], and K. C. Klasing[2], *[1]Universitat Autonoma de Barcelona, Barcelona, Catalonia, Spain, [2]University of California, Davis, Davis.*

The aim of this study was to elucidate the ability of different feedstuffs sources to block the attachment of ETEC (K88) to the intestinal pig epithelium using an in vitro model. An adhesion test was done in polystyrene 96-well plates covered with an IPEC-J2 (intestinal porcine epithelial cell line isolated from the jejunum epithelia of neonatal piglets). Triplicates samples of wheat bran (WB), casein glycomacropeptide (CGMP, Lacprodan, Arla Foods, Denmark), mannan-oligosaccharides (MOS, Bio-Mos, Alltech, USA) or *Aspergillus oryzae* fermentation extract (AO, Fermacto, Molimen S.L., Spain) were evaluated as likely blockers of the ETEC attachment. Feedstuffs were diluted in PBS at 0.8% (w/v), sonicated 3 times, and centrifuged. Supernatant (1mL) of feedstuffs were incubated first with 1mL of an ETEC K88 strain (10^8 cfu/mL diluted in PBS), isolated from a clinical case of colibacillosis in piglets, for 30 min at room temperature and second with the IPEC-J2 monolayer cell culture in the well plates at 37°C/5% CO_2 for 1 h. After that, plates were washed twice with sterile PBS to remove non-attached bacteria and then CO_2-independent media was added to promote the growth of attached bacteria. Plates were incubated at 37°C/10h in a spectrophotometer and optical density (OD, 650 nm) was recorded every 10 min. The OD data were analyzed by nonlinear regression using SAS. The resulting parameters thus obtained were used to calculate the delay time (h) for the cultures to reach an OD of 0.05 ($t_{OD = 0.05}$). Analysis of variance of the $t_{OD = 0.05}$ values between treatments was done using the PROC GLM of SAS. Results showed that CGMP and MOS delayed ($P < 0.05$) $t_{OD = 0.05}$ to 3.4 ± 0.07 and 3.5 ± 0.26 h, respectively, in comparison to the negative control (2.4 ± 0.13 h). The values obtained for WB (3.2 ± 0.05) and AO (3.0 ± 0.06) were intermediate and different ($P < 0.05$) from the negative control. Our results suggest that some dietary ingredients may act as "anti-adhesive" compounds against pathogenic *E. coli*, which may have a positive effect on the intestinal health.

Key words: casein glycomacropeptide, mannan-oligosaccharides, *E. coli* K88

W187 The effects of a galactoglucomannan-arabinoxylan complex on eimeria acervulina infection in broiler chicks. T. A. Faber*[1], R. N. Dilger[1], A. C. Hopkins[2], N. P. Price[3], and G. C. Fahey[1], *[1]University of Illinois, Urbana, [2]Temple-Inland, Diboll, TX, [3]National Center for Agricultural Utilization Research, Peoria, IL.*

Fermentable carbohydrates are thought to enhance the ability of the gastrointestinal tract to defend against pathogenic infection. We hypothesized that a mannose-rich, galactoglucomannan-arabinoxylan (GGM-AX) complex would positively affect the immune status and prevent weight loss resulting from acute coccidiosis (*Eimeria acervulina*) infection. Using a completely randomized design, day-old commercial broiler chicks (n = 160; 4 reps/treatment; 5 chicks/rep) were assigned to one of 4 corn-soybean meal-based diets containing supplemental GGM-AX (0, 1, 2, and 4%) that replaced dietary cellulose. On d 8 post-hatch, an equal number of chicks on each diet were inoculated with either distilled water (sham control) or *E. acervulina* (1×10^6 oocysts). All birds were euthanized on d 7 post-inoculation for collection of cecal contents and duodenal tissue. At 7 d post-inoculation, infected birds fed the 0% GGM-AX treatment had heavier ($P < 0.03$) body weights than infected birds fed 1 or 2% GGM-AX. Feed intake was decreased ($P = 0.01$) by coccidial infection, but not affected by dietary treatment ($P = 0.69$). Cecal pH was greater ($P < 0.01$) in infected birds compared with uninfected birds. As dietary GGM-AX increased, cecal pH linearly decreased ($P = 0.001$), regardless of infection status. Coccidial infection increased ($P < 0.02$) cecal concentrations of propionate, butyrate, and total short-chain fatty acids, but not acetate ($P = 0.28$). Additionally, cecal propionate concentration decreased ($P < 0.01$) as dietary GGM-AX supplementation increased, whereas acetate, butyrate, and total SCFA concentrations were not affected by diet ($P \geq 0.48$). Dietary GGM-AX did not affect mRNA expression of interferon-gamma, interleukin (IL)-6, or IL-15 cytokines in duodenal tissue. An infection x diet interaction ($P = 0.02$) was observed for duodenal IL-12β and IL-1β mRNA expression. Based on these data, we conclude that GGM-AX supplementation was unable to mitigate the negative impact of an acute *E. acervulina* infection in broiler chicks.

Key words: chick, coccidiosis, galactoglucomannan oligosaccharide

W188 The effects of feed-borne *Fusarium* mycotoxins on performance, serum chemistry, and hematology of fryer rabbits. M. A. Hewitt*, M. Brash, and T. K. Smith, *University of Guelph, Guelph, Ontario, Canada.*

Mycotoxins are secondary metabolites produced by fungal synthesis. In many species, the effects of *Fusarium* mycotoxins have been documented. Very few studies, however, have been conducted on rabbits. The objective of the current study was to determine the effects of feeding grains naturally contaminated with *Fusarium* mycotoxins on growth and metabolism of fryer rabbits. Thirty 5-wk old male New Zealand white rabbits were used. Each rabbit was randomly assigned to 1 of 3 diets: (1) a control, (2) contaminated diet and (3) contaminated diet + 0.2% Glucomannan mycotoxin adsorbent (GMA). The control diet contained 0.2µg/g deoxynivalenol (DON), the contaminated diet contained 4.3µg/g DON and the GMA diet contained 4.9µg/g DON. Zearalenone and 15-acetyl DON were minor contaminates. The rabbits were given feed and water ad libitum for 21 d. Feed intake was measured daily and water intake was measured every 3 d. On d 21, blood samples were taken for serum chemistry analysis, and tissue sections were taken for pathology. Data was analyzed by ANOVA using a PROC GLM model. A Tukey test was used to compare least squares means among treatments and comparisons were considered significant at $P \leq 0.05$. Average daily gain was increased in rabbits fed the GMA diet ($P < 0.05$), and feed efficiency and average daily water intake were increased in rabbits fed the contaminated and GMA diet, when compared with controls ($P < 0.05$) (Table 1.1). Urea levels were also increased in rabbits fed the GMA diet and alkaline phosphatase (ALP) levels were decreased in rabbits fed the GMA diet when compared with controls ($P < 0.05$) (Table 1.1). An increase in water consumption could indicate improper kidney function. The increased weight gain seen in rabbits fed both the contaminated and GMA diets could be reflected by the increased water consumption. High urea and low ALP levels are signs of impaired protein metabolism. It was concluded that the feeding of diets naturally contaminated with *Fusarium* mycotoxins could adversely affect protein metabolism in immature rabbits.

Table 1. Effect of feed-borne *Fusarium* mycotoxins[1]

Diet	Average Gain (g)	Feed Efficiency (g/g)[2]	Average Water Intake (ml)	Urea (mmol/L)	Alkaline Phosphatase (U/L)
Control	37.08	0.347	142.49	3.19	212.6
Contaminated	40.33	0.377	173.45	3.57	171.8
GMA	41.02	0.385	184.4	3.85	162.6
SEM	± 1.0	± 0.01	± 7.69	± 0.164	± 12.1
1 vs. 2	NS[3]	0.05	0.02	NS	NS
1 vs. 3	0.026	0.011	0.002	0.024	0.02
2 vs. 3	NS	NS	NS	NS	NS

[1]Values are mean ± SEM; for each diet n=10.

[2]Total Weight Gain/Total Feed Consumption.

[3]$P > 0.05$.

Key words: rabbit, *Fusarium* mycotoxins, water consumption

W189 Effects of plant extracts on peripheral blood immune cells and inflammatory mediators of weaned pigs experimentally infected with a pathogenic *E. coli*. Y. Liu*[1], M. Song[1], T. M. Che[1], J. A. Soares[1], D. Bravo[2], C. W. Maddox[1], and J. E. Pettigrew[1], *[1]University of Illinois, Urbana, [2]Pancosma SA, Geneva, Switzerland.*

A study evaluated the effects of 3 different plant extracts (PE) on immune responses of weaned pigs experimentally infected with a pathogenic F-18 *E. coli*. Weaned pigs (n = 64, 6.3 ± 0.2 kg BW, 21 d old) were housed in individual pens in disease-containment chambers for 15 d: 4 d before and 11 d after the first inoculation (d 0). Treatments were in a factorial arrangement: with or without an F-18 *E. coli* challenge (toxins: LT, STb, and SLT-2; 10^{10} cfu/3 mL oral dose; daily for 3 d from d 0) and 4 diets (a nursery basal diet (CON), 10 ppm capsicum oleoresin (CAP), garlic (GAR), or turmeric oleoresin (TUR)). Blood was collected on d 0, 5, and 11 to measure total and differential white blood cell (WBC) counts and serum tumor necrosis factor-α (TNF-α), interleukin-10 (IL-10), transforming growth factor-β (TGF-β), C-reactive protein (CRP), and haptoglobin (Hp). The *E. coli* infection increased ($P < 0.05$) lymphocytes (LYM), TNF-α, and Hp on d 5, and WBC, neutrophils (NEU), LYM, monocytes (MONO), and Hp on d 11, but decreased ($P < 0.05$) IL-10 on d 5 and TGF-β on d 11 compared with the unchallenged group. In the *E. coli* challenged group, CAP decreased ($P < 0.05$) TNF-α (61.8 vs. 79.6 pg/ml) and Hp (823 vs. 1400 μg/ml) on d 5, and WBC (21.6 vs. 32.2 × 10^3/μl) and NEU (10.3 vs. 17.0 × 10^3/μl) on d 11; GAR decreased ($P < 0.05$) LYM (5.35 vs. 8.25 × 10^3/μl) and Hp (888 vs. 1400 μg/ml) on d 5, and WBC (23.0 vs. 32.2 × 10^3/μl), LYM (7.63 vs. 13.48 × 10^3/μl), and Hp (164 vs. 1272 μg/ml) on d 11; TUR decreased ($P < 0.05$) TNF-α (63.1 vs. 79.6 pg/ml) on d 5 and NEU (10.2 vs. 17.0 × 10^3/μl) on d 11 compared with the CON. In the unchallenged group, on d 5, CAP decreased ($P < 0.05$) Hp; GAR increased ($P < 0.05$) MONO and decreased ($P < 0.05$) Hp compared with the CON. PE did not affect IL-10, TGF-β, and CRP in both sham and *E. coli* challenged groups. In conclusion, the 3 PE tested affected total WBC, the populations of immune cells, and inflammatory mediators in *E. coli*-infected piglets, which may be beneficial to pig health.

Key words: *E. coli*, plant extracts, weaned pigs

W190 Acute toxicity of aqueous extract of *Moringa oleifera* leaf in growing poultry. J. O. Ashong* and D. L. Brown, *Cornell University, Ithaca, NY.*

The objective of the present study was to evaluate the safety of an aqueous extract of *Moringa oleifera* and its impact on feed intake in growing poultry. At 21 d of age, 75 White-leghorn type chicks were weighed and randomly divided into 5 groups, G1, G2, G3, G4 and G5. Chicks in G1, G2, G3, and G4 were gavage (orally) with aqueous moringa extract: 200, 400, 800, 2000 mg/kg BW, respectively, while chicks in G5 were gavage with distilled water (control group). Each group was made up of triplicates with 5 chicks per replicate. All chicks were fed basal chick feed. All the chicks were observed at the first 6 h and once daily thereafter over 14 d for signs of abnormal behavior and/or toxicity and mortality. Daily feed intake and weekly BW were recorded for the duration of the study. Post-trial postmortem examination conducted included weighing of kidney, liver and heart and biochemical analyses such as uric acid, thyroxine (T4), creatinine, aspartate transaminase (AST), alkaline phosphatase (ALP), cholesterol and total protein. Liver and kidney tissues were harvested for histopathological examination. There were no observed signs of abnormal behavior and/or toxicity and mortality in the course of the study. Macroscopic and microscopic observations showed no alterations and differences in the liver and kidneys of G1, G2, G3, G4 and G5 even though the liver weight was heaviest in G4 and lightest in G2. Similarly, there were no differences in feed intake and weight gain among the treatment groups. In the biochemical study, no changes and differences were observed among circulating biochemical indicators ($P > 0.05$); however, ALP decreased ($P < 0.05$) with increasing moringa leaf extract concentration, while total protein and albumin also decreased ($P < 0.05$) with increasing moringa leaf extract from 400 to 2000 mg/kg BW. In conclusion, oral administration of an aqueous extract of moringa at doses of 200, 400, 800 and 2000 mg/kg BW for 14 d to growing poultry did not induce any short-term toxicity and had no impact on feed intake

Key words: *Moringa oleifera*, acute toxicity, poultry

W191 Effects of spray-dried plasma on growth and reproductive responses of pregnant mice to lipopolysaccharide as a model for inflammation in sows. M. Song*[1], Y. Liu[1], J. A. Soares[1], J. J. Lee[1], T. M. Che[1], J. M. Campbell[2], J. Polo[2], J. C. O'Connor[3], and J. E. Pettigrew[1], *[1]University of Illinois, Urbana, [2]APC Inc., Ankeny, IA, [3]University of Texas Health Science Center, San Antonio.*

A study evaluated the effects of spray-dried plasma (SDP) on growth and reproductive responses of pregnant mice (C57BL/6 strain) to lipopolysaccharide (LPS; *Salmonella typhimurium*) as a model for inflammation in sows. The mated female mice (n = 250; 4 replicated groups, 62 or 63 mice/group) were shipped from Bar Harbor, ME to Urbana, IL on the day the vaginal plug was found (gestation day (GD) 1), arriving at the laboratory on GD 3. They were housed in individual cages, randomly assigned to dietary treatments with or without 8% SDP (SDP or CON), and fed for 15 d. The diets were formulated to similar ME, CP, and AA levels without antibiotics. On GD 17, pregnant mice (n = 61; 26.5 ± 1.65 g BW) were randomly assigned to intraperitoneal injections with or without 2 μg LPS in 200 μL PBS (LPS or PBS) and euthanized 6 h (6H) or 24 h (24H) later. Measurements were growth performance, pregnancy loss, fetal death, average live fetal and placental weight (WT), and organ WT (intestine, liver, spleen, and lung). The SDP improved BW gain (6H: 0.13 vs. −0.14 ± 0.12 g, $P = 0.06$; 24H: 0.81 vs. 0.30 ± 0.08 g, $P < 0.05$), feed intake (6H: 0.20 vs. 0.06 ± 0.05 g, $P < 0.05$; 24H: 2.8 vs. 2.4 ± 0.18 g, no significant (NS)), G:F (6H: no data; 24H: 0.30 vs. 0.11 ± 0.03, $P < 0.05$), average live fetal WT (6H: 0.65 vs. 0.56 ± 0.03 g, $P < 0.05$; 24H: 0.76 vs. 0.71 ± 0.02 g, $P = 0.09$), and the ratio between average live fetal and placental

WT (6H: 6.1 vs. 4.9 ± 0.6, $P = 0.07$; 24H: 7.2 vs. 6.4 ± 0.8, NS), and reduced spleen WT (6H: 0.29 vs. 0.35 ± 0.03% of BW, $P = 0.08$ (SDP effect larger under the LPS challenge (interaction, $P = 0.09$)); 24H: 0.29 vs. 0.25 ± 0.01% of BW, NS) compared with the CON. There were no interactions between diet and challenge on the other responses. The LPS challenge reduced BW gain and feed intake, and increased pregnancy loss (48 vs. 0%, $P < 0.05$), fetal death (5.3 vs. 0.6%, $P = 0.08$), and spleen WT compared with the PBS challenge. In conclusion, SDP improved growth performance of pregnant mice and their fetal WT after the challenge, but did not affect pregnancy loss or fetal death.

Key words: mice, reproductive responses, spray-dried plasma

W192 Effects of spray-dried plasma on immune responses of pregnant mice to lipopolysaccharide as a model for inflammation in sows. M. Song*[1], Y. Liu[1], J. J. Lee[1], J. A. Soares[1], T. M. Che[1], J. M. Campbell[2], J. Polo[2], J. C. O'Connor[3], and J. E. Pettigrew[1], *[1]University of Illinois, Urbana, [2]APC Inc., Ankeny, IA, [3]University of Texas Health Science Center, San Antonio.*

A study evaluated the effects of spray-dried plasma (SDP) on immune responses of pregnant mice (C57BL/6 strain) to lipopolysaccharide (LPS; *Salmonella typhimurium*) as a model for inflammation in sows. The mated female mice (n = 125; 2 replicated groups, 62 or 63 mice/group) were shipped from Bar Harbor, ME to Urbana, IL on the day the vaginal plug was found (gestation day (GD) 1), arriving at the laboratory on GD 3. They were housed in individual cages, randomly assigned to dietary treatments with or without 8% SDP (SDP or CON), and fed for 15 d. The diets were formulated to similar ME, CP, and AA levels without antibiotics. On GD 17, pregnant mice (n = 17; 27 ± 1.7 g BW) were randomly assigned to intraperitoneal injections with or without 2 μg LPS in 200 μL PBS (LPS or PBS) and euthanized 6 h later to collect gestational tissues (uterus (U) and placenta (P)). Measurements were pro-inflammatory cytokines (PRO; tumor necrosis factor-α (TNF-α) and interferon-γ (IFN-γ)) and anti-inflammatory cytokines (ANTI; interleukin-10 (IL-10) and transforming growth factor-β1 (TGF-β1)) by ELISA, and total protein (TP) using Bradford's reagent and bovine serum albumin to normalize those cytokines. The LPS challenge increased ($P < 0.05$) PRO and reduced ($P < 0.05$) ANTI in both U and P, except IL-10 in P, compared with the PBS challenge (Table). The SDP reduced ($P < 0.05$) PRO in U and P and ANTI in U only compared with the CON (Table). The SDP attenuated the LPS effect on PRO (interactions: TNF-α in P ($P = 0.09$), IFN-γ in U ($P = 0.08$) and P ($P < 0.05$); Table). In conclusion, SDP attenuated acute inflammation caused by LPS.

Table 1. Effect of SDP on immune responses in gestational tissues of pregnant mice to LPS

Cytokines/ TP	CON PBS	CON LPS	SDP PBS	SDP LPS	SEM	*P*-value LPS	*P*-value SDP	*P*-value Interaction
Uterus, pg/mg								
TNF-α	4.1	9.8	1.7	6.0	1.00	<0.05	<0.05	NS*
IFN-γ	0.33	4.2	0.11	1.8	0.52	<0.05	<0.05	0.08
IL-10	57	44	40	38	3.8	0.09	<0.05	NS
TGF-β1	571	421	317	248	45	<0.05	<0.05	NS
Placenta, pg/mg								
TNF-α	1.7	9.7	1.2	7.1	0.55	<0.05	<0.05	0.09
IFN-γ	0.13	0.79	0.08	0.31	0.07	<0.05	<0.05	<0.05
IL-10	24	26	29	28	5.0	NS	NS	NS
TGF-β1	492	454	299	300	37	NS	<0.05	NS

*NS = not significant.

Key words: immune responses, mice, spray-dried plasma

W193 Wheat bran and casein glycomacropeptide may regulate the immune response of IPEC-J2 cells challenged with enterotoxigenic *E. coli* (ETEC K88). R. G. Hermes*[1], E. G. Manzanilla[1], S. Martin-Orue[1], J. F. Perez[1], and K. C. Klasing[2], *[1]Universitat Autonoma de Barcelona, Barcelona, Catalonia, Spain, [2]University of California, Davis, Davis.*

The objectives of the present study were to measure the innate immune response of the IPEC-J2 cell line challenged with an ETEC (K88) or a non-fimbriated *E. coli* (NFEC), and measure the impact of feedstuffs on the response. Triplicates samples of wheat bran (WB), casein glycomacropeptide (CGMP, Lacprodan®, Arla Foods, Denmark), mannan-oligosaccharides (MOS, Bio-Mos®, Alltech, USA) or *Aspergillus oryzae* fermentation extract (AO, Fermacto®, Molimen, Spain) were evaluated. Feedstuffs were diluted in PBS at increasing doses of 0.1, 0.2, 0.4 and 0.8% (w/v), sonicated 3 times and centrifuged. Then, 1mL of feedstuffs supernatants were incubated (30 min./room temperature) with 1mL of ETEC K88 or NFEC cultures (10^8 cfu/mL, diluted in PBS), added to confluent monolayer of IPEC-J2 cells and incubated for 2 h at 37°C/5% of CO_2. Cells were washed twice with sterile PBS, and IL-8 and TNF-α expression was quantified using Cyclophilin-A, as a housekeeping gene, and related to a non-challenged treatment. Gene expression results were analyzed by ANOVA using the PROC GLM of SAS. The ETEC K88 challenge increased ($P < 0.05$) the inflammatory response, compared with NFEC challenge for IL-8 (33.1 ± 5.44% vs. 6.8 ± 2.42%) and TNF-α (28.9 ± 4.92% vs. 1.8 ± 0.85%) gene expression. Regarding the effect of feedstuffs, the incorporation of WB or CGMP reduced ($P < 0.05$) the IL-8 (7.3 ± 5.26% and 15.4 ± 9.54%, respectively) and TNF-α gene expression (13.0 ± 7.67% and 6.9 ± 3.94%, respectively) in comparison to the AO treatment (IL-8, 35.8 ± 4.08% and TNF-α, 25.9 ± 4.67%). The incorporation of MOS promoted an intermediate response for IL-8 (19.1 ± 6.40%) and similar results to WB and CGMP for TNF-α (13.3 ± 4.49%). In summary our results suggest that WB and CGMP regulate the inflammatory response of IPEC-J2 cells to an ETEC (K88) challenge, likely due to interference in microbial adhesion to the epithelial cells.

Key words: wheat bran, casein glycomacropeptide, *E. coli* K88

W194 Importance of evaluating piglet daily weight gain during the first week after weaning. G. J. M. M. Lima* and L. S. Lopes, *Embrapa, Brazil.*

Performance after weaning is crucial for pig growth. There are few reports describing ADG over the first wk after weaning. Some individuals show low gains while others lose weight (wt) during this period, providing highly variable results. To study wt gain during the first wk after weaning, an experiment was conducted to determine the effects of 4 combinations of lactose sources with or without growth promoter (GP): T1 = whey - GP; T2 = whey + GP; T3 = lactose + GP; T4 = whey permeate + GP. Ninety-six pigs (7.10 ± 0.12 kg) were weaned at 21 d of age and distributed to pens according to a random block design with 8 replicates of 3 animals. Diets met or exceeded 1998 NRC levels and pigs had free access to feed and water. Animals were weighed daily and had no clinical signs of diseases. Diarrhea frequencies were similar among diets (X2 test, $P = 0.69$). Overall average pig wt (n = 96) at d 22, 23, 24, 25, 26, 27 and 28 were 6.90, 6.88, 6.98, 7.17, 7.25, 7.33 and 7.50 kg, respectively, with coefficients of variation (CV) from 11.72 to 12.66%. However, overall average individual ADG for this period were, respectively, −0.205, −0.022, 0.102, 0.184, 0.084, 0.079 and 0.165 kg, with CV ranging from –818.31 to 281.17%. There were no differences in ADG among treatments by ANOVA for any d ($P > 0.35$) or for the first wk period (0.055 kg/d, CV = 123.92%, $P = 0.46$). A diet effect was detected when all individual ADG were combined through multivariate analysis ($P = 0.15$ by Wilks' Lambda test and $P = 0.002$ by Roy's test). Overall frequencies of negative, zero and positive ADG in the first wk period were 16.73, 3.00 and 80.27%, respectively, and there were differences among diets ($P = 0.03$, X2 test). It was detected that T1 (without GP) showed more animals with negative gain in the first wk compared with other treatments ($P < 0.05$, X2 test). It is important to study ADG during the first wk after weaning in these experiments. Multivariate analysis and frequency study of ADG provides useful information for a better understanding of this critical period for pigs.

Key words: Swine, multivariate analysis, X2 test

W195 Acquisition of garlic conditioned preference enhances the flavor hedonic power of porcine digestive peptides (PDP) in post-weaned piglets. J. Figueroa*[1], D. Solà-Oriol[1], S. L. Vinokurovas[1], E. Borda[2], and J. F. Pérez[1], *[1]Universitat Autònoma de Barcelona, Bellaterra, Barcelona, Spain, [2]Bioibérica, Barcelona, Spain.*

Piglets are reluctance to eat unfamiliar ingredients after weaning, which implies that innately preferred ingredients are commonly used in the design of these diets. However, the preference for a novel feed or flavor may be acquired as a result of an association with an intrinsically positive consequence. The aim of the present study was to explore the ability to increase the attraction and hedonism of a protein source in piglets by using synergy between their innate attraction and a flavor conditioned preference. A total of 240 non-deprived weanling piglets were trained during 8 d (alternate sessions) with a 2% Porcine Digestible Peptides (PDP) + 2% Garlic flavor solution and water (Synergy group), and with a 2% Garlic flavor and a 2% PDP solution (Control Group) in odd and even days, respectively. Double choice test (DCHT) between PDP+Garlic v/s PDP in water were performed on d 16, 23 and 30 after weaning. The first contact (number of piglets/pan for the first 15 s; FC) and 30 min solution intake were measured. Data was analyzed by using the GLM procedure of SAS. Higher FC values were observed for PDP+Garlic over PDP solution on d 16 and 23 (4.8 vs. 2.3 and 4.5 vs. 2.8; $P < 0.05$) for the Synergy group. No differences were observed for the Control group. Synergy group showed also a higher intake of PDP+Garlic than PDP at d 30 (773mL vs. 503mL; $P < 0.05$). No differences were observed in the intakes achieved for the Control group. The present results indicate that a garlic conditioned preference may enhance the attraction of PDP solutions, showing a synergy effect. This effect may be used to increase piglet acceptance and reduce neophobia for new feed ingredients.

Key words: protein, piglets, hedonic

W196 Nutrient composition changes in pigs and associated liver from birth to 21 days of age. Y. L. Ma*[1], M. D. Lindemann[1], J. L. Pierce[2], and G. L. Cromwell[1], *[1]University of Kentucky, Lexington, [2]Alltech Inc., Nicholasville KY.*

The objective of this study was to characterize nutrient composition in pigs and associated liver from birth to d 21 of age with specific interest in N and P for use in future determinations of lactation needs of sows for N and P. A week before the expected farrowing day, crossbred gilts (n = 10) were moved to farrowing crates and monitored. Two pigs were randomly selected and euthanized at d 0 (within 2 h after birth; nursing deprived), 7, 14, and 21 from each litter. Pigs (whole body without liver and gastrointestinal tract) and associated liver were analyzed for N, ether extract (EE), P, and total ash on a dry matter (DM) basis. With advancing age, BW increased linearly (1.59, 3.00, 4.63, 6.27 kg; $P < 0.01$), DM increased (19.8, 27.0, 29.2, 30.0%; $P < 0.05$ for linear [L], quadratic [Q], and cubic [C] responses), N decreased (9.77, 8.37, 8.24, 8.40%; $P < 0.01$; Q), EE increased 6-fold from birth to d 7 (5.7, 34.3, 35.8, 37.1%; $P < 0.01$; Q), P decreased (3.49, 2.27, 1.82, 1.78%; $P < 0.01$; Q), total ash decreased, in particular during first 7 d (20.0, 11.9, 10.0, 10.0%; $P < 0.01$; Q), and the unaccounted portion (carbohydrates) decreased, especially for the first 7 d (13.3, 1.5, 2.6, 0.3%; $P < 0.01$; C). As for pig liver, weight increased linearly (44.0, 114.4, 144.5, 190.8 g; $P < 0.01$), DM decreased linearly (29.3, 28.4, 26.2, 25.4%; $P < 0.01$), N increased (6.7, 10.2, 10.1, 10.4; $P < 0.01$; C), EE remained constant (6.8, 6.6, 6.8, 7.4%), total ash increased (4.53, 5.93, 6.16, 5.99%; $P < 0.01$; Q), and the unaccounted portion decreased (47.0, 23.6, 24.0, 21.8%; $P < 0.01$; C) with advancing age. The results characterize the nutrient composition change in pigs and associated liver from birth to 21 d of age, with the greatest change occurring in the first 7 d.

Key words: pigs, body composition, liver

W197 Evaluating performance of dairy replacement calves housed in different group numbers with the same space/calf. K. Shore* and A. Roy, *Grober Nutrition, Cambridge, Ontario, Canada.*

Pre-weaned dairy replacement calves were evaluated for growth and health differences in different group sizes given the same space/calf (2.2 m^2). Sixty-five calves (40.2 ± 4.2 kg BW; 81 ± 3.3 cm height) were used in a 1-way ANOVA model and randomly assigned at arrival to one of 4 treatments: individual (I) pen (n = 23), paired (P) pen (n = 5; 10 calves), small group (SG) of 6 calves (n = 2; 12 calves), large group (LG) of 11 calves (n = 2; 22 calves). All calves were offered 9 L of milk replacer (1.35 kg of dry matter) on a daily basis. I and P calves were offered milk by pail; SG and LG groups were fed by

automatic calf feeder. All milk refusals were recorded; BW and heights were measured weekly. Health was evaluated daily using an adapted version of the University of Wisconsin calf scoring sheet. Calves were on trial for 10 wk, 8 wk on milk replacer, grain and hay and 2 wk on grain and hay only. Water was offered free choice to all calves. Body weight gain was not different between the groups over the 10 wk (I = 61.6 ± 6.2 kg; *P* = 57.0 ± 10.9 kg; SG = 62.0 ± 12.6 kg; LG = 64.4 ± 7.6 kg). There was no difference in ADG between groups throughout the 10 wk (I = 0.881 ± 0.089 kg/d; *P* = 0.829 ± 0.147 kg/d; SG = 0.885 ± 0.179 kg; LG = 0.920 ± 0.109 kg). There was a difference in height to start, such that I and P pens were taller however by 10 wk there was no difference in height (I = 98.2 ± 1.3 cm; *P* = 98.0 ± 2.4 cm; SG = 97.2 ± 3.2 cm; LG = 98.4 ± 3.1 cm). Health was measured in the number of events throughout the trial period, there was a difference between groups such that I (1.7) and P (1.2) were not different from each other but had less events (*P* = 0.04) than group calves (LG = 2.6; SG = 2.3) (LG and SG were not different). Morbidity was highest in the first 2 wk as was mortality. Mortality was greatest in the P group. In summary, the number of calves in a group when given the same space did not affect growth parameters. The number of health events did not increase with more calves in a group.

Key words: calf, group size, milk replacer

W198 Comparison of moisture determination methods for feed ingredients. J. Y. Ahn*, D. Y. Kil, and B. G. Kim, *Department of Animal Science and Environment, Konkuk University, Seoul, Republic of Korea.*

Accurate determinations of moisture content in feed ingredients and mixed diets are very important in animal nutrition experiments, feed sales, and feed storage conditions. While several methods are available for moisture determination in the literature, an oven method drying at 135°C for 2 h (AOAC Method 930.15) is one of the most widely employed procedures for feed moisture analysis. The objective of the present study is to compare oven-drying methods for determining 'loss-on-drying (LOD)' in feed ingredients and mixed diets. Feed ingredients tested in this study included corn, soybean meal (SBM), distillers dried grains with solubles (DDGS), permeate, whey, spray-dried porcine plasma (SDPP), and fish meal. A diet containing these ingredients was also analyzed for LOD. The LOD contents in these samples were determined by oven drying the samples at 135°C for 2 h or at 105°C for 3 h (NFTA 2.2.2.5) in triplicate. Additionally, the samples were dried at 105°C for 6, 9, 12, or 15 h. Drying the samples at 135°C for 2 h resulted in greater LOD contents in corn (12.3 vs. 11.9%), SBM (10.7 vs. 10.3%), DDGS (12.0 vs. 9.3%), permeate (7.5 vs. 3.1%), whey (8.9 vs. 3.0%), SDPP (7.8 vs. 7.5%), and fish meal (8.1 vs. 7.8%) compared with drying at 105°C for 3 h (*P* < 0.05). After drying the samples at 105°C for 3 h, further drying DDGS, permeate, and whey for 12 more h caused more LOD (1.9, 2.3, and 2.3 percentage units, respectively; *P* < 0.01). It was notable that the DDGS and permeate were considerably darkened by drying at 135°C for 2 h. The LOD contents in the individual ingredients were fairly additive: the difference between the calculated LOD contents in the mixed diet based on ingredient analysis and analyzed values ranged from −0.1 to 0.3 percentage units. Taken together, the method of oven-drying at 135°C for 2 h may be inappropriate for determining moisture content in some ingredients, such as DDGS, permeate, and whey, and thus, in diets containing these ingredients.

Key words: drying methods, feed ingredients, moisture content

W199 The effect of diet and creep feed on feed intake by weanling pigs. J. Shea, D. A. Gillis, and A. D. Beaulieu*, *Prairie Swine Centre, Inc., Saskatoon, SK, Canada.*

A growth lag at weaning may be related to delayed initiation of feed intake. The objective of this experiment was to determine if creep feeding, or phase 1 diet complexity, could alleviate this. Trts, arranged as a 2 × 2 × 3 factorial, were 2 BW groups (heaviest [H] and lightest [L] pigs in a weaning group);creep (CR, weaning groups 1–8) or no creep (NoCR, weaning groups 9–15) and 3 diet regimens (complex d 0 to 1, simple d 2 to 14 [Com1]; complex d 0 to 4, simple d 5 to 14 [Com4] and simple d 0 to 14 [Sim14] post-weaning). Pigs were weaned at 28 d of age. Creep feed (commercial phase 1) was available for 1 wk pre-weaning. The heaviest and lightest pigs (n = 48 /wk, 30% of available) from a weaning group were randomized within BW group to one of the diet trts and housed 4 per pen. Diets met nutrient requirements (NRC 1998) but only the complex diet contained whey, plasma, blood meal and fish meal. BW and ADFI were determined on d 0 (weaning), 1, 4, 7 and 14. Pens were videotaped for 24 h post-weaning and at each diet change to enumerate feeder approaches (head over a feeder) per hour. Data were analyzed as a split plot with creep as a main plot, pens within nursery as sub plots and feeder visits as a repeated measure. Post hoc, feeder visits were separated into active (1 to 6 and 18 to 24 h) and resting phases (7 to 17 h post-feeding). CR pigs were 130 g heavier on d 0 (8.49 kg, *P* = 0.35) primarily due to H pigs (creep by BW, *P* = 0.01). NoCR pigs grew faster overall (0.20 vs 0.17 kg/d; *P* = 0.05). H pigs were heavier than L pigs on d 0 (10.40 vs 6.44 kg; *P* < 0.01) but H pigs lost more weight and had lower ADFI during the initial 24 h post-weaning (*P* < 0.01). Overall ADG was greatest in L pigs (*P* < 0.01). Sim14 pigs lost more BW than Com1 or Com4 on d 0 (*P* = 0.02). ADG, d 0 to 14, and final BW were unaffected by diet (*P* = 0.14). During the first 24 h; NoCR had more feeder approaches than CR (*P* = 0.02) and, significant only during the active phase, L pigs more feeder approaches than H. Com4 pigs had more feeder approaches on d 1 and 4 (*P* = 0.05). Weaning wt, creep feed, and diet regimen had only modest effects on growth post-weaning, in pigs housed with minimal competition.

Key words: swine, creep feed, weaning

W200 Effects of creep feed frequency on pre-weaning and post-weaning growth performance and behavior of piglet and sow. J. H. Cho*, S. Zhang, and I. H. Kim, *Dankook University, Cheonan, Choongnam, South Korea.*

This study was conducted to evaluate the effects of creep feeding frequency on pre- and post-weaning growth performance and behavior of piglet and sows. A total of 30 sows (Landrace × Yorkshire) and their litters were employed in this study. Sows were randomly assigned with 1, 2 or 3 + parities into 1 of 3 treatments. Dietary treatments included: 1) CON (creep feeding 3 times daily), 2) TRT1 (creep feeding 4 times daily) and 3) TRT2 (creep feeding 5 times daily). The behavior of sows (nursery, eating and standing) and piglets (eating, sleeping and fighting) in each treatment was observed throughout the experiment. Each piglet was weighed on d 5, 10, 15, 21 and 7 after weaning to evaluate ADG. Sows and piglets were bled on the weaning day to evaluate the blood characteristic. Backfat and estrus interval were investigated to evaluate the effect of flavor supplementation on the sows. Varying creep feed frequency did not affect the pre-weaning and post-weaning piglet growth performance (pre-weaning: ADG = 214 vs 225, 231 g, ADFI = 15 vs 16, 15 g; post-weaning: ADG = 201 vs 206, 208 g, ADFI = 210 vs 214, 219 g, G:*F* = 0.957 vs 0.962, 0.949; *P* > 0.05). Pigs

with different frequency did not affect ($P > 0.05$) the IgG (427.9 vs 456.2, 472.6 mg/dl), epinephrine (282.3 vs 277.7, 290.4 pg/ml), norepinephrine (886.2 vs 870.0, 868.2 pg/ml) and cortisol (1.93 vs 1.83, 1.97μg/dl) concentration, as well as the post-weaning diarrhea scores and behaviors in the current study. Moreover, creep feeding frequency did not affect ($P > 0.05$) the weanling-to-estrus interval (5.36 vs 5.22, 5.28 d) and backfat loss (3.9 vs 3.4, 3.8 mm) of sows in the current study. Varying dietary frequency did not affect ($P > 0.05$) the cortisol (6.72 vs 6.28, 6.47μg/dl), epinephrine (37.15 vs 34.58, 35.39 pg/ml) and norepinephrine (202.8 vs 191.2, 188.4 pg/ml) in this study. No differences ($P > 0.05$) in eating (18.6 vs 19.4, 18.4%), standing (23.8 vs 25.8, 24.6%), and lying times (57.6 vs 54.8, 57.0%) during lactation were noted in the current study. In conclusion, varying creep feeding frequency did not affect the performance and behavior of piglet and sow in this study.

Key words: behavior, creep feed, frequency

W201 Effect of a partial replacement of limestone by a $CaSO_4$-zeolite mixture combined with a slight protein reduction on production indices, egg quality and excreta pH in laying hens. C. Romero*[1], E. M. Onyango[2], W. Powers[3], R. Angel[4], and T. J. Applegate[5], *[1]Universidad Politécnica de Madrid, Spain, [2]East Tennessee State University, [3]Michigan State University, East Lansing, [4]University of Maryland, [5]Purdue University, IN.*

A commercial diet (CM diet; 17.4% CP and 4.37% Ca) was compared with a diet with 35% replacement of limestone by a $CaSO_4$-zeolite mixture (5.76% $CaSO_4$ and 1.18% zeolite) and a 0.4 percentage units reduction in protein content (RE diet) in laying hens. Apparent N retention, egg production, egg composition and excreta pH were measured. Previous studies demonstrated that the RE diet reduced ammonia emissions by 48%. Laying hens (192 total; 48 replicate cages per diet with 2 hens per cage; 1441 ± 135 g initial BW) were fed experimental diets from 33 to 49 wk of age. Apparent N retention averaged 48.2% ($P > 0.05$). Egg production (83.6%) and number of shell-less eggs (0.18%) were not affected by the diet. Eggs tended to be heavier (59.4 vs. 58.8 g/egg, $P = 0.06$) and yolk percentage (29.7 vs. 29.0%, $P = 0.013$) was greater with the RE diet. At 48 wk of age, the total solids content per egg was also greater from hens fed the RE diet (13.2 vs. 12.6 g/egg, $P = 0.032$). Other egg components were not influenced by diet (58.1% of albumen and 9.04% of shell). Feeding the RE diet resulted in a higher specific gravity (1.0786 vs. 1.0656 g/g, $P = 0.014$) only when hens were 44 wk-old. At the end of the experiment, excreta were collected from all cages (excreta from 3 cages were mixed and pooled; 16 pools of excreta per diet). At collection, excreta of hens fed the RE diet had lower pH (5.89 vs. 6.54, $P < 0.001$) and higher moisture content (74.0 vs. 70.9%, $P < 0.001$) than those of hens fed the CM diet. After 7 d of storage, excreta pH of hens fed the RE diet continued to be lower (6.30 vs. 8.36, $P < 0.001$). A slight reduction in dietary protein and replacing a portion of the Ca from $CaCO_3$ with $CaSO_4$ did not affect egg production nor did it impair shell quality. Feeding the RE diet to laying hens resulted in a reduction in excreta pH, even after 7 d of storage, as compared with laying hens fed the CM diet.

Key words: calcium sulfate, egg quality, protein reduction

W202 Dietary sources of selenium in nulliparous sows: The importance of vitamin B_6 status for some aspects of antioxidant status and ovulation during the peri-estrus period. M. Roy*[1,2], I. Audet[1], M.-F. Palin[1], H. Quesnel[3], F. Guay[2], and J. J. Matte[2], *[1]Agriculture and Agri-Food Canada, Sherbrooke, QC, Canada, [2]Laval University, Québec, QC, Canada, [3]Institut National de la Recherche Agronomique, St-Gilles, France.*

In this experiment, it was hypothesized that there is an interaction between pyridoxine (B_6) and selenium (Se) metabolisms for an adequate flow of organic Se (Se-cysteine) toward the glutathione peroxidase (GPX) system in response to oxidative pressure induced by the peri-estrus period in sows. Forty-five gilts received one of the 5 dietary treatments (n = 9/group): 1) basal diet (Se = 0.2 mg/kg and B_6 = 2.5 mg/kg) (C); 2) # 1 + 0.3 mg/kg Na-Se ($MSe0B_6$); 3) # 2 + 10 mg/kg B_6 ($MSe10B_6$); 4) # 1 + 0.3 mg/kg Se-yeast ($OSe0B_6$) and 5) # 4 + 10 mg/kg B_6($OSe10B_6$). Treatments started at first pubertal estrus and lasted up to 3 d after fourth estrus. Blood was collected from all gilts at each estrus. At slaughter, liver and kidneys were collected and corpora lutea were counted. At fourth estrus, blood Se was lower in C vs Se gilts and higher in OSe's vs MSe's (229.0, 251.2, 250.7, 288.9 and 282.6 µg/L in groups 1, 2, 3, 4 and 5, respectively, SE = 7.3)($P < 0.01$) while blood GPX activity was higher in MSe vs OSe gilts and both were higher vs C's (117.6, 148.3, 145.6, 125.6 and 131.9 mU/mg hemoglobin in groups 1, 2, 3, 4 and 5, respectively, SE = 6.4)($P < 0.01$). In spite of Se effects (as in blood, $P < 0.01$) on Se in liver (0.7, 0.8, 0.7, 1.0 and 1.0 µg/g in groups 1, 2, 3, 4 and 5, respectively, SE = 0.1) and kidneys (2.5, 2.5, 2.4, 2.7 and 2.7 µg/g in groups 1, 2, 3, 4 and 5, respectively, SE = 0.1), there was no treatment effect ($P > 0.50$) on GPX activity in these tissues. However, gene expressions of cytosol GPX (GPX1) and Se-cysteine oxidase (control of the flow of Se-cysteine to the GSH-Px system) in both liver and kidneys were 50 to 70% higher in $OSe10B_6$ gilts than in others (interaction Se x B_6, $P < 0.01$). Ovulation rate were 17.4, 16.7, 17.7, 16.9 and 21.2 (SE = 0.9) in groups 1, 2, 3, 4 and 5, respectively (B_6 effect $P < 0.01$, Se effect $P < 0.06$ and interaction B_6 x Se, $P < 0.09$). In conclusion, dietary B_6 is a modulating factor of the metabolic pathway of organic Se toward the GPX system and may be involved in ovarian function leading to optimal ovulation conditions.

Key words: selenium, vitamin B_6, gilt

W203 Effects of high dietary selenium supplementation on fasting plasma glucose and lipid profiles of young pigs. E. Isaacs*, K. Roneker, and X. G. Lei, *Cornell University, Ithaca, NY.*

Recent animal and human studies have shown an intriguing pro-diabetic, hyperglycemic, or hyperlipidemic effect of high dietary intakes of Se that are suggested for cancer prevention. This experiment was conducted to establish a pig model to determine whether a high Se concentration in a corn-soybean meal basal diet (BD) affected plasma glucose concentrations and lipid profiles. A total of 16 weanling pigs (BW = 7.47 ± 0.78 kg) were divided into 2 groups (n = 8/group) and fed the BD supplemented with 0.3 or 1.0 mg Se/kg (as sodium selenite) for 8 wk. Growth performance and fasting plasma glucose, total triglyceride, and total cholesterol concentrations were measured at initial and then biweekly. Weekly or overall ADG, ADFI, and gain/feed efficiency were similar between the 2 dietary Se concentrations. There was no significant effect ($P = 0.1$) of dietary Se supplementation on fasting plasma glucose concentrations (mg/L) (from Wk 0 to Wk 8 = 1207.9 ± 336.8 to 727.9 ± 84.5 vs. 1359.9 ± 169.7 to 845.6 ± 195.6). Likewise, fasting plasma concentrations of total triglyceride and total cholesterol were not different ($P = 0.85$) between the 2 dietary Se groups. In conclusion, supplementing the corn-soy diet with 1 mg of Se/kg for 8 wk might not be sufficient to alter fasting plasma glucose or lipid profiles of weanling pigs.

Key words: glucose, lipid, model pigs, plasma, selenium

W204 Bioavailability of zinc from zinc propionate in chicks. M. A. Brooks*, J. L. Grimes, S. Verissimo, K. L. Murphy, and J. W. Spears, *North Carolina State University, Raleigh.*

The purpose of this experiment was to evaluate the relative bioavailability value (RBV) of Zn propionate (ZnProp) relative to feed-grade $ZnSO_4$ using body weight gain and bone zinc as response criteria. One hundred day-old Ross chicks were fed a semi-purified starter diet deficient in Zn for 7 d post-hatching (22 mg Zn/kg). Chicks were randomly sorted into one of 5 treatments (n = 20) with 5 replicate pens of 4 birds per pen. The experimental control diet (20 mg Zn/kg) differed from the starter diet in that ground corn replaced approximately 30% of the

dextrose and starch present in the semi-purified starter diet. Using corn in the diet increased the level of phytate, an important Zn antagonist in nonruminant animals. The control diet was supplemented with 0, 6 or 12 mg Zn/kg from feed grade $ZnSO_4$ or ZnProp. Chicks were housed in heated, thermostatically controlled Petersime batteries with raised wire floors and fed the treatment diets from 8 to 21 d. Feed and water were offered ad libitum. Individual body weights and feed intake (by pen) were measured at 7-d intervals for determination of gain, feed intake, and feed efficiency (feed:gain). At the end of the study, tibia bones were excised and used for Zn determination. Zinc RBV was determined using $ZnSO_4$ as a standard source by multiple linear regression and slope-ratio methodology. Analyzed supplemental Zn intake was used in the regression analysis. As supplemental dietary Zn increased, there was a dose dependent increase ($P < 0.05$) in feed intake, weight gain, total Zn intake, tibia Zn concentration and total tibia Zn. Feed efficiency (feed:gain) was poorer ($P < 0.01$) in the control diet (0 mg supplemental Zn/kg) compared with Zn addition to the diet, but did not show a dose response with additional Zn ($P > 0.05$). ZnProp RBV was 119%, 116% and 116% using weight gain, tibia Zn concentration, and total tibia Zn, respectively. RBV was greater than $ZnSO_4$ ($P \leq 0.04$) for total tibia Zn, but was not different in regards to weight gain and tibia Zn concentration ($P > 0.05$). In summary, based on these results, bioavailability of Zn from ZnProp is greater than $ZnSO_4$.

Key words: poultry, zinc, relative bioavailability

W205 Effects of copper concentration and source on performance, bile components, copper metabolism and gastrointestinal microbial distribution in nursery swine. M. A. Arnold*[1], J. S. Schutz[1], K. Sellins[1], R. J. Harrell[2], and T. E. Engle[1], *[1]Department of Animal Science, Colorado State University, Fort Collins, [2]Novus International Inc., St. Charles, MO.*

One hundred twenty weaned nursery pigs (6.12 ± 0.56 kg) were utilized in this experiment to determine the effects of Cu concentration and source on performance, bile components, Cu metabolism, and gastrointestinal microbial distribution in nursery pigs blocked by weight and gender and placed in pens containing 5 pigs of similar weight distribution per pen. Pigs were fed one of 4 dietary treatments for 21 or 22d. Treatments consisted of: 1) Control (5 mg of Cu/kg from CuSO4); 2) 250 mg of Cu/kg from CuSO4, (250-sulfate) 3) 75 mg of Cu/kg from Cu-Mintrex Cu (75-Min; Novus International, Inc., St. Charles, MO), and 4) 75 mg of Cu/kg from CuSO4 (75-sulfate). On d 22 and 23, equal numbers of pigs per treatment were slaughtered. Post slaughter, blood, liver, intestinal tissue and contents, and bile samples were obtained. Body weights, ADG, and ADFI were similar across treatments ($P \geq 0.20$). Feed efficiency was greater ($P \leq 0.05$) for pigs receiving 250-sulfate compared with controls (0.53 vs. 0.43 ± 0.03, respectively), and pigs fed 75-Min (0.47 ± 0.03) or 75-sulfate (0.44 ± 0.03) were intermediate. Pigs receiving 250-sulfate had greater ($P \leq 0.05$) bile (7.05 vs. 2.06 ± 0.49; respectively) and liver (124.4 vs. 53.3. ± 24.6; respectively) Cu concentrations than controls. Bile components, intestinal bacterial populations, and small intestine gene expression profiles (Ctr-1, Atox-1, Cox-17, ATP7a, and ATP7b) associated with Cu absorption and homeostasis were similar across treatments ($P \geq 0.20$). Antimicrobial effects of bile (determined by measuring the diameter of the zone of inhibition; mm) tended ($P \leq 0.20$) to be higher for 250-sulfate and 75-Min treatments compared with controls. Data from this experiment indicated that Cu dose influenced pig performance, but dose or source did not influence measured bile components, intestinal bacterial populations, or intestinal gene expression profiles associated with Cu absorption.

Key words: nursery pigs, performance, copper

W206 Different levels of chelated selenium (Se) addition on the performance, and internal and external quality of Japanese quail eggs. V. C. da Cruz*[1], L. C. Carvalho[1], G. do Valle Polycarpo[2], L. H. Zanetti[1], R. F. de Oliveira[1], D. D. Millen[1], R. G. A. Cardoso[1], A. L. C. Brichi[1], M. L. Poiatti[1], and O. J. Sabbag[1], *[1]São Paulo State University, Dracena Campus, Dracena, São Paulo, Brazil, [2]São Paulo State University, Botucatu Campus, Botucatu, São Paulo, Brazil.*

To evaluate the performance, and internal and external quality of eggs of Japanese quail fed diets supplemented with chelated Se, this study was carried out at the São Paulo State University, Dracena Campus, Brazil. 240 7-wk-old birds were distributed in an entirely random design with 5 treatments (T1: control; T2: 0.25 ppm of Se; T3: 0.50 ppm of Se; T4: 0.75 ppm of Se; T5: 1.00 ppm of Se), 8 replications and 6 birds per cage. Water and feed were ad libitum. The feeding was done twice/d, at 0800 h and at 1800 h, and only the empty feeders were filled up. The light program was 18 h light and 6 h dark, using 60-W incandescent light bulbs. The obtained results for the performance indexes (average egg weight, egg yield, egg mass, feed intake, feed conversion per egg mass and feed conversion per egg dozen) from 0 to 40 d (76-d of age) did not present differences ($P > 0.05$) among the treatments. When the different levels of chelated Se addition on the internal and external quality of quail eggs were analyzed, the Haugh Unit (HU) presented quartic effect ($HU = -1.9E\text{-}06\ x^4 + 0.0003\ x^3 - 0.0192\ x^2 + 0.2530\ x + 93.2758$, $P < 0.05$), and so did the albumen height (AH) ($AH = -3.5E\text{-}07\ x^4 + 6.6E\text{-}05\ x^3 - 0.0036\ x^2 + 0.0451\ x + 5.1615$, $P < 0.05$). The yolk height (YH) presented cubic effect ($YH = 6.3E\text{-}06\ x^3 - 0.0008\ x^2 + 0.0192\ x + 10.3502$, $P < 0.05$), and the shell weight (SW) had linear effect ($SW = -0.0003\ x + 0.8768$, $P < 0.05$), and in all those variables, the best result was observed for the eggs of birds that received only inorganic minerals (control treatment). In the other evaluated variables, specific egg weight, albumen index, yolk index and shell thickness, there were no differences ($P > 0.05$) among the treatments. In the studied levels, the microminerals of associated organic sources do not affect the bird performance. The diet supplementation of quail with chelated Se was inefficient in the improvement of bird performance, but it influences the internal quality of the eggs.

Key words: *Coturnix coturnix japonica*, chelated mineral

W207 Recovery of bone mineralization and strength after a marginal dietary calcium deficiency in growing pigs. L. A. Iwicki*, J. L. Reichert, J. R. Booth, D. K. Schneider, and T. D. Crenshaw, *University of Wisconsin, Madison.*

During recovery from dietary energy or amino acid deficiency, animals compensate by improved efficiency of nutrient use. The objective was to determine if efficiency of dietary Ca and P improved in growing pigs after 5 wk consumption of a diet with marginal Ca deficiency. In the first 5 wk (P1), 40 kg crossbred pigs (n = 72/diet) were fed diets with either 70% (LCa) or 115% (HCa) of Ca required (50 to 80 kg). All diets provided 98% of P requirement. During wk 5 to 10 (P2, 80 to 120 kg), pigs were allotted to either continue LCa or HCa diets or were switched in a crossover design to the opposite diet to provide 4 dietary groups of LLCa, LHCa, HLCa, or HHCa. Selected pigs from each sex and diet group were scanned at 40 (n = 6), 80 (n = 24), and 120 (n = 48) kg using dual energy x-ray absorptiometry (DXA, GE

Prodigy v11.4) to determine whole body bone mineral content (BMC). Scanned pigs were killed, femurs were collected, scanned for femur BMC (FmBMC), and subjected to a 4-point bending test (Instron, model 5566). At 80 kg pigs fed LCa had 15.9% less ($P < 0.01$) BMC, 15.2% less ($P < 0.01$) FmBMC, and 29.9% lower femur bending moment (yBM) than pigs fed HCa. Ca and P efficiency was calculated as g retained (derived from DXA scans) per g consumed. Pigs fed LCa until 80 kg were 23.5% more ($P < 0.03$) efficient in Ca use than pigs fed HCa, but were 29% less ($P < 0.001$) efficient in P use. Over the entire trial no differences ($P > 0.20$) were detected in growth or feed consumption. Pigs fed LLCa had expected reductions ($P < 0.05$) in BMC (13.2%, 1966 v 2265 g), FmBMC (9.0%, 67 v 74 g), and yBM (23.1%, 294 v 382 kg/cm) with improved Ca efficiency (28.7%, 0.71 v 0.55), but a reduction in P efficiency (16.1%, 0.34 v 0.40) compared with pigs fed HHCa. Pigs fed the LHCa or HLCa diets had reduced ($P < 0.05$) Ca efficiency (16.5%, 0.60 v 0.71), but improved ($P < 0.05$) P efficiency (7.1%, 0.36 v 0.34) compared with pigs fed LLCa. No evidence was identified that supported improvement in P efficiency in pigs during recovery from marginal Ca deficiency.

Key words: bone mineral content, P efficiency, bone strength

W208 Ionomic profile changes in the intestine, liver, kidney, serum and gall bladder contents due to Cu source and concentration. B. Aldridge*[1], R. F. Power[2], K. A. Dawson[2], and S. Radcliffe[1], *[1]Purdue University, Department of Animal Science, West Lafayette, IN, [2]Center for Animal Nutrigenomics and Applied Animal Nutrition, Nicholasville, KY.*

Eighty crossbred barrows were weaned at 20 ± 1 d of age and used in 2 blocks (5 reps/block) of a 2 × 3 factorial experiment to investigate the effects of Cu source ($CuSO_4$ and Bioplex Cu (Alltech Inc.)) and concentration (4, 25 or 125 ppm) on ionomic profile concentration changes in the proximal jejunum (PJ), liver, kidney (KD), serum and gall bladder contents (GBC). Pigs were blocked by BW and randomly assigned to diets offered in 2 daily feedings at 9% of metabolic BW ($BW^{0.75}$) per day for a total of 14 d. Samples from the PJ, liver, kidney, serum and GBC were frozen and stored at −20°C until ICP-MS mineral analysis. The PROC MIXED procedure in SAS was used to determine the main effects of Cu source and concentration and their interactions on other mineral concentrations. In addition, PROC GLM linear and quadratic contrasts were determined for increasing supplemental Cu. Pig served as the experimental unit. Increasing Cu concentration did not affect ($P > 0.05$) proximal jejunal [Se], but linearly increased liver [Se] ($P < 0.001$) for both Cu sources. [Se] was decreased ($P < 0.05$) by 30% in GBC when Cu was fed at 125 ppm. Feeding Cu at 125 ppm tended to increase ($P = 0.06$) PJ [Fe], while liver stores were not altered ($P > 0.05$). As dietary Cu increased from 0 to 125 ppm, kidney [Fe] linearly decreased ($P < 0.02$), while at all levels [Fe] was greater when fed Bioplex Cu versus $CuSO_4$. Changes in other mineral GBC include ($P < 0.03$) [Zn] and [Mn] which doubled at the 4 ppm dietary [Cu], when compared with the 25 or 125 ppm level from either Cu source. Zn concentration in the KD increased ($P < 0.001$) when [Cu] was supplemented at 125 ppm, whereas in the liver, Bioplex Cu quadratically altered [Zn] through a reduction of [Zn] at the 25 ppm concentration. This similar trend ($P = 0.1$) was noted in the PJ for both Cu sources.Other altered mineral concentrations include increasing [Co] in the kidney and serum ($P < 0.001$), as dietary Cu increased. These results indicate protagonistic/antagonistic ionomic effects can occur in various organs at select dietary Cu concentrations, which can differ between Cu sources.

Key words: copper, pig, ionomics

W209 Microarray analysis of commonly regulated genes in the jejunum of weanling pigs given dietary Cu proteinate or $CuSO_4$. B. Aldridge*[1], R. Xiao[2], D. Mallonee[2], R. F. Power[2], K. A. Dawson[2], and S. Radcliffe[1], *[1]Purdue University, Department of Animal Sciences, West Lafayette, IN, [2]Center for Animal Nutrigenomics and Applied Animal Nutrition, Nicholasville, KY.*

To illustrate the effect that Cu has on metabolic processes and commonly regulated genes, 2 different types of Cu were used to demonstrate Cu specific cellular pathway changes. Thirty crossbred barrows (n = 10/trt) were weaned at 20 ± 1 d of age and used to determine the effect of a 2 wk supplementation of 0 or 25 ppm Cu from Cu proteinate (Bioplex Cu, Alltech Inc., Nicholasville, KY) or $CuSO_4$ to weanling pig diets on gene expression in the proximal jejunum using microarray analysis. Dietary $CuSO_4$ and Bioplex Cu altered the expression of 545 and 387 genes ($P < 0.05$, FC > 1.2), respectively, compared with control fed pigs. Of these genes, 71 transcripts were commonly altered by $CuSO_4$ and Bioplex Cu, indicating Cu-specific cellular functions.Network pathways of these Cu-specific genes are involved in hematological system development, immune cell trafficking and inflammatory response, and include genes such as modulator of frizzled homolog 4 (FZD4), protein tyrosine phosphatase, protein phosphatase 2 (PPP2R1B), aptoptosis 1 (MOAP1), mitogen-activated protein kinase 3 (MAPK3), chemokine receptor 7 (CXCR7), chemokine ligand 2 (CXCL2) and cytochrome c (CYCS). Additional biological networks altered following Cu supplementation include cellular assembly and organizational pathways, neurological and inflammatory disease, as well as cell death, growth and proliferation. Select genes involved include cyclin A2 (CCNA2), vascular endothelia growth factor C (VEGFC), protein kinase (PKIA), phosphoinositide-3-kinase C3 (PIK3C3), and the Na^+ coupled neutral amino acid transporter 6 (NAT-1). Links to fatty acid metabolic related genes include peroxisomal trans-2-enoyl-CoA reductase (PECR) and the fatty acid transporter SLC27A6. Potential alterations to gut permeability are suggested by altered channel proteins: K^+ large conductance calcium-activated channel (KCNMB1) and gap junction protein (GJA1). These data represents novel commonly regulated pathways between $CuSO_4$ and Bioplex Cu point to Cu specific genes and verify transcriptionally Cu related functions involved in apoptosis, cell signaling and cellular immune responses in swine.

Key words: copper, pig, microarray

Nonruminant Nutrition: Mineral and Sow Nutrition

W210 A lactation curve model in sows. A. V. Hansen*[1,2], A. B. Strathe[1], E. Kebreab[1], and P. K. Theil[2], *[1]Department of Animal Science, University of California, Davis, [2]Department of Animal Health and Bioscience, Faculty of Agricultural Sciences, Aarhus University, Blichers Allé 20, 8830 Tjele, Denmark.*

A quantitative description of the functional form of the sows lactation curve is crucial in understanding energy and nutrient partitioning and for estimation of nutrient requirements. The aim of the investigation was to modify a mathematical function and estimate its parameters from milk yield (MY) measurements. Three Danish studies on sows (Yorkshire x Danish Landrace) were used and MY was measured by D_2O dilution technique. The first study included 4 sows (n = 4) and MY was measured on d 4, 11 and 18 of lactation, in the second (n = 8) MY was measured on d 10, 17 and 24 and in the third (n = 48) MY was measured on d 9, 16 and 23, respectively. The litter size (LS) varied from 5 to 14 piglets while litter weight gain (LG) varied from 0.21 to 4.2 kg/d. A modified Gompertz function ($y(t) = (y_m/t_m) \times t \times \log(t_m \times e/t)$, $0 < t \leq t_m \times e$) was adopted and parameterized to include MY at peak lactation (y_m), the time to peak lactation (t_m) and e is the exponentiation to 1. The function is right skewed, and hence the acceleration in MY to peak lactation is faster than the deceleration in late lactation. The function was implemented in a Bayesian hierarchical model where the parameters describing the between sow variability were modeled as log-normally distributed. Its mean structure included covariates study, LS and LG, which were centered before entering the analysis. Non-informative priors were assigned to the parameters as the likelihood should dominate the posterior. The analysis was conducted in WinBUGS. Parameters y_m and t_m were affected by study, LS and LG ($P < 0.05$) as indicated by the 95% credible intervals. The mean MY at peak lactation was 12.7 (12.1; 13.2) kg/d at d 21 (19; 22) and the associated between sow variability in ym and tm was 15% and 24%, respectively. The following relationships were established between parameters and LS and LG ($y_m = \exp(2.54_{(SE:0.02)} + 0.043_{(SE:0.02)} \times (LS-11) + 0.23_{(SE:0.05)} \times (LG-2.7))$) and (($t_m = \exp(3.02_{(SE:0.04)} + 0.027_{(SE:0.03)} \times (LS-11) + 0.74_{(SE:0.09)} \times (LG-2.7))$), which is applicable in predicting MY in sows with known LS and LG. The data analysis also revealed that although LS and LG affected y_m their effects on the shape of the lactation curve were minor.

Key words: milk production, Gompertz, sows

W211 Impact of ergot infested sorghum on the reproductive performance of sows. G. M. Abdelrahim*[1], R. C. Richardson[2], and A. Gueye[3], *[1]Alabama A&M University, Normal, [2]Texas State University, San Marcos, [3]Mt. Ida College, Newton, MA.*

The objective of this research was to evaluate effects of ergot infested sorghum (EIS) in sows' diets on animal and reproductive performance throughout 2 parities, including number of live born pigs (LBP), weight of live born pigs (WLBP), survival of pigs at d 28(S- 28 d), weight gain of pigs at d 28 (W- 28 d), weight gain at d 56 (W- 56 d), lactation feed intake (LFI), lactation weight change (LWC), and weaning-to-estrus interval (WEI). Total alkaloid concentration in the mature ergot sphacelia/sclerotia was 235 mg/kg (77% as dihydroergosine). In the experiment, 18 later-parity sows (BW = 155 ± 17 kg; n = 18) stratified by BW (n = 6 sows/diet) were fed 3 treatments consisting of a sorghum-based control diet mixed with 1) 0% EIS; 2) 5% EIS and 3) 10% EIS (which equaled 0, 11.75 and 23.50 mg/kg, respectively). There was no effect ($P > 0.05$) on LBP, S- 28 d, W- 56 d, and LWC when we fed up to 10% EIS to sows during the first and second parity; similar results were obtained when LBP, S- 28 d, W- 56 d, and LWC data of the 2 parities were combined. An increase in WLBP was observed ($P < 0.05$) when 5- 10% EIS was included in the second parity's diets, although LFI was significantly ($P < 0.05$) reduced when EIS was included in that parity's diets. Although W-28 d was not affected when 10% EIS was included in the first and second parities' diets and when W-28 d data of the 2 parties were combined ($P > 0.05$), piglets weight gain at 28 d was reduced ($P < 0.05$) when 5% EIS was included in the first parity's diet and when W-28 d data of the 2 parities were combined ($P < 0.05$) Although, treatment diets did not affect ($P > 0.05$) WEI of pigs in the second parity and when WEI of the 2 parties were combined ($P > 0.05$), and no response ($P > 0.05$) was recorded when 5% EIS was fed during the first parity, the inclusion of 10% EIS had significantly decreased the WEI ($P < 0.05$). Overall, variables that were affected by the inclusion of ergot sclerotia in the diets were WLBP, W- 28 d, LFI, and WEI.

Key words: ergot alkaloids, sows reproductive performance, sorghum

W212 Improved retention rates and reduced culling for lameness for sows fed a chelated trace mineral blend. J. Zhao*[1], L. Greiner[2], G. Allee[3], M. Vazquez-Anon[1], C. D. Knight[1], and R. J. Harrell[1], *[1]Novus International Inc, St Charles, MO, [2]Innovative Swine Solutions, Carthage, IL, [3]University of Missouri, Columbia, MO.*

Our objectives of this study were to improve sow retention rates by feeding a chelated trace mineral blend (Mintrex, Novus) from weaning and continuing through the reproductive phases. Two sister sow farms with a common grandparent farm were used. One farm was fed an inorganic control (ITM) and the other was fed a Mintrex blend (Zn, Mn, and Cu), which replaced 50% of the ITM, with target supplementation levels of Zn, 165 ppm, Cu, 16 ppm, and Mn, 38 ppm in the final diet. Replacement gilts were blocked by group on the basis of each monthly supply of weaned gilts. The group of sows was the experimental unit for statistical analyses. Results indicated that gilts fed Mintrex (n = 10,725) had lower removal rates than gilts fed ITM (n = 10,729) from first service to farrowing (8.0% vs. 8.8%, $P = 0.04$). Subsequent retention rates were analyzed for sows that were on treatment from weaning to parity 4 (n = 3994 and 4418 for Mintrex vs. ITM, respectively). Sows fed Mintrex had higher ($P < 0.01$) retention rates than sows fed ITM at both Parity 3 and Parity 4 (72.1% for sows fed Mintrex and 63.5% for those fed ITM, respectively). The involuntary removal rate and relative removal rate due to locomotion were reduced with Mintrex supplementation. In gilts, relative removal rates due to locomotion were 9.0 vs 13.8% ($P < 01$) for Mintrex and ITM, respectively. The involuntary removal rates were reduced ($P < 0.01$) for gilts fed Mintrex (17.3%) compared with gilts fed ITM (27.1%). Similar results were observed in sows in that removal rates due to locomotion were reduced by 55% with Mintrex supplementation (10.4% vs. 16.1%; $P < 0.01$) compared with sows fed ITM. The involuntary removal rates were reduced by 45% with Mintrex supplementation (19.4 vs 28.1%; $P < 0.01$) compared with sows fed ITM. Overall mortality was reduced with 8.6% mortality for sows fed Mintrex and 10.4% for those fed the control. In summary, Mintrex is beneficial for maintaining sow skeletal health and improving welfare assessed by higher survival rates to parity 4 and lower removal rates due to locomotion.

Key words: sow, lameness, chelated trace mineral

W213 A blend of chelated trace minerals improved sow cumulative reproduction and farrowing rate. J. Zhao*[1], L. Greiner[2], G. Allee[3], M. Vazquez-Anon[1], C. D. Knight[1], and R. J. Harrell[1], *[1]Novus International Inc., St Charles, MO, [2]Innovative Swine Solutions, Carthage, IL, [3]University of Missouri, Columbia.*

In many commercial units sow output falls considerably short of the potential to produce weaned piglets per her lifetime, with over 50% of sows culled before reaching their third or fourth parity. Our objectives were to determine if feeding a chelated trace mineral blend (Mintrex®, Novus International Inc.) from weaning and throughout the reproductive phases in commercial farms would improve farrowing rates and cumulative reproductive performance. Two sister PRRS-stable sow farms (6,400 sows each) using PIC C22 and C29 genetics with a common grandparent farm were fed either an inorganic control (ITM) or a Mintrex blend (Zn, Mn, and Cu), which replaced 50% of the ITM, with target supplementation levels of Zn, 165 ppm, Cu, 16 ppm, and Mn, 38 ppm in the final diet. Replacement gilts were blocked by group on the basis of each monthly supply of weaned gilts. The experiment was conducted for 3 years from April 2007 to April 2010. To calculate cumulative reproduction performance up to parity 4, only sows within groups that were old enough to produce at least 4 parities were included in the data analyses. This included a total of 8,412 sows for the analyses. Farrowing rate was improved 2.3 percentage units with Mintrex supplementation (86.8% vs. 84.5% for Mintrex and ITM, respectively, $P < 0.001$). The benefit was observed across parities except in parity 2 with farrowing rates of 86.4% vs. 83.6%, 84.9% vs. 83.9%, 87.7% vs. 85.8%, and 88.9% vs. 85.4% from parity one to parity 4 for Mintrex vs. ITM, respectively. Sows fed Mintrex had more total born (44.1 vs. 40.8, $P = 0.02$) and born alive (41.6 vs. 38.9, $P = 0.04$), and tended to have more weaned pigs (36.4 vs. 34.6, $P = 0.07$) compared with those fed ITM. Presence of mummies was not affected by treatment (0.69 vs. 0.67, $P = 0.47$). Sows fed Mintrex had more stillborns compared with sows fed ITM (1.8 vs. 1.2, $P < 0.01$). In summary, sows fed Mintrex had higher farrowing rates and better cumulative production performance up to parity 4.

Key words: sow, chelated trace mineral, reproduction

W214 Improved progeny performance from sows fed a chelated trace mineral blend. J. Zhao*, M. Vazquez-Anon, C. D. Knight, and R. J. Harrell, *Novus International Inc, St Charles, MO.*

Our previous study indicated sows fed Mintrex produced heavier piglets at birth compared with sows fed inorganic mineral. We hypothesized that piglets with heavier birth weights should perform better from weaning to market weight. Trial design consisted of a 2*3 factorial arrangement with 2 progeny sources from sows fed either inorganic trace minerals (ITM) or Mintrex and 3 dietary mineral programs. The 3 dietary mineral programs included an ITM or Mintrex supplementation at 50% of NRC levels (Zn 50 mg/kg, Mn 2 mg/kg, and Cu 3 mg/kg), and ITM at 2X NRC levels. A total of 2400 weanling pigs (PIC, 20 d of age, 6.07 ± 0.07 kg) were randomly allotted to 6 treatments with 16 replications per treatment and 25 pigs per pen. Data was analyzed by PROC GLM for main effect of progeny, dietary minerals, and 2-way interaction. No interaction of progeny source and dietary mineral treatment was observed on performance or carcass traits ($P > 0.10$). Overall, no differences were observed among pigs fed the 3 different dietary mineral programs ($P > 0.10$). The main finding in this trial was the effect of progeny source. No differences were observed in starting pig weights (20 d of age, $P = 0.27$) between progeny source. However, compared with progeny from sows fed ITM, progeny from Mintrex sows were heavier by d 10 post-weaning (8.09 vs. 7.25 kg, $P < 0.01$) and remained heavier until the end of the study on d 161 (118.5 vs. 116.5 kg, $P = 0.02$). During the nursery period (d 0–42), Mintrex progeny ate more ($P < 0.01$), gained more ($P < 0.01$) and were 2.5 kg heavier at the end of nursery ($P < 0.01$) compared with pigs from sows fed ITM. Overall (d 0–161), progeny from sows fed Mintrex ate more (1.75 vs. 1.72 kg/day, $P < 0.01$), gained more (0.701 vs. 0.686 kg/day, $P < 0.01$) and tended to have greater loin depth (47.3 vs. 45.6 cm^2, $P = 0.09$) compared with progeny from sows fed ITM. No treatment differences were observed on G:F, carcass yield, and meat quality traits ($P > 0.10$). In summary, progeny from sows fed Mintrex performed better and had greater loin depth than piglets from sows fed ITM and demonstrates that sow mineral source affects their progeny performance.

Key words: pig, Mintrex, trace mineral

W215 Comparison of serum progesterone concentrations from new and used CIDR in Holstein heifers. J. T. Whitley* and C. S. Whisnant, *North Carolina State University, Raleigh.*

The aim of the present study was to determine the progesterone release and concentrations of used Eazi-Breed CIDR (CIDR) devices when compared with new/unused CIDR's. Although used CIDR have been utilized in synchronization protocols data comparing progesterone (P4) concentrations are limited. Pubertal Holstein heifers (13–14 mo of age, 375 ± 11.5 kg BW) were used and randomly assigned to receive either a new (n = 7) or used CIDR (n = 7). A used CIDR in this study was one that was previously removed in a cow for a period of 7 d, removed, washed, and stored. Washing was done by first rinsing with water followed by rinsing with Nolvasan and being allowed to air dry. Storage was in a climate controlled room in a closed drawer. CIDR was inserted 24 h after treatment with prostaglandin F2 α to induce luteolysis. Blood samples were taken by tail vein puncture at 4 times: just before the CIDR was inserted, 1 h later, 24 h later and finally when the CIDR was removed at the end of 7 d. Blood samples were placed on ice for transport and centrifuged, with serum stored at −20°C until assayed for P4 concentrations using a commercially available RIA validated in our laboratory for use with bovine serum. Data were analyzed using PROC GLM of SAS 9.2 for type of CIDR (new vs. used), time and the time by type of CIDR interaction. Serum P4 concentrations (ng/mL) were not different between types of CIDR (Table 1). Serum P4 concentrations increased ($P \leq 0.01$) from time of insertion to 1 h later and remained elevated at all other times. Both new and used CIDR provided a rapid and sustained increase in serum P4 concentration in Holstein heifers.

Table 1.

CIDR	Time 0	1h	24h	7d
NEW[a]	0.6 ± 0.2	4.2 ± 0.5	5.3 ± 0.6	5.1 ± 0.5
USED[a]	0.7 ± 0.2	4.6 ± 0.5	4.8 ± 0.4	4.4 ± 0.6

[a]P4 concentrations ng/mL.

Key words: progesterone, CIDR, heifer

W216 Correlation between residual feed intake and metabolic parameters of Nellore heifers. R. H. Branco[1], E. Magnani[1], L. T. Egawa[1], T. L. Sobrinho[2], S. F. M. Bonilha[1], M. E. Z. Mercadante*[1], J. N. S. G. Cyrillo[1], and L. A. Figueiredo[1], *[1]Instituto de Zootecnia, Sertãozinho, São Paulo, Brasil, [2]Faculdade de Ciências Agrárias e Veterinárias, Jaboticabal, São Paulo, Brasil.*

Selection against residual feed intake (RFI) has the potential to improve feed efficiency without affecting growth performance or body size, but measuring this trait in cattle is costly. Identification of RFI physiological indicators may facilitate early detection of more efficient heifers. The objective of this study was to examine correlations among RFI, growth performance and metabolic parameters. Nellore heifers (n = 32) from Instituto de Zootecnia – Sertãozinho, São Paulo, Brazil, with averages of 364 kg for BW and 502 d for age were evaluated. Animals were classificated for RFI: low RFI (≤mean + 0.5 SD; n = 17) and high RFI (≥mean + 0.5 SD; n = 15). Creatine phosphokinase, IGF-I, leptin and cortisol were analyzed. Pearson correlations among variables were calculated by CORR procedure of SAS, and significant correlation between RFI and DMI (Table 1) was found. However, RFI was not correlated with ADG, once the animals classified as more or less efficient show no difference in the gain. Also correlations between RFI and metabolic parameters were not detected. Cortisol was negatively correlated to leptin, suggesting that animals under stress have lower intake, since the increase in serum cortisol levels lead to reductions in leptin, and this related to the regulation of energy metabolism and feeding behavior. In this study, the animals were not subjected to stress. Thus, more research is needed to identify physiological and genetic markers, which can explain the variations in the physiological bases of the RFI.

Table 1. Pearson correlations among metabolic parameters blood and efficiency measures in Nellore heifers

	ADG	RFI	CPK	IGF-I	LEP	CORT
DMI	0.078ns	0.60**	−0.42*	0.079ns	−0.35ns	0.17ns
ADG		0.074ns	0.38ns	0.098ns	−0.057ns	0.33ns
RFI			−0.19ns	−0.027ns	0.026ns	0.068ns
CPK				0.10ns	0.21ns	0.04ns
IGF-I					−0.07ns	0.06ns
LEP						−0.52**

ns: $P > 0.1$; *$P < 0.05$; **$P < 0.01$; ***$P < 0.0001$. CPK=creatine phosphokinase; LEP=leptin; CORT=cortisol.

Key words: beef cattle, efficiency, metabolism

W217 Follicular and ovulatory responses following superovulation treatment with rFSH and HMG in dairy cattle. M. Poorhamdollah*[1], H. Kohram[1,2], and A. Nejati-Javaremi[1], *[1]Department of Animal Science, Faculty College of Agriculture and Natural Resources, University of Tehran, Karaj, Iran, [2]Department of Clinical Sciences, Faculty of Veterinary Medicine, Shahid Chamran University, Ahvaz, Iran.*

The unpredictability in the FSH/LH ratio of gonadotropin preparations is considered to be a factor causing variability of superovulatory responses. The aim of this study was to investigate the superovulatory responses in terms of follicular and ovulatory responses during a superovulatory treatment with rFSH and HMG together. Five Holstein dairy cows were selected randomly from the university herd. The estrous cycles were synchronized by 2 successive injections of PGF2α (vetglan, cloprostenol, Aburaihan, Iran) 11 d apart. Treatments for superovulation were initiated between d 9 to 14 of the estrous cycles with 10 successive injections of 4 shots of rFSH (Gonal-F, Follitropin α, Serono, Switzerland) and 6 shots of HMG (human menopausal gonadotropin, Merional, hFSH-hLH, IBSA, Lugano) at 12-h intervals. A single prostaglandin F2α injected with the 4th injection of HMG. The ovaries of all cows were examined by ultrasonography (B mode; Pimedical, Falco 100, 8 MHz) on d 9 (day of initiation of the superovulatory treatment), 10, 11, 12, 13, 14 (day of estrus following superovulation) for follicular and ovulatory response, and 7 d after estrus for number of CL and number of non-ovulation follicles. All follicles measured at their largest diameter size. The results showed that the mean number of large follicles (≥7mm) at estrus, CL and non-ovulation follicles at 7- days after estrus were 11.2 ± 1.8, 9.4 ± 1.5 and 1.8 ± 0.8, respectively. There was a high positive correlation (84 and 58%) between the number of CL and the mean number of large follicles at estrus and the number of small follicles (≥4mm) at initiation day of

superovulatory treatment (d 9), respectively. In conclusion, there was a high ovulatory response, high positive correlation between number of ovulated follicles at estrus and numbers of CL 7 d after estrus. Also, the homogeneity between follicles following superovulatory treatment when rFSH and HMG are used together for inducing superovulation was high.

Key words: superovulation, Gonal-f, HMG

W218 Adipocyte cell turnover in subcutaneous fat of heifers related to adipocyte cell size. D. Germeroth, S. Häussler*, H. Akter, and H. Sauerwein, *University of Bonn, Germany.*

Adipose tissue mass results not only from adipocyte volume, but also from their number, the latter being determined by cell proliferation and cell loss. In humans, adipocytes probably perish with increased size through apoptosis. In obese subjects apoptosis is presumably overcompensated by emergence of new cells. We hypothesized that the rate of apoptosis and cell proliferation in cattle might depend on adipocyte size. Subcutaneous tailhead fat was collected from 12 non-lactating, non-pregnant Simmental heifers (mean BCS = 5) and from 25 early lactating (d 1 to 105 in milk) Holstein heifers (mean BCS = 3) from different feeding trials. Deparaffinized sections (12 µm) were used for apoptosis detection (TUNEL method); cell proliferation was characterized on cryosections (14 µm) using Ki67-staining. Bovine lymph nodes (apoptosis) and liver (Ki67) were used as positive and negative controls. The portion of apoptotic and proliferating cells was calculated from the mean number of positive stained cells/mean number of total cells x 100. Parametric (Students t-Test) and non-parametric (Mann-Whitney-U-test and Spearman's Rank correlation) tests were used to evaluate the data (SPSS), differences were considered significant at $P \leq 0.05$. The adipocytes from Simmental were larger ($p \leq 0.001$) than from Holstein heifers with mean areas of 8230 ± 240 µm^2 and 5146 ± 491 µm^2, respectively. Adipocyte area and apoptotic portion were negatively correlated ($r = -0.614$; $p \leq 0.001$), represented by a higher apoptotic portion for heifers having small adipocyte size (11.37 ± 2.21%) compared to animals with larger ones (1.03 ± 0.59%). In addition, low cell proliferation rates were observed in both Simmental (0.43 ± 0.44%) and Holstein (0.02 ± 0.01%) heifers. Reduction of adipocyte size as observed in early lactating heifers seems to be accompanied by increased apoptosis in fat cells. This loss of cell number is nowhere near enough compensable by cell proliferation. In conclusion, the rate of apoptosis rather than cell proliferation depends on adipocyte size in cattle.

Key words: apoptosis, cell proliferation, adipocyte size

W219 Effect of short-term supplementation and temporary weaning on follicular liquid composition in first-calved Hereford cows. L. Veloz[1,2], M. E. Trobo[1,2], C. García Pintos[1,2], C. Viñoles[2], and M. Carriquiry*[1], *[1]School of Agronomy, UdelaR, Montevideo, Uruguay, [2]National Research Institute for Agriculture, Tracuarembó, Uruguay.*

To evaluate the effects of short-term supplementation and temporary weaning on follicular fluid composition, first calved Hereford cows (n = 32, 388 ± 7 kg BW and 3.6 ± 0.2 units of BCS, scale 1–8) in anestrus and their calves (120 ± 2 kg BW) were used in a randomized block design with a 2 × 2 factorial arrangement of supplementation (SUP vs. CON), and temporary weaning (with and without), before initiation of the breeding period (103 ± 1 d postpartum). The supplement (2.5 kg/cow of rice bran, 90.3% DM, 10% CP, 9% EE, 14% NDF) was fed daily for 23 d and calves were temporary weaned by applying nose plates for 14 d. Cows were injected with 3 prostaglandin (PG) injections 11 d apart. Thirty-six hours after the last PG injection, cows were castrated and all follicles >5 mm were dissected and follicle fluid was aspirated to determine metabolite and hormone composition. Means from a mixed analyses were considered to differ when $P < 0.05$. Follicle size did not differ among groups and averaged 7.0 ± 0.5 mm. Concentrations of estrogen tended ($P = 0.08$) to increase with suckling restriction (4651.1 vs. 1155.2 ± 1777.3 pmol/L). In contrast, progesterone concentrations tended ($P = 0.10$) to increase with supplementation (102.6 vs. 147.0 ± 18.5 ng/mL). The estrogen/progesterone ratio tended to increase ($P = 0.08$) with suckling restriction (34.1 vs 10.0 ± 14.3). Glucose concentrations were greater in SUP than CON cows (50.8 vs. 57.6 ± 2.5 mg/dL) and suckling restriction tended ($P = 0.08$) to increase glucose in follicular fluid (56.6 vs. 51.7 ± 2.5 mg/dL). Follicular fluid concentrations of NEFA and cholesterol were not affected by nutritional treatment, suckling restriction, or their interaction. Concentrations of estrogen, glucose, and cholesterol as well as the ratio estrogen/progesterone increased with follicle size. In conclusion, nutrition and/or suckling restriction before initiation of the breeding period, in primiparous beef cows in grazing conditions, affected the microenvironment of follicles which could affect reproductive performance

Key words: nutrition, suckling control, ovary

W220 Estrus quantification of early lactation cow cervix physiology: An economical farm innovation. A. Nikkhah*, M. A. Sirjani, and A. A. Assadzadeh, *University of Zanjan, Zanjan, Iran.*

The objective was to quantify cow cervix morphology during estrus phases. Cervix distinctness, central positioning, motility and mucosal secretions were scored daily on a 5-scale basis during proestrus (PE), standing estrus (SE), diestrus (DE) and metestrus (ME) phases in 4 black-white multiparous Holstein cows (50 ± 14 d in milk, 31 ± 3.6 kg milk yield, 643 ± 66 kg BW, 3.0 ± 0.18 BCS) on multiple occasions (n = 8). The design was a split-plot with estrus phases as plots. The cervix was video-recorded using a farm apparatus of 45 cm length and 2.7 cm diameter, with internal electrical settings, external polyvinyl cover, front lights, and terminal wires connected to a laptop computer with an image processing program. The score of 1 represented cervices with fully distinct, central, stable, and mucosal manifestation, and the score of 5 described fully non-separate, non-central, motile, and non-mucosal cervices. Data were analyzed as mixed models with fixed effect of estrus phase (plot) plus random effects of 'cow within phase' and residuals. Regression was used to relate changes of rectal temperature (RT) and cervix morphology. Results demonstrated a significant ($P < 0.01$) differential order, for SE > PE > DE > ME of an increased cervix distinctness (1.00, 1.20, 3.10, 3.62), greater central positioning (1.13, 1.50, 3.73, 4.15), greater stability (decreased motility) (1.00, 1.50, 2.58, 4.33), and greater mucosal secretions (1.00, 1.50, 3.88, 4.13), respectively, on SE vs. non-SE. The RT was not different ($P = 0.51$) among ME, DE, PE and SE, respectively (38.66, 38.33, 38.58, and 38.83°C ± 0.22). Minor links were found between RT and cervix morphology on SE vs. non-SE phases ($P > 0.20$), except for cervix central positioning (y) and RT (x) changes during ME vs. SE ($y = 3.34 - 1.9\ x$)($P = 0.07$). The innovative method proves to be easily applicable to differentiate cervices on different estrus phases in dairy cows. Its cost-effectiveness (<200 $US) encourages further research on monitoring reproductive tract health and physiology.

Key words: estrus, physiology, quantification

W221 Effects of maternal metabolizable protein level in late gestation on circulating amino acid concentrations in the ewe and the fetus. L. A. Lekatz*[1], M. L. Van Emon[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.*

We have previously reported that feeding 60% of MP requirements during the last third of gestation decreases fetal weight, without altering placental weight, compared with controls by d 130. We hypothesize this fetal weight reduction is due to a decrease in circulating amino acids. Our objective was to examine the effects of maternal MP level during late gestation on circulating amino acid concentrations in the ewe and fetus. Multiparous ewes (n = 11) carrying singletons were assigned with receive an isocaloric diet with 60% (60, n = 4), 80% (80, n = 4), or 100% (100, n = 3) of MP requirements from d 100 until d 130. At surgery on d 130, blood was collected from the maternal saphenous artery (maternal artery, MA), uterine vein of the pregnant horn (UVP), umbilical vein (UMBV) and umbilical artery (UMBA) and amino acids were analyzed. In the MA, Gly was lower ($P = 0.04$) in the 100 compared with the 80 and 60 ewes (226 vs. 369 and 408 ± 46.1 nmol/ml). In the UVP, Ser, Gly, and Gln were each lower ($P \leq 0.04$) in the 100 compared with the 80 and 60 ewes (27.3 vs. 38.0 and 40.9 ± 2.91 nmol/ml, 178 vs. 367 and 417 ± 60.8 nmol/ml, and 192 vs. 229 and 246 ± 11.4 nmol/ml for Ser, Gly, and Gln, respectively). In the UMBV, Gly was lower ($P = 0.04$) and Val was greater ($P = 0.04$) in the 100 compared with the 80 and 60 ewes (429 vs. 734 and 648 ± 74.9 nmol/ml and 323 vs. 235 and 175 ± 36.4 nmol/ml for Gly and Val, respectively). In the UMBA, Gly was lower ($P = 0.02$) and Leu was greater ($P = 0.03$) in the 100 compared with the 80 and 60 ewes (388 vs. 641 and 595 ± 56.7 nmol/ml and 219 vs. 132 and 101 ± 28.0 nmol/ml for Gly and Leu, respectively). Also, Val and Ile were greater ($P \leq 0.05$) in the 100 compared with the 60 ewes (302 vs. 156 ± 33.3 nmol/ml and 113 vs. 50.0 ± 16.0 nmol/ml, for Val and Ile, respectively), with the 80 ewes being intermediate (214 ± 33.3 nmol/ml and 69 ± 16.0 nmol/ml for Val and Ile, respectively). Overall, it appears that decreasing maternal MP from 100% to 80 or 60% of requirements alters amino acid concentrations in both maternal and fetal circulations.

Key words: amino acids, metabolizable protein, pregnancy

W222 Functional genomics and role of integrin beta 5 in cattle fertility. L. Koenig[1], X. Wang[1], A. Kaya[2], S. Bridges[1], and E. Memili*[1], *[1]Mississippi State University, Mississippi State, [2]Alta Genetics, Inc., Watertown, WI.*

Fusion of male and female gametes at the fertilization is one of the most important events in mammalian developmental biology. Integrins play multiple roles in fertilization, embryogenesis, and implantation. We recently identified a single nucleotide polymorphism in Integrin Beta 5 (ITGB5) associated with bull fertility. Functional significance of this mutation and roles of ITGB5 in fertilization and early embryogenesis are not known. The objectives of this study were to: 1) identify conserved sequence domains and motifs between bovine ITGB5 protein with mouse, human, dog, and rat ITGB5 proteins, 2) determine expression patterns of itgb5 transcripts in bovine oocytes and early embryos and analyze the results using one way analyses of variance (ANOVA), and 3) determine ITGB5 protein expression in sperm from bulls of varying fertility. Comparative functional genomics, reverse transcriptase real time PCR, and immunoblotting were used to accomplish our objectives. Our results showed that 1) There is an extraordinary degree of conservation (>90% identity of amino acid sequences) of ITGB5 across the mammals indicating that this protein may serve a very important functional role in many species, 2) Transcripts of ITGB5 were highly expressed in bovine oocytes and early embryos; highest expression was at the 2-cell ($P < 0.05$), and 3) ITGB5 protein was detectable in bull spermatozoa. These results provide molecular evidence that ITGB5 is expressed in bovine gametes and embryos and might play important roles at the onset of mammalian development. The findings will help us better understand early mammalian development and identify molecular biomarkers for fertility.

Key words: cattle, fertility, integrin

W223 Male goat vocalizations stimulate LH secretion and estrous behavior in sexually experienced but not in sexually inexperienced goats. J. A. Delgadillo*, J. Vielma, H. Hernández, J. A. Flores, G. Duarte, I. G. Fernández, and G. Fitz-Rodríguez, *Centro de Investigación en Reproducción Caprina, Universidad Autónoma Agraria Antonio Narro, Torreón, Coahuila, Mexico.*

The objective of the current study was to determine the response of sexually inexperienced and experienced goats to buck vocalizations by measuring their secretion of LH and estrous behavior. Males (n = 3) were rendered sexually active during the non-breeding season by exposure to 2.5 mo of long days (16 h of light by d) from November 1st. From 20 d of age, females were isolated from any auditory, visual and tactile cues from males so that, once in adulthood, they had no sexual experience. By contrast, a group of females had visual, auditory, olfactory and tactile contact with male goats, but copulations were prevented by a fence. On April 4th (d 0; 11:00 h) a stimulus group (n = 5) of anestrous females was exposed to photoperiod treated males in a light proof-building; under these conditions, males produced vocalizations that were reproduced through a microphone-amplifier-loudspeaker system. The anestrous sexually inexperienced and experienced groups (n = 6 each, females had 15 mo of age,) were kept in 2 open pens and exposed during 5 consecutive days to the buck vocalizations coming from the males exposed to stimulus females. LH pulsatility was determined every 15 min from 4 h before to 8 h after introducing the males. Behaviors were recorded twice daily. The LH pulses frequency was analyzed by a 2-way ANOVA with repeated measurements (group and time). The estrous behavior was compared by the Fisher exact test. The number of LH pulses did not differ between sexually inexperienced and experienced goats before exposition to vocalizations of bucks (0.4 + 0.2 in both groups; $P > 0.05$). In contrast, vocalizations induced an increase of pulses of LH in experienced (1.7 + 0.4) but not in inexperienced females (1.0 + 0.3; $P < 0.05$). The frequency of mounting attempts (50) and the acceptance of mounts (36) were greater in experienced than in inexperienced females (1 and 7, respectively; $P < 0.01$). These results indicate that the lack of sexual experience of females is associated with low endocrine and behavioral responses to buck vocalizations.

Key words: caprine, sexual behavior, endocrine activity

W224 Profiling bioenergetics and metabolic stress in cells derived from commercially important fish species. B. Beck* and A. Fuller, *Stuttgart National Aquaculture Research Center, Stuttgart, AR.*

As organisms intimately associated with their environment, fish are sensitive to numerous environmental insults which can negatively affect their cellular physiology. For our purposes, fish subject to intensive farming practices can experience a host of acute and

chronic stressors such as changes in dissolved oxygen, temperature, and water quality; all of which can result in metabolic perturbations on a cellular level. Thus, in the present study, we sought to further our understanding of cellular metabolism in fish and to examine the stress response of cells derived from commercially relevant fish species (catfish, white bass, fathead minnow). We employed a Seahorse Bioscience XF24 Extracellular Flux (EF) Analyzer, an instrument which detects changes in oxygen (O2) levels and pH within the media directly surrounding cells. By measuring the O2 consumption rate (OCR), an indicator of mitochondrial respiration, we determined that all cells tested exhibited a markedly aerobic phenotype (OCR > 100 pMol/min). Simultaneously, we measured the extracellular acidification rate (ECAR), an indicator of glycolysis, and found that in all cell lines tested the ECAR was very low (<5 mpH/min). Next, we performed a mitochondrial function protocol whereby compounds modulating mitochondrial respiration were sequentially exposed to cells (oligomycin→FCCP→rotenone). For each cell type, this assay provided us with basal and maximal OCR, O2 consumption dedicated to ATP production, O2 consumption from ion movement across the mitochondrial inner membrane, the reserve respiratory capacity, and O2 consumption independent of Complex IV of the electron transport chain. From these informative bioenergetic parameters we generated distinct metabolic signatures for each cell type. These findings are the first description of EF technology employed on fish cell lines and provide key proof-of-concept data demonstrating the utility of fish cells as tools for modeling bioenergetics. We hope to extend these findings to develop assays predictive of how fish may cope with cellular insults encountered in production settings.

Key words: extracellular flux, mitochondria, bioenergetics

W225 Conjugated linoleic acid and rosiglitazone attenuate lipopolysaccharide-induced TNF-α production by bovine immune cells. M. C. Perdomo and L. Badinga*, *University of Florida, Gainesville.*

Lipopolysaccharide (LPS) modulates innate immunity through alteration of cytokine production by immune cells. The objective of this study was to examine the effect of exogenous conjugated linoleic acid (CLA) and peroxisome proliferator-activated receptor gamma (PPAR-γ) agonist, rosiglitazone, on LPS-induced tumor necrosis factor α (TNF-α) production by cultured blood from prepubertal Holstein heifers (mean age = 5.5 mo). Compared with unstimulated cells, addition of LPS (10 μg/mL) to the culture medium increased peripheral blood mononuclear cell (PBMC) proliferation up to 2.5-fold. Co-incubation with interferon gamma (IFN-γ, 5 ng/mL) further stimulated ($P < 0.01$) the proliferative response to LPS. Lipopolysaccharide increased ($P < 0.01$) TNF-α concentration in cultured whole blood in a dose- and time -dependent manner. The greatest TNF-α stimulation occurred after 12 h of exposure to 1 μg/mL of LPS. Co-incubation with trans-10, cis-12 (t10,c12) CLA isomer (100 μM) or rosiglitazone (10 μM), a PPAR-γ agonist, decreased LPS-induced TNF-α production by 13 and 29%, respectively. Linoleic acid (LA) and cis-9, trans-11 (c9,t11) CLA isomer had no detectable effects on LPS-induced TNF-α production. The PPAR-γ agonist-induced TNF-α attenuation was reversed when blood was treated with both rosiglitazone and GW9662, a selective PPAR-γ antagonist. Addition of rosiglitazone to the culture medium tended to reduce NF-κBp65 concentration in nuclear extracts isolated from cultured PBMC. Results demonstrate that LPS is a potent inducer of TNF-α production in cultured bovine blood, and that t10,c12 CLA and PPAR-γ agonists attenuate the TNF-α response to LPS in vitro. Additional studies are needed to fully characterize the involvement of NF-κB in LPS-signaling in bovine blood cells.

Key words: CLA, TNF-α, cattle

W226 Influence of nitrogen and sulfur intake on bovine uterine pH. J. K. Grant*[1], P. Steichen[2], C. L. Wright[1], K. A. Vonnahme[2], M. L. Bauer[2], J. S. Jennings[3], and G. A. Perry[1], *[1]Department of Animal and Range Sciences, South Dakota State University, Brookings, [2]Department of Animal Science, North Dakota State University, Fargo, [3]Alltech Animal Nutrition, Brookings, SD.*

Previous research has reported that high protein and sulfur intake decreases uterine pH in cattle. Therefore, the objective of this study was to determine the effect of high N and S intake on uterine pH. Holstein and Angus-cross heifers (n = 20; 337.5 ± 8.4 kg of BW) were randomly assigned to 1 of 4 diets: control (C; 13.4% CP and 0.17% S); high N (N; C plus urea supplement to achieve 18.5% CP); high S (S; C plus calcium sulfate to achieve 0.43% S); or both high N and S (NS). Diets were individually fed at 2.6% of BW using Calan gates and estrus was synchronized to occur on d 12 after the experiment began. Blood samples were collected daily to determine plasma urea nitrogen (PUN), sulfate (d 0, 3, 7, 11, and 15), and progesterone concentrations. Uterine pH was measured on d 15, 19, 23, and 27 (d 3, 7, 11, and 15 of the estrous cycle). There was a treatment, time, and treatment x time interaction ($P < 0.01$) on PUN concentrations. Starting on d 2, PUN concentrations were increased in N and NS, which were not different ($P > 0.05$), compared with C and S ($P < 0.01$), which were not different ($P > 0.05$). There was an effect of treatment ($P < 0.01$) on sulfate concentrations, with concentrations being increased in S compared with C, N, and NS ($P \leq 0.01$), with NS increased compared with C ($P = 0.04$). In addition, sulfate concentrations were increased on d 3 compared with d 7 ($P = 0.04$) and 15 ($P < 0.01$), but there was no treatment x time interaction ($P = 0.81$). There was no effect of treatment ($P = 0.55$) or a treatment x time interaction ($P = 0.16$) on progesterone concentrations, but there was an effect of time ($P < 0.01$), with increasing concentrations after estrus consistent with normal CL formation. Uterine pH was increased in N and NS compared with C ($P < 0.02$), while S was not different from any treatment ($P > 0.11$). There was no effect of time ($P = 0.26$) or treatment x time interaction ($P = 0.71$) on uterine pH. In summary, uterine pH was increased in N and NS compared with C, while S was intermediate, and correlated with increased PUN concentrations.

Key words: nitrogen, sulfur, uterine pH

W227 Influence of sperm fertility-associated antigen status on nulliparous Nelore heifer fertility at first-service timed AI. J. C. Dalton*[1], L. Deragon[2], J. L. M. Vasconcelos[3], A. Ahmadzadeh[4], and R. F.G. Peres[5], *[1]University of Idaho, Caldwell, [2]Alta Genetics Brazil, Uberaba, MG, Brazil, [3]FMVZ-UNESP, Botucatu, SP, Brazil, [4]University of Idaho, Moscow, [5]Agropecuária Fazenda Brazil, Barra do Garças, MT, Brazil.*

The objective was to determine whether the presence of sperm fertility-associated antigen (FAA; a 31 kDA heparin binding protein) can be used to assess potential fertility of sperm for use at first-service timed AI (TAI). Following determination of FAA status by use of a lateral flow cassette, 6 Nelore bulls were selected based on FAA status (FAA-negative: n = 3; FAA-positive: n = 3) and their ability to produce neat semen with characteristics equal to or greater than 70% morphologically normal sperm and 60% estimated progressive motility

before cryopreservation. Ejaculates were collected by artificial vagina and extended semen was cryopreserved in 0.25-mL straws (30×10^6 sperm). Nulliparous Nelore heifers (n = 617) at a single location in Mato Grosso, Brazil, were evaluated for body condition score (BCS; 1–5 scale) and enrolled in a first-service TAI program. On d 0 heifers received an intravaginal insert containing 1.9 g progesterone (CIDR) and an injection of estradiol benzoate (2.0 mg i.m.). On d 7, all heifers received an injection of prostaglandin $F_{2\alpha}$ (12.5 mg i.m.). On d 9 CIDR inserts were removed and all heifers received an injection of estradiol cypionate (0.6 mg i.m.) and an injection of eCG (200 IU i.m.). On d 11, all heifers received TAI 48 h after CIDR removal. Fertility, as measured by pregnancy/TAI (P/TAI), was different ($P = 0.04$) between FAA-positive and FAA-negative bulls (33.7% vs. 40.7%, respectively). There was no effect of AI technician or BCS on P/TAI. In this study using a limited number of bulls (FAA-negative: n = 3; FAA-positive: n = 3) and TAI, it appears that FAA-negative status was not a limiting factor as nulliparous Nelore heifers achieved greater P/TAI with sperm from FAA-negative bulls. These results appear to be contradictory to a previous report of greater fertility following the use of FAA-positive bulls in AI (Sprott et al., J. Anim. Sci. 2000:78:795–798).

Key words: sperm, timed AI, fertility

W228 Feeding rumen-protected polyunsaturated fatty acids (PUFA) to high-producing dairy cows: II. Effects on serum concentrations of progesterone and insulin. M. M. Reis[1], R. F. Cooke[2], B. I. Cappellozza[2], and J. L. M. Vasconcelos*[1], *[1]UNESP – Faculdade de Medicina Veterinária e Zootecnia, Botucatu, SP, Brazil, [2]Oregon State University–Eastern Oregon Agricultural Research Center, Burns.*

The objective was to determine if the productive and reproductive benefits of rumen-protected PUFA supplementation to high-producing dairy cows are due to increased circulating concentrations of progesterone (P4) and insulin. In this study, 765 primiparous and multiparous lactating Holstein cows, with estimated production of at least 9,000 kg of milk/yr, were randomly allocated approximately 30 d postpartum to 1 of 10 free stalls, where they remained throughout the lactation. Each free stall was assigned randomly to receive a diet, balanced to meet the nutritional requirements of lactating dairy cows, without (control) or with (PF) the inclusion of 250 g/cow daily of a rumen-protected PUFA source (Megalac-E; QGN, Rio de Janeiro, Brazil). Control and PF diets were iso-energetic and iso-nitrogenous, and the PUFA source was offered during the first feeding of the day (0600 h). Between 45 and 60 d postpartum, cows were randomly assigned to fixed-time AI (TAI) or embryo transfer (ET). Blood samples were collected 7 d after TAI or on the day of ET for determination of serum P4 and insulin concentrations. Primiparous PF cows had greater ($P < 0.01$) P4 concentrations compared with control cohorts (4.4 vs. 3.2 ng/mL, respectively), whereas no treatment differences were detected in multiparous cows ($P > 0.61$). Similarly, PF primiparous tended ($P = 0.08$) to have greater insulin concentrations compared with control cohorts (10.5 vs. 7.5 μIU/mL, respectively), whereas no treatment differences were detected in multiparous cows ($P > 0.43$). When P4 and insulin were analyzed independently of treatments, primiparous cows with insulin concentrations equal or greater than the median (7.35 μIU/mL) had greater ($P < 0.01$) P4 concentrations compared with primiparous cows with insulin below the median (5.4 vs. 3.3 ng/mL, respectively). The same outcome, however, was not detected among multiparous cows ($P > 0.29$). In summary, rumen-protected PUFA supplementation at 250 g/d increased circulating concentrations of P4 in primiparous lactating cows, which may be attributed to concurrent increases in insulin concentrations.

Key words: PUFA, insulin, progesterone

W229 Feeding rumen-protected polyunsaturated fatty acids (PUFA) to high-producing dairy cows: I. Effects on milk production and reproductive performance. M. M. Reis[1], R. F. Cooke[2], S. Soriano[4], F. L. Aragon[3], M. B. Veras[3], and J. L. M. Vasconcelos*[1], *[1]UNESP – Faculdade de Medicina Veterinária e Zootecnia, Botucatu, SP, Brazil, [2]Oregon State University–Eastern Oregon Agricultural Research Center, Burns, [3]Pioneiros Veterinary Clinic, Carambei, PR, Brazil, [4]Colorado Dairies, Araras, SP, Brazil.*

The objective was to determine if rumen-protected PUFA supplementation benefits performance and reproduction of high-producing dairy cows. In this study, 1,083 primiparous and multiparous lactating Holstein cows, with estimated production of at least 9,000 kg of milk/yr, were randomly allocated approximately 30 d postpartum to 1 of 10 free stalls, where they remained throughout the lactation. Each free stall was assigned randomly to receive a diet, balanced to meet the nutritional requirements of lactating dairy cows, without (control) or with (PF) the inclusion of 250 g/cow/d of a rumen-protected PUFA source (Megalac-E; QGN, Rio de Janeiro, Brazil). Control and PF diets were iso-energetic and iso-nitrogenous, and the PUFA source was offered during the first feeding of the day (0600 h). Milk production and composition were evaluated during the initial 43 wk of lactation. Between 45 and 60 d postpartum, cows were randomly assigned to fixed-time AI (TAI), embryo transfer (ET) or conventional AI. Pregnancy was verified by transrectal ultrasonography 60 d after TAI, ET or AI. Results were analyzed using the PROC MIXED and GLIMMIX of SAS. Cows receiving PF had greater ($P < 0.01$) milk production compared with control (38.7 vs. 36.2 kg/cow/d, respectively). However, PF cows had reduced ($P < 0.01$) milk protein and fat content compared with control cows (3.09 vs. 3.11% of protein and 3.42 vs. 3.55% of fat, respectively). Still, PF cows had greater ($P < 0.01$) fat corrected milk production (3.5% milk fat) compared with control cows (37.3 vs. 36.0 kg/cow/d, respectively). Independently of breeding procedure (TAI, AI, or ET), no treatment effects were detected on first service pregnancy rates (18.7 vs. 20.2% of pregnant cows/total cows for PF and control, respectively; $P = 0.78$) or number of services required for pregnancy (2.23 vs. 2.28 services per pregnancy for PF and control cows, respectively; $P = 0.73$), even when milk production served as covariate. In summary, rumen-protected PUFA supplementation to high-producing dairy cows enhanced milk production without impairing reproductive performance.

Key words: PUFA, milk production, reproduction

W230 Puberty induction in Nelore heifers receiving eCG and/or estradiol cypionate at the end of the estrus synchronization protocol. A. Rodrigues[1], R. Peres*[3], A. Lemes[2], T. Martins[1], F. Aono[1], M. Pereira[1], H. Graff[3], E. Carvalho[3], and J. L. M. Vasconcelos[1], *[1]FMVZ-UNESP, Botucatu, SP, Brazil, [2]ESALQ-USP, Piracicaba, SP, Brazil, [3]Agropecuaria Fazenda Brasil, Barra do Garça, MT, Brazil.*

The aim of this study was to evaluate if eCG and/or estradiol cypionate (ECP) administration at the end of an estrus synchronization protocol containing a previously used (4th use) intravaginal progesterone device (CIDR) increases induction of puberty in prepubertal Nelore heifers. Heifers were evaluated for puberty status 7 d before and at CIDR insertion (d 0) via transrectal ovarian ultrasonography and classified as prepubertal if a corpus luteum was not detected. Only prepubertal heifers were utilized in the present study. After CIDR removal (d

12), heifers detected in heat were inseminated according to the Trimberger system for 7 d, whereas 8 d after CIDR removal heifers not detected in estrus were again evaluated for corpus luteum presence. Data were analyzed by logistic regression using PROC LOGISTIC of SAS. In Exp. 1, 896 heifers were used and randomly received 200 IU of eCG (G2) or no treatment (control) at CIDR removal (d 12). Heifers that received G2 had greater ($P < 0.01$) puberty induction and heat detection compared with control (71.9 and 53.3% of puberty induction and 34.3 v. 27.5% heat detection rate, respectively). Conception rates were not affected ($P > 0.10$) by treatments (45.1 vs. 43.5% for G2 and control, respectively). In Exp. 2, 401 heifers randomly received G2, 200 IU of eCG + 0.5 mg ECP (G3), or control at CIDR removal (d 12). Heifers that received G3 had greater ($P = 0.01$) estrus detection and puberty induction compared with G2 and control heifers (56.1, 34.8 and 21.5% estrus detection rate and 88.3, 75.0 and 45.6 puberty induction, respectively). Conception rate were similar ($P > 0.10$) among treatments (46.7, 34.7, and 33.3 for control, G2, and G3, respectively). In Exp 3, heifers randomly receive 0.5 mg of ECP (E1), G2, G3, or control at CIDR removal (d 12). Heifers receiving G3 had greater ($P = 0.02$) puberty induction compared with E1, G2, and control (88.7, 75.3, 82.2, and 57.9%, respectively). In conclusion, the use of ECP, eCG, and particularly eCG + ECP at CIDR removal increased the number of Nelore heifers cycling and detected in heat at the beginning of the breeding season.

Key words: heifers, estradiol and eCG, puberty

W231 Repeated exposure to human chorionic gonadotropin causes development of antibodies in some lactating dairy cows. J. O. Giordano*, M. C. Wiltbank, and P. M. Fricke, *Department of Dairy Science, University of Wisconsin-Madison, Madison.*

Our objective was to determine if repeated exposure of lactating dairy cows to human chorionic gonadotropin (hCG) would induce an antibody (Ab) response against hCG. Cows (n = 45) enrolled in a synchronization of ovulation experiment either received an hCG injection (hCG; 2000 IU i.m.) or no treatment (CON) at 18 d after a timed AI. A subgroup of cows (n = 27) from the original group received a 2nd hCG injection 35 d after the 1st injection, and another subgroup (n = 18) of cows received a 3rd hCG injection 35 d after the 2nd hCG injection. Blood samples were collected at 0, 7, 14, 21, and 28 d after hCG or CON. A binding radioimmunoassay for hCG Ab was used to detect hCG Ab in serum samples. A positive Ab response (6.34% bound) was defined as 3 standard deviations above CON binding. The proportion of cows presenting an Ab response at 0 and 14 d after hCG was compared through one tailed Fisher's exact test, whereas difference in Ab bound at 0, 7, 14, 21, and 28 d was compared with PROC MIXED of SAS. No cows had hCG Ab at Day 0 before 1st hCG. At 14 d after 1st hCG, no difference ($P = 0.48$) was observed between CON (0/22) and hCG (1/20) cows for percentage Ab positive. At 2nd hCG, no difference ($P = 0.59$) was observed on Day 0 between CON (0/11) and hCG (1/16) cows, whereas a tendency ($P = 0.06$) was observed at 14 d [(CON = 0/5) vs. (hCG = 8/16)]. At the 3rd hCG injection no difference ($P = 0.16$) was observed on Day 0 between CON (0/6) and hCG (4/12) cows, whereas a greater ($P = 0.05$) proportion of hCG cows (6/9) had hCG Ab at 14 d vs. CON cows (0/4). Treatment, time, and treatment by time affected ($P < 0.05$) the average % Ab bound after the 2nd and 3rd hCG injection. Cows that received hCG had greater % Ab Bound at 7, 14, 21, and 28 d after hCG, with the greatest binding observed at 14 d. We conclude that some but not all lactating dairy cows developed an Ab response after repeated exposure to hCG and that maximum response is observed within 14 d of hCG injection.

Key words: hCG, immune response, dairy cow

W232 Synchronization of dairy heifers with a modified 5-day CIDR-$PGF_{2\alpha}$-GnRH timed AI protocol. J. Howard*[1,2], K. Carnahan[1], C. Autran[1], J. Branen[2], R. Kasimanickam[3], G. Sasser[2], and A. Ahmadzadeh[1], *[1]University of Idaho, Moscow, [2]BioTracking LLC, Moscow, ID, [3]Washington State University, Pullman.*

It has been shown that the use of a CIDR insert, in conjunction with a GnRH-$PGF_{2\alpha}$ fixed time AI(TAI) protocol improves pregnancy per AI (P/AI). But due to variability in the results of previous studies it is not clear whether the 1st GnRH administration at the time of CIDR insertion in a 5-d CIDR protocol improves P/AI in heifers. The objective of this experiment was to evaluate the effect GnRH at the time of CIDR insertion, in a 5-d CIDR-Cosynch timed artificial insemination (TAI) protocol on P/AI in dairy heifers. Holstein replacement heifers (n = 234), received a CIDR on d 0. Subsequently heifers were paired by age and assigned randomly to receive either 100 ug of GnRH (GnRH-CIDR; n = 117) or no GnRH treatment (Control; n = 117). On d 5, the CIDR was removed and all heifers received 25 mg $PGF_{2\alpha}$ (d 5). On d 8 (72 h after CIDR) all heifers received GnRH and TAI. Estrus activity was monitored using tail chalk methods from d 5 to d 8. Pregnancy was diagnosed by ultrasound and a Pregnancy specific protein B (PSPB) based ELISA (BioPRYN) on d 32 and 45 after AI. Blood samples were collected in a subgroup of heifers (n = 113) on d 0 to determine progesterone (P4) concentrations. There was no effect of bull or technician on P/AI on d 32 or d 45. Mean P4 concentrations on d 0 were not different between groups and averaged 3.6 ± 0.5 ng/mL. Pregnancy per AI did not differ between treatments (GnRH CIDR 57.2% vs. Control 61.5%) on d 32 or 45. Only 18% of heifers were not detected in estrus and P/AI was less ($P < 0.05$) in heifers that were not detected in estrus (41.8% vs. 63.3%). The results of this experiment indicate GnRH administration at CIDR insertion, in 5-d CIDR-Cosynch may not have beneficial effects on P/AI in Holstein heifers.

Key words: dairy heifer, timed AI, GnRH

W233 Prepartum 2,4-thiazolidinedione administration increases plasma tumor necrosis factor alpha in transition dairy cows. K. M. Schoenberg*[1], K. L. Perfield[2], J. K. Farney[3], B. J. Bradford[3], and T. R. Overton[1], *[1]Cornell University, Ithaca, NY, [2]Elanco Animal Health, Greenfield, IN, [3]Kansas State University, Manhattan.*

Thiazolidinediones (TZD) are potent ligands for peroxisome proliferator–activated receptor–gamma (PPARγ), and TZD administration has been shown to alter lipid metabolism and energy status in transition dairy cows. Tumor necrosis factor α (TNFα) is an inflammatory cytokine which may also play a role in metabolic health during the transition period. The objective of this experiment was to determine the effect of prepartum TZD administration on plasma TNFα and further characterize TNFα throughout the transition period. Holstein cows (n = 31) entering their second or greater lactation were administered 0, 2.0, or 4.0 mg TZD/kg BW by intrajugular infusion once daily from 21 d before expected parturition until parturition. Plasma samples were analyzed for TNFα on d –14, –3, –1, 1, 3, 7, 35, and 49 relative to parturition via a recently developed bovine TNFα enzyme-linked immunosorbent assay (ELISA). Results were analyzed with a mixed model including repeated measures over time and a covariate sample collected at d –22. Data transformation was required to meet assumptions of normality for statistical analysis and values reported are back-transformed. Independent of day, plasma TNFα was increased linearly

by increasing TZD dose (2.63, 3.72, 3.95 pg/mL; $P = 0.01$). The temporal pattern (effect of day; $P < 0.01$) for plasma TNFα was such that it lowest (2.85 pg/mL) during the postpartum period (d + 7 to d + 49), highest (4.18 pg/mL) during the prepartum period (d −14) and intermediate (3.32 pg/mL) during the transition period (d −3 to +3). Contrasts of the effect of period showed that prepartum values were significantly different from both the transition period ($P < 0.01$) and the postpartum period ($P < 0.001$). These results suggest that TNFα may be an important metabolic regulator during the transition period. Somewhat surprisingly, TZD administration increased TNFα concentrations independent of day relative to calving. The effects of TZD on TNFα may be confounded in this case with effects on other regulators such as leptin.

Key words: transition cow, thiazolidinedione, tumor necrosis factor alpha

W234 Effect of dietary β-glucan on growth performance, fecal microbial shedding and immunological responses after lipopolysaccharide challenge in weaned pigs. T. X. Zhou*, B. U. Yang, and I. H. Kim, *Dankook University, Cheonan, Choongnam, South Korea.*

Two experiments were conducted to investigate the effects of β-glucan on growing performance and immune function in weaned pigs after LPS challenge. In Exp. 1, 40 weaned pigs (7.89 ± 0.84 kg of BW and 21 ± 2 d of age) were used in a 28 d feeding trial. All pigs were randomly allotted to 1 of 2 treatments (0 or 0.1 g/kg of β-glucan in the diet) with 4 replicate pens per treatment and 5 pigs per pen. Dietary β-glucan decreased ($P < 0.05$) the number of *E. coli*. In Exp. 2, a total of 20 weaned barrows (6.69 ± 0.24 kg of BW and 21 ± 2 d of age) were used to investigate the immunological response after LPS challenge. Pigs were fed 0 or 0.1 g/kg dietary β-glucan for 42 d. On d 42, pigs (n = 5) in each treatment were injected i.p. with *E. coli*. lipopolysaccharide or sterile saline solution at a concentration of 100 μg/kg of BW. Dietary β-glucan increased leukocytes counts at 2, 4 and 6 h, and lymphocyte concentration at 2, 4 and 6 h, and LPS challenge increased ($P < 0.05$) leukocytes counts at 2, 4, 6, and 8 h and increased ($P < 0.05$) lymphocyte concentration at 2, 4, and 6 h post-challenge and a interaction ($P < 0.05$) was observed. LPS challenge increased the rectal temperature at 2, 4, 6, and 8 h post-challenge. Dietary β-glucan reduced plasma TNF-α concentration while LPS challenge increased ($P < 0.05$) blood TNF-α concentration at 2, 4, and 6 h. Dietary β-glucan increased ($P < 0.05$) the concentration of the cluster of differentiation antigens 4 and 8 (CD4+ and CD8+) cells at 2, 4, 6 h and 4, 6 h post-challenge, respectively, and LPS challenge increased ($P < 0.05$) CD4+ and CD8+ cell concentrations at 2, 4 and 6 h post-challenge; an interaction ($P < 0.05$) between β-glucan and LPS challenge was observed. The CD4+: CD8+ ratio was decreased ($P < 0.05$) by LPS challenge and dietary β-glucan at 2, 4, 6 and 8 h post challenge and a interaction ($P < 0.05$) was observed at 4 and 6 h post challenge. In conclusion, dietary β-glucan can decrease *E. coli* numbers but not affect growth performance in weaned pigs and offer benefits on immune function in weaned pigs challenged with LPS.

Key words: beta-glucan, lipopolysaccharide challenge, pigs

W235 Difference in the expression of components of the GHR/IGF-I axis in follicular granulosa cells and corpus luteum in cows. A. Schneider[1,2], L. F. M. Pfeifer[1], M. N. Corrêa[1], and W. R. Butler*[2], *[1]Universidade Federal de Pelotas, Pelotas, RS, Brazil, [2]Cornell University, Ithaca, NY.*

The aim of this work was to evaluate the difference in the expression of components of the GHR/IGF-I axis in follicular granulosa cells and corpus luteum (CL) in cows. Expression of IGF-I in granulosa cells is controversial, even though it is easily detected in the CL. Ovaries were collected from cows during slaughter. Follicles (7 estrogen-active follicles [EAF] and 7 atretic follicles [ATF]) were dissected from the stroma, FFL was aspirated and the follicle walls immersed in RNALater. To recover granulosa cells, follicular walls were removed from the RNALater, halved, scraped and washed with cold saline. Granulosa cells were recovered by centrifugation at 2000 x g for 3 min. The CL (n = 7) were also dissected. Total RNA was isolated and real-time PCR used to evaluate suppressor of cytokine signaling (SOCS-1, −2 and −3), GHR, IGF-I, IGF-II and ERα mRNA expression according to the ΔΔCt method. Estradiol (E2), progesterone (P4) and IGF-I were evaluated in FFL. In EAF and ATF, FFL E2 concentration was 137 ± 40 and 21 ± 6 ng/mL, with E2/P4 ratio of 2 and 0.4, respectively. IGF-I in FFL was 96 ± 18 and 85 ± 25 ng/mL for EAF and ATF, respectively. Expression of GHR, IGF-I, IGF-II, SOCS-1 and SOCS-2 mRNA was higher in the CL than EAF and ATF. GHR mRNA expression was 8 times higher, while IGF-I mRNA was 25 times higher in CL than in follicles. SOCS-3 and ERα expression was not different between CL and follicles. No difference between EAF and ATF for the genes studied was found. Regarding follicles, SOCS-2 was correlated to GHR ($r = 0.62$, $P < 0.05$), ERα ($r = 0.87$, $P < 0.0001$) and FFL E2 ($r = 0.55$, $P < 0.05$). In the CL, SOCS-2 was correlated to GHR ($r = 0.85$, $P < 0.05$) and ERα ($r = 0.85$, $P < 0.05$). The IGF-I and SOCS-2 to GHR ratio was lower ($P < 0.01$) in follicles than CL, which indicates that there is more IGF-I and SOCS-2 mRNA production per unit of GHR in the CL. In sum, SOCS-2 and IGF-I mRNA expression in EAF was not different from ATF, although SOCS-2 expression was correlated to FFL E2 concentration. Moreover, GHR effectiveness in stimulating IGF-I seems reduced in the follicle when compared with the CL.

Key words: granulosa cells, GHR, IGF-I

W236 Functional genomics of liver in purebred beef cows in two forage allowances during gestation and lactation period. J. Laporta*[1], G. Greif[2], P. Zorrilla[2], H. Naya[2], G. J. M. Rosa[3], and M. Carriquiry[1], *[1]Facultad de Agronomía, Universidad de la República, Montevideo, Uruguay, [2]Instituto Pasteur, Montevideo, Uruguay, [3]University of Wisconsin, Madison.*

In rangeland conditions, pasture quality and availability vary throughout the year affecting energy balance of pregnant and lactating beef cows. A large microarray experiment was conducted using purebred cows (PU; Angus and Hereford) in high (H) and low (L) forage allowances (10 vs. 6 kg DM/100kgLW/d) to study liver gene expression during gestation and lactation periods. Four cows per treatment (PU-H and PU-L) were used. Total RNA was extracted from liver biopsies (−170, −15, +15 and +60 d relative to parturition). Integrity and quality were evaluated using Agilent 2100 Bioanalyzer (RIN 6.4±0.4). A single-channel microarray analysis was performed using Agilent 4x44K Bovine Gene Expression array. Data was normalized, filtered, and a 2-way ANOVA, to evaluate the effect of time and forage allowances, was performed using GeneSpring (v11.5) Software. Significance levels were adjusted for multiple testing using a false discovery rate of 0.2. Out of 806 differentially expressed genes (DEG), 795 changed only across time (140 ±2.5 fold change), and 12 with forage allowance. There were no significant interactions between time and forage allowance. The DEG were clustered to study expression profiles and a Gene Set Enrichment Analysis was performed. More than 15 significant ($P \leq 0.01$) gene sets across time (only for −170 vs. −15 d) with posi-

tive (IGFI-MTOR pathway, spliciosome, and MAPK pathway) and negative (PPAR signaling pathway, triacylglyceride biosynthesis, and pyruvate metabolism, etc.) enrichment scores (ES) were identified. Only PPAR signaling pathway was enriched in −15 vs. +15 d. Steroid metabolism, cholesterol biosynthesis, glucogen and glycogenolysis, among others, were positively enriched for +15 vs. +60 d. Only four genes sets were significantly ($P \leq 0.01$) and negatively enriched when high vs. low forage were compared: amine hormones, glucose SLC sugar transporters, neuotransmitter release and MAPK signaling pathway. These results contribute to understand liver function in regulating alterations in metabolism in response to the level of nutrition and physiological stage in beef cattle along the year on grazing conditions.

Key words: microarrays, liver, grazing

W237 Conjugated linoleic acids (CLA) and lactation related changes of serum amyloid A3 (SAA3) and IL-6 mRNA abundance in different bovine tissues with a focus on different adipose depots. B. Saremi*[1], M. Mielenz[1], D. von Soosten[2], S. Dänicke[2], and H. Sauerwein[1], *[1]Institute of Animal Science, Physiology and Hygiene Unit, University of Bonn, Bonn, North Rhine-Westphalia, Germany, [2]Institute of Animal Nutrition, Friedrich-Loeffler-Institute (FLI), Federal Research Institute for Animal Health, Braunschweig, Lower Saxony, Germany.*

The adipokine SAA3 is linked to obesity and insulin sensitivity of adipose tissue (AT) and respective inflammatory response, at least in mice. SAA3 is not related to the plasma concentrations of SAA. In contrast, SAA3 could be found in medium of cultured adipocytes. SAA3 is known to be upregulated by IL-6 in mice. In dairy cows, CLA interfere with energy homeostasis and fat metabolism by milk fat reduction. We hypothesized that the mRNA abundance (Ab) of SAA3 and IL-6 could be affected by CLA or days postpartum. From 25 Holstein heifers, 5 animals were slaughtered on d 1 postpartum. Remaining heifers were randomly allocated to CLA (Lutrell pure, BASF, Germany, n = 10) or control fat supplementation (Silafat, BASF, n = 10) each at 100 g/d. Five animals per group were slaughtered at d 42 or 105. Liver, skeletal muscle, udder, pancreas and fat samples [subcutaneous (Sc) (chest, wither and tail head) and visceral (Vc) (mesenterial, omental and retroperitoneal)] were collected. Total RNA was analyzed by qPCR. Pearson correlation and statistical analysis using the general linear model or non parametric tests were done in SPSS 17 ($P < 0.05$). Decreasing Ab of SAA3 from d 1 to d 42 and 105 was observed in all tissues except mesenterial AT in which SAA3 was constantly expressed. In ScATs and muscle tissue, CLA reduced SAA3 Ab in comparison to control group regardless of time. In general, 2 to 26 fold differences in the SAA3 Ab in different ATs compared with omental AT (highest SAA3 Ab) were observed. IL-6 Ab was reduced from d 1 to d 42 and 105 in ScATs and vice versa in liver. IL-6 Ab was neither affected by CLA nor correlated to SAA3 Ab. In conclusion, a regulatory effect of IL-6 on SAA3 in mice was not supported for dairy cattle. Reduced SAA3 Ab in ScATs and muscle regarding to CLA, might be a hint of local anti-inflammatory effects of CLA and improved insulin sensitivity in these tissues.

Key words: SAA3, IL-6, adipose tissue

W238 Role of nuclear receptors in the metabolism of boar taint compounds in Leydig cells. M. A. Gray* and E. J. Squires, *University of Guelph, Guelph, Ontario, Canada.*

Boar taint is an unpleasant odor and taste caused by accumulation of androstenone and 3-methylindole (3MI, skatole) in fat of male pigs. The objective of this work was to determine the effects of the nuclear receptors constitutive androstane receptor (CAR), pregnane X receptor (PXR), and farnesoid X receptor (FXR) on the production of total 16-androstene steroids (16A) and androgens (AND) from pregnenolone (PREG) in Leydig cells. Treatment of Leydig cells with CAR or PXR agonists resulted in 25.0 ± 2.7% and 26.0 ± 2.8% conversion of PREG to 16A, respectively, which was significantly ($P < 0.05$) higher than the 16.0 ± 2.2% conversion found with the DMSO control. Treatment with a FXR agonist did not significantly affect conversion of PREG to 16A. Conversely, treatment with agonists for CAR, PXR and FXR significantly ($P < 0.05$) decreased the percentage of PREG converted to AND to 40.8 ± 2.6%, 40.2 ± 1.9%, and 46.2 ± 3.9%, respectively, compared with the DMSO control (58.8 ± 4.7%). Treatment of Leydig cells with 3MI did not significantly alter 16A or AND production. Activation of CAR, PXR, or FXR all resulted in significant upregulation of several genes involved in the conversion of PREG to 16A or AND, as measured using real-time PCR. Although transcription of CYP17A1, the enzyme that converts PREG to both AND and 16A, was not significantly altered, expression of CYB5A and CYB5R1 increased with activation of each receptor. These genes are accessories to CYP17A1 and increase CYP17A1 andien-β synthase activity instead of 17α-hydroxylase and C17,20 lyase activities, thus favoring 16A production over AND production. Treatment with 3MI resulted in decreased expression of key target genes for each receptor, indicating that skatole acts as an inverse agonist for these receptors. Taken together, the functional and transcriptional effects of transactivation of CAR, PXR, and FXR suggests that activation of these receptors favors the production of 16A, and thereby will result in an increase in boar taint.

Key words: boar taint, nuclear receptor, steroidogenesis

W239 Effects of heat stress on Na^+/K^+ATPase activity in growing pigs. S. C. Pearce*, A. J. Harris, N. K. Gabler, and L. H. Baumgard, *Iowa State University, Ames.*

Na^+/K^+ATPase pumps are involved with cellular transport processes, osmotic balance and account for a substantial portion of whole body energy expenditure. However, how heat stress (HS) affects Na^+/K^+ATPase activity in various tissues has not been studied in a porcine model. Crossbred gilts (n = 48; 35 ± 4 kg BW) were housed in constant climate controlled rooms in individual pens and exposed to 1) thermal neutral (TN) conditions (20°C; 35–50% humidity) with ad libitum intake (n = 18), 2) HS conditions (35°C; 20–35% humidity) with ad libitum intake (n = 24) or 3) pair-fed (PF in TN conditions [PFTN], n = 6: to eliminate confounding effects of dissimilar feed intake [FI]). Pigs were sacrificed at 1, 3, or 7d of environmental exposure and jejunum, longissimus dorsi (LD), and liver samples were collected and analyzed for Na^+/K^+ATPase activity. HS pigs had an increase ($P < 0.01$) in body temperature (39.3 vs. 40.8°C), a doubling in respiration (54 vs.107 bpm) and an immediate decrease in FI (47%; $P < 0.05$) which continued through d7; by design PFTN controls FI mirrored the HS group. Over the 7d period, TN pigs had increased ADG compared with the HS pigs (1.14 vs 0.24 kg/d) while HS pigs lost 2.7 kg BW. Overall, compared with the TN pigs, HS pigs had increased LD Na^+/K^+ ATPase activity (52%; $P = 0.06$). There was an environment by day interaction in jejunum Na^+/K^+ATPase activity as it was markedly increased (175%; $P < 0.05$) on d1, but returned to TN levels by d3. Liver Na^+/K^+ATPase activity was not different between the TN and HS pigs. However, PFTN pigs had decreased pump activity compared

with the HS and TN pigs (30%; $P = 0.06$). Irrespective of environment, TN pigs tended to have tissue differences in Na^+/K^+ATPase activity ($P = 0.08$) as liver activity was lower (27%) compared with jejunum; LD was not different from either tissue. These data indicate HS induces tissue specific increases in Na^+/K^+pump activity and suggests that ion pump energy expenditure (and presumably total body energetic cost) increases during a thermal load and is more pronounced during acute HS.

Key words: heat stress, energetics, Na^+/K^+ pump

W240 Serum shock did not synchronize clock gene expression in primary bovine hepatocyte cultures. C. A. Kurman*, M. M. McCarthy, L. M. Nemec, and T. F. Gressley, *University of Delaware, Newark.*

Circadian rhythms are regulated by clock gene expression. In the liver, clock genes are controlled by hormonal and neural signals to result in 24 h patterns of metabolism and nutrient availability. Studying circadian rhythms in vitro requires artificial synchronization of clock gene expression, accomplished by serum shock in monogastric hepatocyte culture systems. Our objective was to determine whether serum shock of primary bovine hepatocyte cultures would synchronize clock gene expression patterns. Monolayer cultures were established from hepatocytes isolated from a 1 wk old Holstein bull calf. At 0 h, cells were serum shocked for 2 h with 50% fetal bovine serum (FBS) followed by 0% FBS for 46 h (treatment = SS) or treated with media containing 10% FBS for 48 h (NSS). Cells were harvested every 4 h and mRNA was isolated. The mRNA levels of 7 clock genes were quantified relative to control genes (RPS9 and β -actin) using qPCR. The experiment was conducted on 2 occasions (Exp. 1 and Exp. 2). Results were statistically evaluated using a model containing fixed effects of treatment, hour, and their interaction. We expected to observe: 1) characteristic 24 h clock gene expression patterns, and 2) more distinctive patterns for SS compared with NSS. Contrary to this hypothesis, anticipated treatment time interactions were observed only for *Per2* in Exp. 2 (Table 1). Although treatment and hour affected various clock genes in each experiment (Table 1), effects of time and treatment were not consistent with published monogastric studies. The serum shock protocol used in these experiments was unsuccessful at synchronizing bovine hepatocyte clock gene expression.

Table 1.

		Treatment			*P*-value		
	Gene	NSS	SS	SEM	Treat.	Hour	Treat × Hour
Exp. 1	Clock	2.04	1.38	0.22	0.04	0.15	0.63
	Per1	1.7	1.94	0.14	0.25	0.75	0.7
	Per2	2.96	2.32	0.15	0.005	0.001	0.98
	Cry1	2.54	2.22	0.08	0.01	0.05	0.54
	Cry2	2.41	1.84	0.25	0.12	0.87	0.99
	CK1ε	2.38	1.96	0.09	0.002	0.04	0.95
Exp. 2	Clock	2.26	2.06	0.1	0.17	0.18	0.32
	Per1	2.11	2.01	0.08	0.4	0.05	0.49
	Per2	1.93	1.93	0.07	0.91	0.001	0.05
	Cry1	2.41	2.33	0.11	0.61	0.05	0.75
	Cry2	2.1	2.13	0.13	0.87	0.02	0.93
	CK1ε	1.79	1.75	0.11	0.83	0.01	0.31

Key words: clock gene expression, hepatocytes, serum shock

W241 Effect of short-term supplementation in hepatic gene expression in cycling Hereford cows grazing native pastures. F. Bialade[1], A. L. Astessiano*[1], M. P. Grignola[1], J. Laporta[1], C. Viñoles[2], and M. Carriquiry[1], *[1]School of Agronomy, UDELAR, Montevideo, Uruguay, [2]Research Institute for Agriculture, Tacuarembo, Uruguay.*

Short-term supplementation before the breeding season has been associated with an increase in early pregnancy rate, however, the metabolic changes involved in this response are not clear. To evaluate the impact of a short-term energy supplementation before the breeding season on changes on the hepatic gene expression associated with the GH-IGF axis, adult non-gestating nonlactating Hereford cows (n = 9) were used in a randomized block design. Cows (478 ± 11 kg BW, 5.3 ± 0.1 units BCS, scale 1–8) were allocated to 2 groups: control, non-supplemented (CON, n = 5) and supplemented (SUP, n = 4). The supplement consisted in 2.5 kg of rice barn/cow (90.3%DM, 10%CP, 9%EE, 14% NDF) offered daily for 23 d. All cows grazed on native pastures (forage availability of 603 kg DM/ha). Liver biopsies were obtained at the beginning (d 0) and end (d 23) of the supplementation treatment. The abundance of mRNA of growth hormone receptor (GHR), insulin-like growth factor-I (IGF-I), IGF binding proteins-2 (IGFBP2),-3 (IGFBP3), and insulin receptor (INSR) were measured by real time RT-PCR normalized by hypoxanthine phosphoribosyltransferase (HPRT) and β-actin as endogenous controls. Means from a mixed model analysis were considered to differ when $P < 0.05$. Cow BCS did not differ between groups and increased, for all cows, 0.6 ± 0.1 units of BCS during the supplementation period. The expression of all 5 genes: GHR (0.66 vs. 0.57 ± 0.10), IGF-I (0.54 vs. 0.89 ± 0.47), IGFBP2 (4.41 vs. 4.41 ± 1.23), IGFBP3 (1.04 vs. 0.80 ± 0.12), INSR (19.10 vs. 31.06 ± 5.30) mRNAs did not differ ($P > 0.15$) between CON and SUP cows. Expression of GHR and IGFBP3 mRNA (r = 0.62, $P = 0.005$), GHR and INSR mRNA (r = 0.45, $P = 0.056$) and INSR and IGFBP3 mRNA (r = 0.57, $P = 0.011$) were positively correlated. We conclude that short-term energy supplementation before the breeding period has no effect on hepatic gene expression associated with the GH-IGF axis in grazing cyclic beef cows in good BCS.

Key words: mRNA, cattle, nutrition

W242 Effect of charcoal extracted bovine follicular and testicular fluids on testes and endocrine organ weights of pre-pubertal male rabbits. A. H. Ekeocha*, *University of Ibadan, Ibadan, Oyo, Nigeria.*

The effect of charcoal-extracted bovine follicular and testicular fluids on testes and endocrine organ weights of pre-pubertal male rabbits was investigated. A total of 15 young male rabbits of various strains with age range of 11–12 weeks old and weighing 1.0 ± 0.2kg were randomly divided into 3 groups, each consisting of 5 rabbits. The treated groups and the control group were injected intramuscularly with charcoal-extracted bovine follicular fluid, charcoal extracted bovine testicular fluid and charcoal treated distilled water respectively, at the rate of 0.2mL per rabbit on every other day and on 3 different occasions. After administration of the different treatments, testes weight and endocrine organ weights were conducted or carried out. Endocrine organ weights included: thyroid gland, adrenal gland, pituitary gland and kidney. There were no significant differences ($P > 0.05$) in paired testes weights among the 3 different groups. There were no significant differences ($P > 0.05$) in paired thyroid gland, paired adrenal gland between control and treated groups. Contrarily there was a significant increase ($P < 0.05$) in paired kidney weights between testicular fluid treated groups and control and follicular fluid treated groups. There

was a significant decrease ($P < 0.05$) in pituitary gland weight between control and treated groups. Administration of charcoal extracted bovine follicular and testicular fluids to pre-pubertal male rabbits decreased the weights of pituitary gland, which implies that the administration of inhibin to immature rabbits affects the hypo-thalamo-pituitary function as well as block FSH dependent steps in spermatogenesis.

Key words: charcoal extracted, testes, male rabbits

W243 *Caspase* 3 is upregulated in murine spermatogonia and Leydig cells treated with aflatoxin B_1. K. J. Austin*, R. R. Cockrum, K. L. Speiser, and K. M. Cammack, *University of Wyoming, Laramie.*

Aflatoxin B_1 is hepatotoxic and carcinogenic in a variety of livestock species including cattle, sheep and swine. In addition to poor performance and health, AFB_1 in food sources can lead to infertility in livestock, rodents and humans. The objective of these experiments was to examine the molecular mechanisms associated with reduced fertility using male mice as the model. Specifically, apoptosis and *Caspase* 3, a primary activator of protein cleavage and DNA fragmentation, were investigated. Male ICR mice 4 wk of age were treated with 50 μg/mL BW AFB_1 (n = 9) or placebo consisting of corn oil/ethanol (n = 9) daily for 45 d via IP injection. Following treatment, males were mated to 4 females each for 8 d to determine number of pups sired. Males were then sacrificed for testes collection. Spermatogonia and Leydig cell lines were cultured in vitro and treated with 0, 5, 10 or 20 μg/ mL AFB_1 (n = 3 wells/treatment) for 20 h . Effects of treatment were estimated using the GLM procedure of SAS. Message for *Caspase* 3, as analyzed by semi- quantitative real- time RT-PCR, did not differ ($P = 0.20$) in testes of treated males compared with control males. However, spermatogonia treated with 10 μg/mL AFB_1 showed an upregulation ($P = 0.004$) of *Caspase* 3 when compared with control (0 μg/mL AFB_1) treated cells. Tunel staining of spermatogonia also showed an increase ($P = 0.03$) in the number of positively stained cells in the treated cultures (5 and 10 μg/mL AFB_1) compared with control cultures. Leydig cells treated similarly showed greater ($P = 0.02$) message for *Caspase* 3 at the 10 and 20 μg/mL levels than controls. This is the first report to our knowledge linking aflatoxicosis to apoptosis in reproductive tissues. Results imply that apoptosis may be in part responsible for damage to the testes/testicular cells, resulting in decreased testosterone levels and reduced fertility. More research is needed to determine other components of the apoptotic pathway affected by AFB_1, and whether the upregulation in *Caspase* 3 observed in this study occurred as a direct result of insult with AFB_1.

Key words: apoptosis, *Caspase* 3, aflatoxin

W244 Muscle resident adipogenic progenitors are fiber type specific, Pax3/Myf5-independent and form white adipocytes by default. Y. Q. Liu* and S. H. Kuang, *Purdue University, West Lafayette, IN.*

Ectopic accumulation of adipose tissue in skeletal muscles (intermuscular fat, IMF) has been associated with muscle wasting, insulin resistance and diabetes. However, the developmental origin and regulation of postnatal progenitors that give rise to IMF in comparison to other fat depots are unclear. We found that adipogenic progenitors are more enriched in slow than fast muscles. Cre/LoxP-mediated lineage tracing demonstrated that IMF progenitors are exclusively derived from a Pax3/Myf5-independent lineage and readily differentiate into white adipocytes in culture. In contrast, brown adipose tissue progenitors are derived from a Pax3/Myf5 double positive lineage. Interestingly, progenitors residing in anatomically distinct white adipose depots are all from a Myf5-independent lineage but are heterogeneous for Pax3 lineage dependence. Diphtheria toxin-mediated lineage ablation confirmed that Myf5 cell lineage is required for brown, but not white, adipocyte differentiation. In addition, ablation of Myf5-dependent myogenic lineage enhances adipocyte differentiation, whereas ablation of aP2- dependent adipocyte lineage impairs muscle regeneration in vivo. In old mice, reduced myogenic capacity is accompanied by accumulation of IMF. Finally, we showed that Dlk1 inhibits the differentiation of both white and brown adipocytes. These results demonstrate surprising heterogeneity of tissue-specific adipogenic progenitors and dynamic interactions between skeletal muscle and adipose tissues.

Key words: intermuscular fat, Myf5, Pax3

W245 Effect of urea on interferon-tau response in the bovine endometrium. A. Ahmadzadeh*, T. Davis, and K. Carnahan, *University of Idaho, Moscow.*

High concentrations of blood and uterine urea associated with high dietary protein have been shown to reduce fertility in dairy cows. The objective of this study was to determine the direct effects of urea on protein expression of the endometrial cells of the bovine uteri in response to interferon-tau (IFN-tau) in vitro. The objective was to determine the direct effect of urea on the production of 2 IFN- tau stimulated proteins, ISG15 and Mx1 in bovine endometrial (BEND) cells. Bovine endometrial cells were cultured to 80% confluency and treated with media containing 0, 5, 7.5, or 10 mM urea for 24 h. Subsequently, BEND cells were challenged with 0 or 10,000 antiviral units of recombinant IFN-tau and cells were incubated for an additional 24 or 36 h in media containing 0, 5, 7.5, or 10 mM urea. Cells were in culture for the same period of time regardless of treatment and then harvested. BEND cells were lysed with MPER and the protein concentrations determined by the Bradford assay. Proteins were separated by SDS-page and subjected to Western blot analysis and immunoblotting to assess the production of Mx1 and ISG15. Based on optical density of the images on x-ray film from a chemiluminescent signal, IFN-tau increased ($P < 0.01$) Mx1 and ISG15 production regardless of treatment after 24 and 36 h. There was no effect of urea treatment or urea by IFN-tau interaction on Mx1 and ISG15 production after 24 ($P = 0.9$) or 36 h ($P = 0.4$) of culture. Moreover, there was no effect of either 24 or 36 h or time by urea treatment interaction on the production of Mx1 and ISG15, in response to IFN-tau. These results show that there is no disruption of IFN- tau-stimulated Mx1 or ISG15 production, when BEND cells were exposed to various concentrations of urea in vitro.

Key words: urea, interferon-tau, bovine endometrial cells

W246 Short-term supplementation and temporary weaning on metabolic and endocrine parameters in anestrous and cyclic Hereford cows grazing native pasture. A. L. Astessiano*[1], L. Veloz[1,2], C. García Pintos[1,2], M. E. Trobo[1,2], F. Bialade[1], C. Viñoles[2], and M. Carriquiry[1], *[1]School of Agronomy, UDELAR, Montevideo, Uruguay, [2]National Research Institute for Agriculture, Tacuarembo, Uruguay.*

Two experiments were conducted to study the effect of a short-term supplementation (Exp.1 and 2) and temporary weaning (Exp.1), before initiation of the breeding period, on metabolic and endocrine parameters in grazing beef cows. In Exp.1 primiparous beef cows (n = 32, 3.6 ± 0.02 BCS) in anestrus were used in a randomized block design with a 2 × 2 factorial arrangement of short-term supplementation (non-

supplemented, CON vs. supplemented, SUP) and temporary weaning (with vs. without). In Exp.2, adult non-gestating nonlactating beef cows (n = 15, 5.3 ± 0.1 BCS) were used in a randomized block design with 2 treatments: CON vs. SUP. The supplement consisted in 2.5 kg of rice bran/cow (90.3% DM, 10% CP, 9% EE, 14% NDF) offered daily for 23 d (Exp.1 and 2) and temporary weaning was performed by applying nose plates to calves for 14 d (Exp.1). Blood samples were collected 3 times a week during the treatments. Means from mixed analyses differed when $P < 0.05$. In Exp.1, cow BCS was not affected by treatments. Insulin concentrations were greater ($P < 0.01$) in temporary weaned than suckled cows (2.31 vs. 1.29 ± 0.21 uU/mL), but plasma glucose and cholesterol did not differ among groups. Concentrations of NEFA were greater ($P = 0.04$) in SUP-suckled than in SUP-temporary weaned and CON cows (0.48 vs. 0.33 ± 0.05 mmol/L). In Exp.2, BCS did not differ between groups and increased 0.6 ± 0.1 units during the period evaluated. Insulin (2.89 vs. 3.80 ± 0.55 uU/mL) and glucose (1.1 vs. 1.2 ± 0.05 mmol/L) concentrations were lower ($P = 0.04$) in SUP than CON cows but this effect was most evident in wk 2 and 3. Plasma NEFA did not differ between treatments but cholesterol was greater ($P = 0.01$) in SUP than CON cows (281.9 vs. 234.6 ± 11.3 mg/dL). Metabolic/endocrine changes reflected a better energy balance in short-term supplemented and temporary weaned primiparous cows in anestrus whereas short-term supplementation in cycling cows with good BCS altered glucose/insulin metabolism.

Key words: cattle, nutrition, hormones

W247 Liver gene expression of GH-IGF1 axis and fatty acid metabolism genes of beef cows on grazing conditions. I: Winter-gestational period. J. Laporta*, A. L. Astessiano, V. Gutierrez, A. C. Espasandín, P. Soca, and M. Carriquiry, *Facultad de Agronomía, Universidad de la República, Montevideo, Uruguay.*

In spring-calving cows on rangeland conditions pregnancy occurs in winter, period of limited forage availability, affecting the energy balance of beef cows. Adult pregnant cows (n = 32) in a factorial arrangement of genetic group (Angus and Hereford, vs. their crosses; PU vs. CR) and forage allowances (6 vs. 10kgDM/100kgLW/d; LO vs. HI) were used to evaluate the hepatic expression of somatotropic axis genes (*insulin like growth factor I*, IGF1; *IFG1 binding protein 3 and 2*, BP3, BP2; *growth hormone receptor*, GHR; *GHR isoform-1A*, GHR1A), fatty acid oxidation genes (*acyl-CoA oxidase-1 palmitoyl*, ACOX1; *acyl-CoA dehydrogenase very long chain*, ACADVL), *peroxisome proliferator activated receptor-α* (PPARA) and, *fibroblast growth factor-21* (FGF 21).Means from a mixed model were considered to differ when $P \leq 0.05$. Liver biopsies were collected in May, August, September and, October (110 ± 10, 210, 240 and 270 ± 3 d of gestation, dgest). Expression of GHR, PPAR, and FGF21 mRNA were not affected ($P > 0.18$) by any of the factors. Abundance of GHR1A and IGF1 mRNA decreased from 110 to 270 dgest (20 to 9 ± 3; 1.6 to 0.9 ± 0.02, respectively; $P < 0.013$), and BP3 tended ($P = 0.10$) to decrease only at 210 dgest to return thereafter to initial values. The BP2 mRNA increased ($P = 0.002$) at 240 dgest and remained elevated until 270 dgest. Abundance of ACOX mRNA increased throughout gestation in winter, and ACADVL mRNA increased at 240 dgest, returning to initial values at 270 dgest ($P < 0.01$). Expression of BP3, BP2 and ACOX1 mRNA during winter-gestation also depended on cow genetic group ($P < 0.045$). The BP3 mRNA decreased at 210 and 240 dgest in PU, whereas it increased at 240 dgest in CR cows. The BP2 mRNA was greater in PU than CR cows at 110 dgest, and BP2 mRNA increased in both groups (PU at 270 and CR at 240 dgest). The ACOX1 mRNA increased earlier in gestation in PU (210 dgest) than CR cows (240 dgest). Dynamics of the GH-IGF1 axis genes and the increased expression of \β;–oxidation genes in the liver reflect changes required to meet energy demands of pregnancy during winter in beef cows on grazing conditions

Key words: somatotrophic axis, energy balance, cattle

W248 Liver gene expression of GH-IGF1 axis and fatty acid metabolism genes in beef cows on grazing conditions. II: Peripartum and lactation period. J. Laporta*, A. L. Astessiano, V. Gutierrez, A. C. Espasandín, P. Soca, and M. Carriquiry, *Facultad de Agronomía, Universidad de la República, Montevideo, Uruguay.*

Beef cows in rangeland conditions are subjected to climate variations that affect pasture growth and variability as cow physiological stage changes from pregnancy to calving and lactation, altering their energy balance. Adult pregnant cows (n = 32) in a factorial arrangement of genetic group (Angus and Hereford, vs. their crosses; PU vs. CR) and forage allowances (6 vs. 10kgDM/100kgLW/d; LO vs. HI) were used to evaluate the hepatic expression of somatotropic axis genes (*insulin like growth factor I*, IGF1; *IFG1 binding protein 3 and 2*, BP3, BP2; *growth hormone receptor*, GHR; *GHR isoform-1A*, GHR1A), fatty acid oxidation genes (*acyl-CoA oxidase-1 palmitoyl*, ACOX1; *acyl-CoA dehydrogenase very long chain*, ACADVL), *peroxisome proliferator activated receptor-α* (PPARA) and, *fibroblast growth factor-21* (FGF 21).Means from a mixed model analysis were considered to differ when $P < 0.05$. Liver biopsies were collected at −15 ± 3, 15 ± 3 and 60 ± 3 d relative to parturition, dpp). Expression of IGF1, GHR and, GHR1A were not affected ($P > 0.45$) by any of the factors evaluated. The BP3 and BP2 mRNA abundance decreased ($P < 0.015$) from −15 to 15 dpp, to return then to initial values at 60 dpp. The BP3 mRNA was also affected by the interaction between genetic group and time ($P = 0.04$), while it was not affected in CR cows, it decreased markedly at 15 dpp in PU cows. The expression of BP2 mRNA tended to be greater ($P = 0.09$) in LO than HI cows. The mRNA abundance of 2 key genes involved in fatty acid oxidation varied across time; ACADVL mRNA tended to increase ($P = 0.10$) at 60 dpp, whereas ACOX1 mRNA decreased ($P = 0.004$) from −15 to 15 dpp to return to elevated initial values at 60 dpp. Hepatic PPARA and FGF21 mRNA were not affected ($P > 0.60$) by any of the factors evaluated. We describe the dynamic of the GH-IGF axis during the peripartum and lactation period in beef cows on grazing conditions. Only IGFBPs mRNA abundance was altered. The increase of ACADVL mRNA and the elevated levels of ACOX mRNA can reflect the need to oxidize fatty acids during postpartum period to meet energy demands of lactation.

Key words: somatotropic axis, fatty acid oxidation, cattle

W249 Uterine gene expression in beef cows grazing different forage allowances of native pastures. M. Carriquiry*[1], F. Bialade[1], M. P. Grignola[1], P. Soca[1], A. C. Espasandín[1], C. Viñoles[2], and A. Meikle[3], *[1]School of Agronomy, UdelaR, Montevideo, Uruguay, [2]National Research Institute for Agriculture, Tracuarembó, Uruguay, [3]School of Veterinary Sciences, UdelaR, Montevideo, Uruguay.*

The aim of this study was to evaluate the effect of long-term nutrition at 2 different forages allowances of native pastures on uterine gene expression in beef cows. Adult cows (Angus, Hereford and F1 crossbred) were used, from May 2007 to May 2010, in a complete randomized block design with 2 forage allowances throughout the year (6 vs. 10 kgDM/100kgBW/d; LO vs. HI) . At the end of the third year, at 178 ± 15 d postpartum, cows were synchronized with 2 prostaglandin (PG)

injections 11 d apart and slaughtered 32 ± 1 h after the last PG injection. Uterine tissue from the middle third of the uterine horn ipsilateral to the corpus luteum was collected from all cows that had at least 2 previous ovulations (n = 8 and 6 for HI and LO, respectively). Relative expression of estrogen (ERα) and progesterone (PR) receptors, growth hormone receptor (GHR), insulin-like growth factor-I (IGF-I), IGF-II, IGF receptor-1 (IGFR1), IGF binding proteins (IGFBP) −2, −3, −4, −5, and −6 mRNA was determined using SYBR-Green real time PCR and normalized to the expression of hypoxanthine-phosphoribosyltransferase and β-actin mRNA. Data were analyzed with a mixed model that included forage allowance and block as fixed and random effects, respectively. At slaughter, cow BCS did not differ ($P = 0.318$) between groups and averaged 3.9 ± 0.08 (scale 1–8). Expression of ERα, PR, GHR, IGF-I, IGF-II, IGFBP3, IGFBP5, and IGFBP6 mRNA did not differ ($P > 0.128$) between forage allowances. However, uterine IGFBP2 tended ($P = 0.092$, 0.30 vs. 0.15 ± 0.08) to be greater and IGFBP4 mRNA was greater ($P = 0.017$, 2.52 vs. 1.25 ± 0.97) in LO than HI cows. Uterine GHR mRNA was correlated ($P < 0.017$) to ERα (r = 0.65), IGFBP4 (r = 0.60) and IGFBP5 (r = 0.69) mRNA while IGF-I mRNA was negatively correlated ($P = 0.043$, r = −0.53) to IGFBP5 mRNA and IGF-II mRNA was positively correlated ($P = 0.023$, r = 0.58) to IGFBP6 mRNA. Nutritional plane may influence IGF availability in the uterus of beef cows indirectly through changes in expression of IGFBPs.

Key words: cattle, grazing, reproduction

W250 The effect of leptin on primary cultured adipocytes of pigs. J. Liang, X. Zhang, Y. Zheng, S. Pan, R. Zhao, and X. Yang*, *Nanjing Agricultural University, Nanjing, P. R. China.*

To investigate the effect of leptin on primary cultured adipocytes of pigs and the possibly mechanism mediated by perilipin. SV cells were separated from subcutaneous adipose tissue of weaned piglet. Cells were cultured to 80% confluence followed by differentiation for 3 d, then treated with 10–8 M and 10–7 M leptin respectively for 4h (short-term treatment) or 48h (long-term treatment). Oil-red O and immunofluorescence histochemistry were used to identify adipocytes, lipid droplets and perilipin. Cultured media were collected for quantization of glycerol content. Perilipin, HSL and ATGL mRNA levels were determined by Real-time RT-PCR. Activity of lipases (HSL and ATGL) was determined. Perilipin and phosphorylated perilipin protein levels were quantitated by Western blot analysis. The results showed that after leptin treatment for 4h, the viability of cells was increased significantly in 10–7 M leptin group; cells in 10–7 M and 10–8 M groups released significantly more glycerol than in the control; Perilipin, HSL and ATGL mRNA expression were significantly increased by 10–7 M leptin treatment, whereas 10–8 M leptin treatment increased the mRNA expression of ATGL only; there was no alteration of lipase activity and perilipin content, and the phosphorylation of perilipin was even not observed in both concentration groups. After leptin long-term treatment for 48h, cells in 10–7 M and 10–8 M groups released significantly more glycerol than in the control; Perilipin mRNA was downregulated by 10–8 M leptin; the perilipin protein content showed downregulate tendency ($P = 0.1$) in 10–7 M leptin group, whereas the phosphorylated perilipin content were detected significantly higher in both treatment groups. The results indicate that the mechanism of the glycerol release in adipocyte induced by leptin short-term and long-term treatment may be different. The leptin short-term treated influence mRNA expression of related genes, and long-term leptin treatment increased lipolytic activity of adipocytes possibly by activating phosphorylation of perilipin.

Key words: adipocyte, leptin, perilipin

W251 Injection of 100 µg of GnRH 31 d after AI does not reduce pregnancy loss in lactating dairy cows. A. L. A. Scanavez*, L. G. D. Mendonça, P. R. B. Silva, J. G. N. Moraes, and R. C. Chebel, *Department of Veterinary Population Medicine, University of Minnesota, St. Paul.*

Objectives of the current study were to determine whether treatment with 100µg of GnRH 31 ± 3 d after artificial insemination (AI) reduces pregnancy losses and whether exposure to heat stress affects this outcome. Lactating cows from 2 dairies were enrolled in the study at 31 ± 3 d after AI. At enrollment cows were grouped by parity and number of AI and assigned to 1 of 2 treatments in a ratio of 1:2. Cows assigned to the GnRH treatment received 100 µg of GnRH at 31 ± 3 d after AI and cows assigned to the control treatment did not receive GnRH. All cows were examined by manual palpation per rectum at 38 ± 3 d after AI (first pregnancy diagnosis) and those diagnosed pregnant were re-examined 66 ± 3 d after AI (second pregnancy diagnosis). Data regarding daily temperature and humidity were recorded and temperature humidity index (THI) was calculated from 4 weeks before to 9 weeks after AI. At pregnancy diagnosis 38 ± 3 d after AI there were 606 pregnant GnRH cows and 1,303 pregnant control cows. No cows were exposed to heat stress (THI > 72) between AI and pregnancy diagnosis and average THI between AI and first pregnancy diagnosis was 53.0 ± 0.1. Average THI from AI to first pregnancy diagnosis was 58.9 ± 0.1 and average THI between first and second pregnancy diagnosis was 63.9 ± 0.1. Average THI from AI to the second pregnancy exam was 60.1 ± 0.1, cows were exposed to 0.5 ± 0.1 week with weekly average THI > 72, and 21.1% of cows were exposed to at least one week of heat stress (weekly average THI > 72). Pregnancy loss from 38 ± 3 to 66 ± 3 d after AI was not ($P = 0.42$) affected by treatment (GnRH = 5.9, control = 5.1%). Similarly, site ($P = 0.94$), parity ($P = 0.99$), and exposure to heat stress did not affect pregnancy loss from 38 ± 3 to 66 ± 3 d after AI. Average projected 305-d milk yield was 11,218.6 ± 42.2 kg and projected 305-d milk yield affected ($P < 0.01$) pregnancy loss from 38 ± 3 to 66 ± 3 d after AI because cow in the lower 2 quartiles (Q1 = 2.7 and Q2 = 4.2%) had smaller ($P < 0.07$) incidence of pregnancy loss than cows in the higher 2 quartiles (Q3 = 7.7 and Q4 = 6.9%). Treatment with GnRH 31 d after AI does not reduce pregnancy loss regardless of exposure to heat stress.

Key words: dairy cow, pregnancy loss, GnRH

W252 Replacing grain and silage with wheat distiller grains affects feeding behavior of finishing beef cattle. W. Z. Yang*[1], T. A. McAllister[1], J. J. McKinnon[2], and K. A. Beauchemin[1], *[1]Agriculture and Agri-Food Canada, Research Centre, Lethbridge, AB, Canada, [2]Department of Animal & Poultry Science, University of Saskatchewan, Saskatoon, SK, Canada.*

A study was conducted to evaluate DMI and feeding behavior of feedlot beef steers fed diets that varied in the proportion of wheat dried distillers grains with solubles (DDGS), with DDGS replacing barley grain or silage. Eighty crossbred steers (486 ± 28 kg) were randomly allotted to 8 pens (2 pens per treatment). The pens were fitted with the GrowSafe system and the steers were tagged with transponders enabling continuous recording of feeding behavior of individual steers, including frequency and duration of visits to the feed bunk and individual feed intake. Steers were fed 1 of 4 diets: control, low (25DDGS), medium (30DDGS), and high (35DDGS) wheat DDGS (DM basis). The control diet consisted of 15% barley silage, 85% barley grain concentrate; the 3 DDGS diets were formulated by substituting 20% barley grain and 5, 10 and 15% silage, respectively, with 25, 30 and 35% wheat DDGS such that the 35DDGS diet contained no silage. In comparison to control, calves fed 25DDGS had greater ($P < 0.01$) DMI (9.5 vs. 11.3 kg/d) and feeding time (84 vs. 112 min/d), but feeding rate (115 vs. 108 g/min), meal frequency (9.3 vs. 10.8, meal/d), and meal length (9.9 vs. 10.9 min/meal) were not different. With increasing substitution of wheat DDGS for silage, DMI (11.3 to 10.7 kg/d; $P < 0.05$), feeding time (112 to 89 min/d; $P < 0.01$), and meal length (10.9 to 8.3 min/meal; $P < 0.01$) linearly decreased, but feeding rate (108 to 134 g/min) and meal frequency (10.8 to 15.4 meal/d) linearly increased ($P < 0.01$). The results indicate that feeding a diet containing moderate levels of wheat DDGS with adequate silage increased DMI but longer feeding time was required. In contrast, when diets contained minimal (i.e., 5%) or no silage, steers increased feeding rate and meal frequency to consume more feed.

Key words: feeding behavior, feedlot beef cattle, wheat DDGS

W253 Inclusion of anti-phospholipase A2 antibody (aPLA2) to backgrounding diet enhanced feed efficiency in growing beef calves. V. R. G. Mercadante*, K. M. Bischoff, T. E. Black, G. H. L. Marquezini, N. DiLorenzo, and G. C. Lamb, *North Florida Research and Education Center, University of Florida, Marianna.*

We determined whether supplementation of anti-phospholipase A2 antibody (aPLA2; BIG BEEF, Aova Technologies, Madison, WI) for growing beef cattle would alter voluntary DM feed intake and feed efficiency of growing calves. Individual performance and daily DMI was measured on 70 crossbred weaned calves (53 steers and 17 heifers) during a 70-d period using a GrowSafe system (GrowSafe Systems Ltd., Alberta, Canada) at the University of Florida NFREC Feed Efficiency Facility. All calves where submitted to a 21-d period of adaptation to facilities and diets. Calves were fed a growing forage-based TMR diet (0.97 Mcal NEg/kg DM, 14.7% CP) to support growth rates of 1 kg/d (NRC, 1996). Calves were blocked by weight and sex and then assigned to pens to receive either no additional supplement (Control, n = 35) or receive a supplement that delivered aPLA2 at an inclusion rate of 0.6% of the dietary DM (BIG BEEF, n = 35). Body weight (BW) was recorded at 14-d intervals over the 70-d period. Linear regression of BW against day on test was used to establish ADG. Initial BW (245.5 ± 5.3 kg and 246.2 ± 5.3 kg for Control and BIG BEEF, respectively; $P = 0.93$), final BW (318.6 ± 5.8 kg and 317.7 ± 5.8 kg for Control and BIG BEEF, respectively; $P = 0.91$), and ADG (1.01 ± 0.03 kg and 1.01 ± 0.03 kg for Control and BIG BEEF, respectively; $P = 0.99$) were similar between treatments. However, daily DMI was greater ($P < 0.0001$) for Control (8.47 ± 0.19 kg) than BIG BEEF (7.87 ± 0.19 kg). In addition, G:F tended ($P = 0.10$) to be greater for BIG BEEF (0.1294 ± 0.004) than Control (0.1206 ± 0.004) and residual feed intake was greater ($P < 0.01$) for Control (0.624 ± 0.291 kg/d) than BIG BEEF calves (−0.624 ± 0.291 kg/d).We conclude that the supplementation of anti-phospholipase A2 (BIG BEEF) for growing beef cattle decreased daily DMI while maintain ADG, therefore, improving feed efficiency.

Key words: beef cattle, feed efficiency, phospholipase A2

W254 Productive performance during fattening phase of Nelore fed diets with two concentrate levels. G. S. Firmino*[1], I. S. Silva[1], F. A. Barbosa[2], S. L. S. Cabral Filho[1], J. F. B. Guedes[1], G. A. Carneiro[1], F. F. Gouveia[1], and J. F. A. Oliveira[1], *[1]University of Brasília - UnB, Brasília, DF, Brazil, [2]Federal University of Minas Gerais - UFMG, Belo Horizonte, MG, Brazil.*

The experiment evaluated the performance of feedlot cattle divided into 2 experimental groups and submitted to 2 diets during 90 d. The herd consisted of 30 bulls aged 22 mo, with an initial average body weight (IBW) of 350.25 kg, which were divided into 2 groups of 15 animals per treatment. The experimental groups were: DIE70 - concentrate (corn grain, sunflower meal, soybean hulls, urea and mineral) and corn silage at a ratio of 70:30 on dry matter and DIE85 - concentrate (corn grain, sunflower meal, soybean hulls, urea and mineral) and corn silage in proportion of 85:15 on a DM basis. The experiment was conducted in a completely randomized design with 2 treatments and 15 repetitions (n = 30). The average initial body weight (IBW), final body weight (FBW), average daily gain (ADG) and hot carcass yield (HCY) were compared by Duncan test with significance level of $P < 0.05$. There was no statistical difference ($P > 0.05$) between IBW with averages of 344.86 kg and 351.61 kg and also between the FBW, 444.66 kg and 441.77 kg for the treatments DIE70 and DIE85 respectively. The ADG and HCY among treatments DIE70 and DIE85 did not differ; the values were 1.16 kg for DIE70 and 1.04 kg for DIE85, and 57.26% for DIE70 and 57.04% for DIE85. In this study, the 85% concentrate diet did not improve animal performance compared with diets containing 70% of concentrate.

Key words: performance, carcass, beef cattle feedlot

W255 Effect of maternal feed efficiency as growing heifers and lactating cows on feed intake and performance of their suckling offspring. K. M. Bischoff*[1], T. E. Black[1], V. R. G. Mercadante[1], G. H. L. Marquezini[1], C. C. Chase[2], S. W. Coleman[2], and G. C. Lamb[1], *[1]North Florida Research and Education Center, University of Florida, Marianna, [2]USDA-ARS, SubTropical Agricultural Research Station, Brooksville, FL.*

We determined whether suckling calf DMI and performance was associated with feed efficiency, feed intake, and performance of their dam as a growing heifer or lactating cow. Feed efficiency was established in

74 growing heifers that subsequently gave birth to their second calf as 3-yr old cows. For the heifer and cow phases, females had a 14-d acclimation period before initiating a 70-d feed efficiency test period. Individual daily feed intakes were recorded using the GrowSafe System (GrowSafe Systems Ltd., Alberta, Canada) to determine average DMI. A forage-based diet consisting of 86.7% Tifton 85 Bermudagrass silage, 12.4% dried distillers grains plus soluble, 0.7% range mineral, and 0.2% salt was fed ad libitum to cow-calf pairs. Cows were milked on d 14 (lactation d 28 ± 7) and d 70 (lactation d 84 ± 7) of the test to determine individual energy corrected milk (ECM). Average DMI of calves was determined by the sum of DMI of feedstuffs and the DMI of ECM from suckling. Weights of calves were collected on d 0 and 70. During the 70-d test calves had ADG of 0.51 kg/d and consumed 0.44 kg/d of feed and 3.98 kg/d ECM (0.52 kg/d on a DM basis). The correlation between total DMI of calf and residual feed intake (RFI) of dam during lactation ($P = 0.88$, r = 0.0191) or RFI of dam as a heifer were similar ($P = 0.97$, r = 0.004). In addition, there was no correlation between DMI of the dam as a lactating cow ($P = 0.172$, r = 0.160) or as a heifer ($P = 0.34$, r = 0.112) to the total DMI of the calf. The gain:feed (G:F) of the calf was not correlated to dam RFI as a cow ($P = 0.30$ r = −0.125) or heifer ($P = 0.74$ r = 0.039). There was no correlation in DMI from feed consumed to DMI from ECM ($P = 0.50$, r = 0.080). However, there was a correlation between G:F and DMI of feed of the calf ($P < 0.001$, r = 0.424); however, there was no correlation between DMI of ECM consumed and the G:F of calves ($P = 0.04$, r = −0.238). We conclude that DMI and performance of suckling calves is not related to feed efficiency, feed intake, and performance of their dam as a growing heifer or lactating cow.

Key words: calf performance, dry matter intake, feed efficiency

W256 Temperament evaluation of Nelore (*Bos indicus*) cattle in Brazilian commercial cow-calf operations. M. Meneghetti*[2], R. F. Cooke[1], B. I. Cappellozza[1], D. W. Bohnert[1], and T. C. Losi[3], *[1]Oregon State University–Eastern Oregon Agricultural Research Center, Burns, [2]Pfizer Animal Health, São Paulo, SP, Brazil, [3]Lageado Consultoria Agropecuária, Mineiros, GO, Brazil.*

Temperament impacts several production parameters in beef cattle, including growth and reproduction. Excitable temperament is frequently detected in *Bos indicus* breeds such as Nelore, which represents the majority of the beef cattle in Brazil – country that holds the largest commercial cattle herd, and is the main exporter and second main producer of beef in the world. However, there is a lack of research studies characterizing temperament of Nelore cattle. Therefore, efforts to determine incidence of excitable temperament and its effects on productivity of Nelore cattle will benefit not only beef production in Brazil, but also availability of beef in many parts of the planet. The objective of the present study was to evaluate temperament in Nelore brood cows, assess the incidence of aggressive cattle in commercial ranches, and correlate temperament measurements with production traits. A total of 855 lactating, multiparous Nelore cows, from 4 different commercial cow-calf ranches (ranch 1, n = 231; ranch 2, n = 195; ranch 3, n = 236; ranch 4, n = 193) were evaluate for BCS, chute core (CS; 1 to 5 scale), and exit velocity (EV; m/s using infrared sensors) when processed for AI. Based on EV and CS (±1 SD from the mean), cows were classified as docile, moderate, or aggressive. Across all ranches, CS and EV were correlated ($P < 0.01$, r = 0.47). A ranch effect was detected ($P = 0.05$) because the correlation coefficient between CS and EV different among ranches (0.47, 0.65, 0.45, and 0.72 for ranches 1, 2, 3, and 4, respectively), which is likely due to differences in the design of the handling facilities. No significant correlations were detected among CS or EV with BCS ($P > 0.11$). Across all ranches, 12% of cows were classified as docile, 74% were classified as moderate, and 14% were classified as aggressive. In conclusion, temperament did not influence BCS of Nelore beef cows at the beginning of the breeding season. However, additional efforts to determine if temperament affects other production parameters in Nelore beef cows are warranted due to the reduced proportion of docile cattle in commercial cow-calf ranches in Brazil.

Key words: Nelore, temperament, productivity

W257 Influence of propionate salt levels on young cow reproductive performance. J. A. Walker*, G. A. Perry, and K. C. Olson, *South Dakota State University, Brookings.*

A supplementation study was conducted to evaluate level of propionate salt on young cow performance. Two- and 3-yr-old cows (n = 60) were allocated to one of 3 treatments at calving. Propionate salt was incorporated in a protein supplement (30% CP, 73% TDN) at a rate of 0, 80 or 160 g/d of propionate salt. Cows were individually supplemented twice weekly at 1.14 kg/d. Cows had access to pasture and hay (6.9% CP, 59.7% TDN). Blood was collected weekly to determine postpartum interval (≤1 ng P_4/ml). Weights and BCS were assigned at calving, end of supplementation, start of breeding season, and weaning. No differences in cow weight ($P = 0.11$) and BCS ($P = 0.17$) were found between treatments. Cow weight changed through the study ($P < 0.01$, 418, 443, 468 and 475 kg for calving, end of supplementation, start of breeding season and weaning, respectively). Cow ADG had a treatment by period interaction ($P < 0.05$): ADG displayed a quadratic response ($P < 0.05$) to levels of propionate salt during the supplementation period with 80 g displaying the highest ADG, but no response during the end of supplementation to breeding or breeding to weaning periods. Cow BCS changed through the study ($P < 0.01$, 4.46, 4.87, 4.90 and 4.73 for calving, end of supplementation, start of breeding season and weaning, respectively). Cows BCS increased during supplementation ($P < 0.01$, 0.42) and decreased from breeding to weaning (−0.17). Calf weight was not different ($P = 0.38$) between treatments. Calf weight increased through the study ($P < 0.01$, 36.1, 101.3 and 197 kg at birth, start of breeding season, and weaning, respectively). Pregnancy rates did not differ between treatments ($P = 0.24$). Pregnancy rates differed by cow age ($P < 0.01$, 77% and 100% for 2- and 3-year-olds, respectively). Cows initiating estrous cycles before the breeding season were greater ($P < 0.05$) for 160 g (47.6%) compared with 0 g (15.6%) and tended to be greater than 80 g ($P < 0.10$, 20.0%). Based on ultrasonography, 3-year-old cows conceived earlier ($P < 0.01$, 183.7 d) than the 2 year cows (207.0 d). Propionate salt did not influence cow weight or BCS; however, propionate salt did influence reproductive performance.

Key words: propionate salt, young beef cows

W258 Methane emission potential and nutritional composition of four *Panicum* sp. forage genotypes in the Brazilian Cerrado region. L. Bezerra da Silva*[1], S. L. S. Cabral Filho[1], R. Guimarães Júnior[2], A. L. Abdalla[3], A. K. B. Ramos[2], and F. D. Fernandes[2], *[1]Universidade de Brasília, Brasília, Distrito Federal, Brasil, [2]Embrapa Cerrados, Planaltina, Distrito Federal, Brasil, [3]Universidade de São Paulo, Piracicaba, São Paulo, Brasil.*

Four genotypes of *Panicum* sp. were evaluated, namely 2 accessions called PM34 and PM46, as well as 2 commercial cultivars, *Panicum maximum* 'Massai' and *Panicum maximum* 'Mombaça'. The purpose of the evaluation was to evaluate nutritional features, and to assess methane emission potential ensuing from the respective chemical composition characteristics of each genotype. The experiments were conducted both at an EMBRAPA unit called Cerrados, which is located in Planaltina town, Federal District (DF) and at the Animal Nutrition Laboratory on the Federal University of Brasília – UnB, within the period from September 2007 to May 2010. The genotypes' methane emission potential was assessed by applying the semi-automated in vitro gas production technique combined with the gas chromatography method concerning methane gas production at 8, 12 and 24 h post-inoculation. The split plot and split block experiment design with 3 repetitions was the experimental approach employed in laboratory analyses. Tukey's test at 5% probability level was applied to compare the means obtained and the data analysis was performed by using the SAS software (2000 version). The dry matter rate was 24.88%, and the neutral detergent fiber (NDF), non-fiber carbohydrate and NDF-nitrogen rates were respectively 67.85%, 11.34%, and 52.58%. Significant differences ($P < 0,05$) were found among the analyzed cultivars in respect to cumulative gas production (CGP), dry matter digestibility (DMD), amount of methane gas produced (ACH_4), as well as the amount of methane gas produced by each gram of dry matter digested (CH_4GDMD). It was observed that CH_4GDMD was negatively related to the level of non-fiber carbohydrates (−0.9063) and positively related to the percentage of nitrogen linked to the neutral detergent fiber (NDF) in the genotypes analyzed (0.9925). In conclusion, a higher methane emission potential was observed for the genotype PM34 after 24 h fermentation, which presented a higher CH_4GDMD rate (32.37 mL/g) combined with a lower DMD rate (35.92%) ($P < 0.05$).

Key words: bovine, semi-automated in vitro gas production technique, greenhouse-effect gases

W259 Methodology for estimating intermuscular, subcutaneous, and intramuscular fat in primal cuts. M. J. McPhee*[1,2], J. P. Siddell[1,2], B. J. Walmsley[1,2], W. H. Johns[1,2], and P. L. Greenwood[1,2], *[1]Cooperative Research Centre for Beef Genetic Technologies, Armidale, NSW, Australia, [2]Industry and Investment NSW, Armidale, NSW, Australia.*

In this study 6 whole beef rumps (3.67 to 5.05 kg) were purchased to evaluate the accuracy of estimating subcutaneous (SUB) and intermuscular (INTER) fat content from computer-aided tomography (CT)-scanned images. A full dissection by 2 operators of SUB and INTER fat was used to evaluate the accuracy of the CT prediction. The rumps were scanned using a Picker Ultra Z Spiral CT scanner (Philips Medical Imaging Australia, Sydney NSW) in the Meat Science CT unit at the University of New England Meat, Armidale. Voltage and current were set at 130 kV and 100 mAs, respectively. A pitch of 1.5, field of view of 480 mm, slice thickness of 5mm and distance between slices of 15mm were used. One hundred and 10 axial slices from 6 primal cuts were created. Total fat and lean in each rump were calculated using image analysis software. Boundaries for fat and lean were set at 10 to 128 and 129 to 210 gray scale units, respectively, with an image diameter of 487mm. INTER fat was removed from each slice using an elliptical tool in ImageJ (public domain software). Images only containing SUB fat were then analyzed to estimate the amount of SUB fat (kg). INTER fat (total fat – SUB fat) was calculated by difference. The SUB and INTER fat dissections were weighed and vacuum packed. Bags were then scanned to determine the amount of fat and lean in each dissected fat depot. The ratio of SUB and INTER fat to the dissected weight (kg) was used to account for any associated errors. The linear relationships between scanned (y) vs. dissected (x) fat for total, sub, and inter fat were $y = 1.0x + 0.02$ (SE = 0.22; $AdjR^2 = 0.98$), $y = 0.92x + 0.01$ (SE = 0.01; $AdjR^2 = 0.99$), and $y = 0.98x + 0.07$ (SE = 0.02; $AdjR^2 = 0.83$), respectively. These results demonstrate that fat deposition in beef primal cuts from scanned data are feasible and can be done with a high degree of accuracy. The amount of intramuscular fat has also been estimated from the scanned images of a Beef Cooperative Research Centre serial slaughter investigating marbling and fat distribution in Angus, Hereford, and Wagyu × Angus steers after SUB and INTER fat has been removed from each slice using the elliptical tool in ImageJ.

Key words: beef cattle, fat deposition

W260 The influence of two levels of concentrate on the performance characteristics and carcass yield in Nellore cattle in *Brachiaria brizantha* compared to Marandu pastures. G. A. Carneiro*[1], F. A. Barbosa[2], S. L. S. Cabral Filho[1], R. V. Oliveira[1], G. S. Firmino[1], C. E. Souza[1], F. F. Gouveia[1], and J. F. A. Oliveira[1], *[1]University of Brasilia, Brasilia, DF, Brazil, [2]Federal University of Minas Gerais, Minas gerais, MG, Brazil.*

The aim of the study was to evaluate the effects of 2 levels of concentrate on the performance characteristics and carcass yield in cattle in *Brachiaria Brizantha* compared with Marandu pastures. The experimental period went from August 2010 to January 2011. The animals used were 30, 22 mo-old Nellore steers with average initial body weight of 330.42 kg, divided into 2 treatments: SCONF 1 – average daily intake of the concentrate (corn, sunflower bran, soybean hulls, urea and minerals) offered at 0.91% the average body weight (ABW; dry matter - DM); SCONF 2 – average daily intake of the concentrate (corn, sunflower bran, soybean hulls, urea and minerals) offered at 1.42% the ABW in DM. The experiment was conducted in a randomized block design with 2 treatments and 3 replications. The Duncan test was used with 5% significance for comparison of treatments for performance and animal's carcass yield. The average final BW obtained was 477.94 kg, therefore there was no statistical difference in the average daily gain (ADG) and in the carcass yield between treatments SCONF 1 and SCONF 2 (ADG 0.867 kg/head/day for both treatments, and carcass yield of 56.00% for SCONF 1 and 56.03% for SCONF 2 ;$P > 0.05$). The 1.42% daily intake in DM of the concentrate did not improve weight gain and carcass yield compared with the daily intake of 0.91% in DM.

Key words: beef cattle, weight gain, grass

W261 Two methods to estimate milk yield in beef cattle grazing systems. A. C. Espasandin*, A. Casal, V. Gutierrez, M. Cadenazzi, and M. Carriquiry, *School of Agronomy, UdelaR, Uruguay.*

The objective of this work was to compare 2 different methods to estimate milk yield (MY) of a beef cattle herd at the Experimental Station Bernardo Rosengurtt, School of Agronomy, Uruguay. Hereford, Angus and F1-crosbred (n = 24) primiparous cows were used to estimate MY, once a month from birth to weaning, with Weight-suckle-weight (WSW) and Milking Machine (MM). All cows grazed native

pasture (2300 kg MS/ha of forage allowance). Two groups were created, each group with one method to estimate milk yield, and then the method was inverted. In WSW method calves were weighted before and after suckling (weight losses by urine and feces were registered previously). Difference between pre and post-suckling weights was recorded as estimated milk production of the dam. In MM method, cows were milked in the morning and afternoon, after receiving oxytocin. Milk was weighted in the afternoon. Estimations of MY, adjusted to 24 h, were analyzed with a repeated measures model including of sex of calves, month of lactation, group, cow breed, calf breed as fixed effects, postpartum days as a covariate, and the cow(breed) as random effect. To compare the 2 methods (WSW or MM), the effect was included in the previous model. Reproducibility of the 2 methods was studied by the Gage r&R (repeteability&Reproducibility) variance components. The MY estimated along lactation period was different between the 2 methodologies, WSW method estimates more MY than MM method. The Effect of method was significant ($P < 0.03$). The r&R coefficients range 83% (r = 0.72 and R = 0.41) suggesting low correlations. MM method estimates the potential capacity of the cow to produce a quantity of milk in a delimited period. Whereas, WSW method estimates milk consumption of calves but it is not an accurate method to estimate the real milk production of the dams. Standard errors analysis for the 2 methods show different variation associated to the estimated mean. The mean variation coefficient was 6% and 18% in MM and WSW method, respectively. Based on variability observed in this experiment, MM method is a more accurate method to estimate milk production in beef cattle systems.

Key words: beef cattle, Gage r&R, milk yield

W262 Comparison of spring and fall calving beef herds grazing endophyte-infected tall fescue. B. T. Campbell*[1], W. M. Backus[1], M. C. Dixon[2], R. J. Carlisle[2], and J. C. Waller[1], *[1]The University of Tennessee, Knoxville, [2]Research and Education Center at Ames Plantation, Grand Junction, TN.*

Twenty years of production records for spring and fall calving cows were obtained from the Research and Education Center at Ames Plantation. The cow herds were under the same management for the years contained in the study and all cows were strictly culled for reproductive failure and low performance. The cows primarily graze tall fescue (*Lolium arundinaceum* Schreb.) with the wild-type endophyte (*Neotyphodium coenophialum*) that induces the signs of tall fescue toxicosis. The spring herd was comprised of 551 cows and 1548 calves and the fall herd was comprised of 463 cows and 1834 calves respectively. The average age of cows in the spring herd was 4 years old, ranging from 2 to 11; and the average age of cows in the fall herd was 5 years old ranging from 2 to 12 respectively. Data were analyzed for calving interval, number of calves born, birth weight of calves, weaning weight of calves, adjusted 205-d weaning weight, average daily gain (ADG) from birth to weaning, and weight/day of age. The data were analyzed using a randomized block design in SAS 9.2. The spring calving herd had a shorter calving interval by an average of 10 d ($P < 0.05$), and produced fewer calves per cow ($P < 0.05$). The fall calving herd averaged 4 calves per cow while the spring calving herd only averaged 3. Calves born in the spring had higher birth weights than those born in the fall ($P < 0.03$), and spring born calves had higher ($P < 0.001$) adjusted 205-d weaning weights than fall born calves. The calves born in the spring had an ADG from birth to weaning of 1.03 kg/day while the calves born in the fall averaged 0.98kg/day. Fall born calves were lighter at birth than spring born claves and had lower weaning weights than spring born calves. However, spring calving cows had a higher replacement rate than fall calving cows. Higher replacement rates in the spring calving herd could be the result tall fescue toxicosis, a problem during the breeding season of spring calving cows. In contrast fall calving cows are bred during winter when tall fescue is dormant and tall fescue toxicosis is not a problem.

Key words: fescue, calving season, production

W263 Influence of winter and spring pasture allowance on growth and reproductive performance on beef replacement heifers. B. L. Bailey*, K. M. Krause, and T. C. Griggs, *West Virginia University, Morgantown.*

The objective of this study was to compare heifer growth and reproductive performance following 2 pasture allowances during the winter and following spring grazing season. Three 5-ha fields were selected as blocks in a randomized complete block design for application of grazing treatments. All fields had been in long-term hay and/or pasture production and contained cool-season grass-legume mixtures (orchardgrass, tall fescue, smooth bromegrass, quackgrass, red and white clovers). Seventy-two spring born heifers of primarily Angus background and 247 kg mean body weight (BW) were allocated to grazing treatments (12 hd/replicate of a treatment) for the entire developmental period November 12, 2009 - May 24, 2010 (194 d). The treatments consisted of daily herbage dry matter (DM) allocation of 3.5 (LOW) or 7.0 (HIGH) % of BW. The winter grazing period began November 12 and ended December 20. During the winter feeding period (December 21 - April 19) haylage (6.2 kg DM/hd/d) was fed and supplementation of soybean hulls (1.8 kg DM/hd/d) occurred January 20 - April 19. Spring grazing began April 20 and ended May 24. BWs were determined every 2 weeks and blood samples were taken on d 13, 41, 71, 109, 139, 155, 169, and 180. Heifers were subjected to a 58 d breeding season. Average daily gains (ADG) for the entire developmental period were 0.56 vs. 0.63 kg/d ($P = 0.12$) for LOW vs. HIGH heifers. During the winter grazing period ADG were 0.37 vs. 0.63 kg/d ($P < 0.05$) for LOW vs. HIGH heifers. For the winter feeding period ADG were 0.34 vs. 0.39 kg/d ($P = 0.31$) and for the spring grazing period 1.43 vs. 1.36 kg/d ($P = 0.38$) for LOW vs. HIGH heifers. Proportion of heifers who had reached puberty, and BW at the onset of the breeding season did not differ between treatments (60% vs. 60%, $P = 1.0$; and 357 vs. 369 kg; $P = 0.12$, for LOW vs. HIGH). Pregnancy rates did not differ (LOW: 74%, HIGH: 81%). We interpret these results to indicate that delaying the majority of weight gain until late in heifer development may decrease costs of winter feeding without detrimental effects on reproductive performance.

Key words: beef heifers, grazing, reproductive performance

W264 Cow and calf separation to improve reproductive performance of first-calf Nellore beef cows under tropical conditions. P. G. M. A. Martins*[1,2], C. A. A. Torres[1], A. B. Mancio[1], W. F. Souza[1], G. C. Lamb[3], and J. D. Arthington[2], *[1]Universidade Federal de Viçosa, Departamento de Zootecnia, Viçosa, Minas Gerais, Brazil, [2]University of Florida, Range Cattle Research and Education Center, Ona, [3]University of Florida, North Florida Research and Education Center, Marianna.*

Our objectives were to compare the effects of an early Nellore-calf weaning, to cows kept with their calves and a 72-h calf withdrawal on measures of performance of first-calf beef cows. Seventy-six primipa-

rous, Nellore cow-calf pairs were randomly allotted to 3 treatments: EW (early weaned); TW (temporary weaned for 72 h); and CON (control – cows remained with their calves throughout the study). Treatments were initiated at the start of a 90-d breeding season, starting on November 2009. Cow and calf BW, and cow BCS were determined at d 0, 30, 63 and 90 of the study. Blood samples were collected over 90 d, 10 d apart for determination of progesterone concentrations. Resumption of cyclicity was defined as the first sampling day when progesterone concentrations were ≥1.5 ng/mL for 2 consecutive sampling dates. Pregnancy was diagnosed by transrectal ultrasonography on d 63 and 53 d after the end of the breeding season. Cow and calf BW did not differ at the beginning of the breeding season ($P > 0.10$; BW = 365 ± 28.3 and 106 ± 14.5, respectively), as well as cow BCS. However, at the end of the breeding season, cow BW was greater for EW cows, compared with TW and CON ($P < 0.10$; BW = 440 ± 35.4; 404 ± 33.4; 398 ± 30.3, respectively). Cow BCS was also greater for EW cows, compared with TW and CON cows ($P < 0.10$; average BCS = 4.5; 3.8; 3.8, respectively; SEM = 0.10). For calf measures, TW and CON calves had greater BW, compared with EW since December, reflecting on BW at the normal weaning time ($P < 0.10$; BW = 164 ± 19.1; 201 ± 23.7; 196 ± 20.2 for EW, TW, and CON calves, respectively). By d 10 of the breeding season (corresponding to aproximately120 d postpartum), more ($P < 0.05$) EW cows were cycling than TW and CON cows. Pregnancy rate was 84.0 and 96.0% for EW, 60.0 and 84.0% for TW, and 46.2 and 80.8% for CON during and after the breeding season, respectively. In the first year of the study, early calf weaning improved cow pregnancy rate, BW and BCS, but resulted in impaired BW gain of EW calves.

Key words: body condition score, progesterone, weaning

W265 Relationships between performance and residual feed intake in Bonsmara heifers when confinement fed or on pasture. L. M. Wiley*[1,2], T. D. A. Forbes[1], A. N. Hafla[2], C. M. Hensarling[1], B. G. Warrington[1], and G. E. Carstens[2], *[1]Texas AgriLife Research, Uvalde, [2]Texas A&M University, College Station.*

Over 2 years, Bonsmara heifers (n = 60 and 55/yr, yr 1 BW 264 ± 6.1, yr 2 BW 281 ± 5.1) were individually fed a forage-based diet (2.07 Mcal ME/kg DM, 13.1 g CP/kg DM) using Calan gates at College Station, TX. Feed intake was recorded daily, animals were weighed weekly for 70 d, and residual feed intake (RFI) was calculated as the difference between actual dry matter intake (DMIc) and expected DMI from linear regression of DMI on ADG and mid-test $BW^{3}0.75$. Heifers were ranked by RFI, and those with the lowest (n = 12, LRFI) and highest (n = 12, HRFI) RFI were transported to Uvalde TX, and placed on pasture. Animals were weighed weekly over a 56 d period, 3 10-d intake measurement trials (2 trials in yr 1) were conducted using n-alkanes. Estimates of forage DMI were calculated daily and averaged within trials. RFI was computed as described above using forage intake estimates. In both yr, estimates of DMI were lower in LRFI than HRFI animals under confinement feeding (8.4 ± 0.78 vs 11.0 ± 1.11, and 8.5 ± 0.23 vs 10.5 ± 0.22 kg DM/d for years 1 and 2 respectively, $P < 0.01$). On pasture, LRFI animals had lower DMI than HRFI (8.8 ± 0.77 vs 9.1 ± 0.91 and 7.7 ± 0.11 vs 7.9 ± 0.16 kg DM/d, for yr 1 and 2 respectively) but the differences were not significant ($P > 0.1$) Estimates of ADG were not different between LRFI and HRFI within feeding situations or yr. In the confinement trials, F:G was correlated ($P < 0.01$) with ADG (−0.53 and −0.83 for yr 1 and 2. respectively) but not with DMI. During the pasture trials, F:G was correlated ($P < 0.001$) with ADG (−0.88 and −0.88 for yr 1 and 2, respectively) but not with forage DMI. In both yr, RFI during the confinement trials was not correlated with ADG, but was correlated ($P < 0.001$) with DMI and F:G. Forage RFI in yr 1 was not correlated with ADG or FCR, but was correlated with forage DMI, while in yr 2 RFI was correlated with DMI and F:G but not ADG. There were no correlations between RFI measured during the confinement and pasture trials. These data suggest that daily variation in forage DMI prevents accurate forage RFI estimation if using a limited number of estimates of DMI

Key words: feed conversion, alkane, gain

W266 Effect of birth weight, early feed intake, and average daily gain of calves before weaning on their performance after weaning and during first lactation. C. M. Matuk*[1], M. Chahine[1], A. Bach[2,3], B. Ozer[1], M. E. de Haro Marti[4], J. B. Glaze[1], and T. Fife[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 birth weight, early feed intake, and average daily gain (ADG) on performance was analyzed in a group of 755 replacement Holstein calves raised on a large commercial dairy operation in southern Idaho. Individual feed intake was recorded 4 times a week during the last 3 wk that calves were individually hutched (56 d of age). Based on their individual feed intake, calves were classified as control (randomly chosen without considering their level of feed intake, CTL, n = 80), ′high eaters′ (highest feeding level quartile, HIGH, n = 200), ′low eaters′ (lowest feeding level quartile, LOW, n = 200) and ′medium eaters′ (the remainder of calves, MED, n = 275). Weight was recorded at birth, and at wk 6, 9 and 12. During data collection, calves were housed at a calf raising facility from birth to approximately 7 mo of age, at a heifer raising facility from 7 mo until heifer reached 247 d of pregnancy and then moved to the dairy where calving occurred. Milk production (305 d mature equivalent, 305ME) records were obtained from the dairy computerized record system for all heifers that calved. Data were analyzed using PROC MIXED and PROC CORR in SAS (SAS Inst. Inc., Cary, NC). Out of the 755 heifers included in the study, 206 were culled (27.3%) and 491 have calved to date (65.0%). Out of the 206 culled heifers, 60 were lost at the calf raising facility (29.1%; 26 sold, 34 dead), 126 at the heifer raising facility (61.2%; 111 sold, 15 dead) and 20 at the dairy (9.7%; 12 sold, 8 dead). Intake classification did not a have a significant effect on cull rate. There was no significant correlation between birth weight and 305ME or between ADG and 305ME. First lactation milk production (305ME) did not differ between feed intake classification and averaged 11553 ± 150 kg for the HIGH group (n = 124), 11483 ± 145 kg for the MED group (n = 123), 11408 ± 174 kg for the LOW group (n = 92) and 11201 ± 255 kg for the CTL group (n = 43). In this study, birth weight, early intake and ADG of calves did not have an effect on their first lactation 305ME milk yield.

Key words: calves, 305ME

W267 Different periods offering chromium oxide (Cr_2O_3) as external marker to evaluate the intake of cattle treated with different diets under feedlot. R. A. Mandarino*[1], F. A. Barbosa[2], I. S. Silva[1], C. F. Lobo[1], S. L. S. Cabral Filho[1], G. A. Carneiro[1], and G. S. Firmino[1], *[1]University of Brasilia, Brasilia, DF, Brazil, [2]Federal University of Minas Gerais, Minas Gerais, MG, Brazil.*

The aim of this study was to evaluate the dry matter intake of cattle using 2 distinct periods of supply of chromium (10 g once daily) as a

marker of consumption of feedlot cattle treated with 3 different diets. The feedlot experiment was conducted from August to November 2009, during 96 d. The herd was composed of 12 zebu cattle with a average age of 23 mo with initial body weight of 364.68 kg. The treatments were the different periods of supply of chromium with 5 d (CR5) and 7 d (CR7) repeated twice in the period of feedlot. The diets were: 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. A randomized scheme in a 2 × 3 factorial divided as follow: CR5SIL, CR5PEL, CR5GRN, CR7SIL, CR7PEL and CR7GRN. The Duncan test at 5% probability level was applied to compare the means obtained. The average final body weight was 471.88 kg. The periods of infusion were not different statistically ($P > 0.05$) for any of the repetitions. The results of dry matter intake showed 2.21%, 2.28%, 1.82%, 2.16%, 1.87% and 1.68% of body weight for CR5SIL, CR7SIL, CR5PEL, CR7PEL, CR5GRN and CR7GRN respectively. All the results showed no interactions either for treatments or the diets ($P > 0.05$) indicating that a shorter period of infusion of chromium can be recommended to reduce the time of this methodology to estimate dry matter intake.

Key words: chromium, markers, supplements

W268 Total and inorganic phosphorus content of an array of feedstuffs. J. P. Jarrett*[1], M. D. Hanigan[1], R. Ward[2], P. Sirois[3], and K. F. Knowlton[1], *[1]Virginia Polytechnic Institute and State University, Blacksburg, [2]Cumberland Valley Analytical Services, Inc., Maugansville, MD, [3]Dairy One, Ithaca, NY.*

Recent investigations suggest that bioavailability coefficients of phosphorus (P) in various feedstuffs may be inaccurate. Surveys of dairy nutritionists suggest that overfeeding of P in dairy rations may stem from a lack of confidence about forms of P and availability of those forms to ruminants. Quantifying variation of P-containing compounds in feed may help improve estimates of P bioavailability. Seventy-two feed samples were received from 2 commercial labs. Total P (TP), inorganic P (Pi), and the percentage of TP that is inorganic were analyzed using the MEANS procedure of SAS. The effect of geographic region and feed class (forages, concentrates, and by-products) was analyzed with the MIXED procedure of SAS. Total P was greater ($P < 0.05$) in concentrate and by-product feeds than in forages but there was no consistent effect of feed class on Pi quantity ($P > 0.10$). However, Pi as a percent of TP was higher ($P < 0.05$) in forages as compared with concentrates and by-products. Region had no effect on TP and Pi concentration. Data characterizing variation of P-containing compounds in feedstuffs may allow better estimations of P availability and more accurate feeding recommendations.

Table 1.

	Total P (μg/g of DM)		Inorganic P (μg/g of DM)		Pi (percent of TP)	
	SD	Mean	SD	Mean	Mean	SD
Corn silage	2177	486	2191	589	99.8	9.4
Grass hay	2367	1094	1752	1231	65.2	28.7
Soybean meal 48%	8008	247	565	79	7.0	0.8
Corn gluten	10116	2399	6452	5085	57.3	40.2
Whole cottonseed	6282	1204	623	159	10.3	3.5
By class[1]						
Forages	2421[a]	553	1939	476	77.4[a]	6.2
Concentrates	5308[b]	580	1077	499	26.9[b]	6.5
By-products	6670[b]	474	2085	408	30.3[b]	5.3

[1]Means within a column with different superscripts are significantly different.

Key words: bioavailability, inorganic phosphorus, total phosphorus

W269 Protein-energy mineral supplementation of Nellore bulls in the growing phase at *Brachiaria brizantha* 'Marandu' during the rainy season. C. F. Lobo*[1], F. A. Barbosa[2], R. A. Mandarino[1], G. A. Carneiro[1], and S. L. S. Cabral Filho1[1], *[1]University of Brasilia, Brasilia, DF, Brazil, [2]Federal University of Minas Gerais, Minas Gerais, MG, Brazil.*

This experiment was designed to evaluate the effects of 2 types of protein-energy-mineral supplementation and mineral supplementation on the performance of Nellore bulls in the growing phase, during the rainy season, from December to April, in *Brachiaria brizantha* 'Marandu'. A total of 60 Nellore bulls were used, with average initial BW of 227 kg. The treatments were: MS – control, complete mineral supplement; SUP1 – protein-energy mineral supplement with slow release urea, with an average daily intake of 0.36% BW; SUP2 – protein-energy mineral supplement with conventional urea, with an average daily intake of 0.36% BW. The experiment was conducted in a randomized block design with 3 treatments and 4 replications. The Duncan test was used to evaluate animal performance. There was a difference ($P < 0.06$) between SUP1 and MS, with ADG of 0.585 and 0.477 kg/h/d, respectively. The gain obtained with SUP1 in comparison to MS promoted additional gains during the rainy season. There was no difference ($P > 0.06$) in ADG between MS and SUP2, with gains of: 0.477 and 0.496 kg/h/d, respectively. There was no difference ($P > 0.06$) between supplements SUP1 and SUP2, and their ADG equal to 0.585 and 0.496 kg/h/d. There was no significant yield difference between SUP1 and SUP2. As for MS, SUP1 was superior and SUP2 was equivalent, indicating the viability of using SUP1 in the rainy season.

Key words: grass, performance, protein

W270 Requirements for continuous ammonia-NH_3 sampling when using relaxed eddy accumulation from concentrated animal feeding operations. C. D. Gambino*[1], J. M. Ham[2], E. Allwine[1], P. O'Keeffe[1], S. N. Pressley[1], B. K. Lamb[1], and K. A. Johnson[1], *[1]Washington State University, Pullman, [2]Colorado State University, Fort Collins.*

Improved understanding of requirements for measuring ammonia (NH_3) volatilization from concentrated animal feeding operations (CAFO) is needed to design mitigation strategies and better acquire

national NH_3 emission inventories currently required by the United States Environmental Protection Agency. Real time NH_3 concentrations at feedlots can be difficult to measure because ambient temperature, relative humidity (RH), dust interference, and sampling line length can negatively impact the sample stream to the NH_3 analyzer. The compounding effect of these variables increases the potential for imprecise measurements. A review of the literature measuring NH_3 concentrations from feedlots indicates that the necessary concentration range for an NH_3 analyzer to be useful in conjunction with an REA approach to flux measurements must satisfy detection from 194 - 1766 ppbv. One commercial NH_3 analyzer that shows promise to be used for feedlot NH_3 measurements is the Picarro G1103 analyzer for NH_3 and H_2O. The objective of this work was to test the robustness of the Picarro for use in feedlot NH_3 measurements. Laboratory tests were conducted to determine potential interferences to the continuous analyzer's detection sensitivity. A Picarro NH_3 analyzer drew samples from the up or down canister every 30 s. Laboratory tests on the adapted system moved to establish an ideal square wave for analyzer response time. Picarro NH_3 analyzer response time was determined for line loss associated with temperature fluctuations of −20°C - 80°C, concentration differences of 100 ppbv-2500 ppbv, RH ranges from 0% - 100%, and dust interference within the optical cell. Lines, as well as up- and down-eddy canisters were maintained at desired temperatures using heat tape and incubators, respectively. Test concentrations matched extremes found during summer campaigns of 194 - 1766 ppbv- NH_3, corresponding to fluxes 68 - 128 ug- NH_3 m^{-2} s^{-1}. The validation and optimization of the REA-Picarro continuous sampling system provides an option for long sampling periods to improve characterization of NH_3 losses from feedlots.

Key words: ammonia, REA, measurement

W271 Effects of weaning strategy on growth and stress in beef calves. M. E. Howe*, L. B. Krebs, and E. G. Brown, *Stephen F. Austin State University, Nacogdoches, TX.*

The market demands alternative strategies to traditional weaning that will lead to more pounds of product produced and less stress in the weaned calf. To compare alternative strategies with traditional abrupt weaning, 39 crossbred calves and their cows were used to evaluate stress and performance. Cows and calves were assigned to 4 treatment groups based on calf body weight and parity of the cow. Treatments include anti-suckling device (day −4 to 0) followed by fenceline (day 0 to 42; n = 10); anti-suckling device followed by abrupt removal from cow (day 0 to 42; n = 10); no anti-suckling device (day −4 to 0) followed by fenceline (day 0 to 42; n = 10); and no anti-suckling device followed by abrupt removal from cow (day 0 to 42; n = 9). All calves remained with their cows when anti-suckling devices were fitted to the calf. At weaning (day 0), anti-suckling devices were removed. Calves were placed in a pasture adjacent to their cows for fenceline weaning and abrupt calves were moved to a remote location away from their cows at weaning. Cows and calves were weighed on d −4,-2, 0, 2, 4, 14, 28, and 42. Body condition scores (BCS) were determined on cows on d −4, 0, 14, 28, and 42. Blood samples were collected from cows and calves on d −4, 0 and 4 to determine complete blood count. Data was analyzed using Proc GLM of SAS. ADG and BCS was not significantly different ($P = 0.05$) among treatment groups for the cows or calves. There was no difference ($P > 0.06$) in lymphocytes or neutrophils for calves pre-weaning (d −4) or post-weaning (d 4). Results from this study suggest that alternative weaning strategies did not result in an increase in performance of the calves compared to traditional weaning.

Key words: stress, weaning

W272 Whole herd enteric methane emission estimates in three contrasting dairy systems. S. Utsumi*[1], D. Beede[1], S. Zimmerman[2], and P. Zimmerman[2], *[1]Michigan State University, East Lansing, [2]C-Lock Technology Inc., Rapid City, SD.*

Effects of contrasting feeding systems (FS) on diurnal patterns of enteric methane (CH4) emissions per cow, footprint per unit of milk, and frequency of milking of a herd of Holstein cows (n = 61) managed with an automatic milking system (AMS) was quantified in this pilot study. Feeding systems were: pasture grazing (GRASS); total mixed ration (TMR); and, pasture grazing plus TMR (pTMR) lasting 17, 34, and 84 d, respectively. Voluntary milking with one single-stall AMS was applied at variable rates of 4 to 2 milkings/day based on days in milk and milk yield (MY). Cows received in addition to basal diets in the FS, 1 kg of concentrate per 4 kg of milk. The mass flux (MF) of eructed and expired CH_4 during individual milkings (n = 12,584) was estimated with the Greenfeed system (C-Lock Technology Inc., Rapid City, SD), using detected changes in CH_4 concentration, air flow and known amounts of gas tracer. Repeated measures analysis of hourly CH_4 fluxes and ANOVA and Pearson correlation of calculated daily CH_4 fluxes and milking variables were conducted ($P < 0.05$). Hourly CH_4 fluxes were affected by a significant FS by hour interaction likely influenced by differences in daily feed intake patterns among FS. Pasture grazing resulted in greater hourly CH_4 fluxes during night hours (2100 to 0500 h), whereas hourly CH_4 fluxes in pTMR and TMR increased immediately after the TMR feeding at 0500 h. Daily CH_4 fluxes did not differ among FS (average = 389 ± 15 g), but GRASS, pTMR and TMR differed in daily milking frequency (2.6, 2.9 and 3.0; SE = 0.1) and MY (22, 25 and 29 kg/cow per d; SE = 1.2). Differences in MY explained the diluted CH_4 footprint per unit of milk in TMR compared with GRASS (15 vs. 19 gCH_4/kg milk; SE = 1) and the intermediate footprint value for pTMR (17 ± 1 gCH_4/kg milk). No correlation between daily CH_4 fluxes and MY was detected in the 3 FS. However, significant negative correlations between milk yield and CH_4 emissions per unit of milk in GRASS (r = −0.67), pTMR (r = −0.72) and TMR (r = −0.79) highlight the importance of a high milk production as a common strategy to dilute CH_4 emissions among dairy systems.

Key words: methane, dairy systems, automatic milking

W273 Withdrawn

W274 Effect of feeding frequency and protein supplementation on methane production by Holstein cows. P. C. Aikman*, J. A. N. Mills, C. K. Reynolds, and L. A. Crompton, *School of Agriculture, Policy and Development, University of Reading, UK.*

Open-circuit calorimetry and IGER Behavior Recorders were used to measure methane production and eating behavior in 4 Holstein cows (259 ± 13 d in milk) receiving one of 4 treatments in a 4 × 4 Latin Square with 5 wk periods. The frequency of feeding and dietary CP concentration varied between treatments. Treatments consisted of an ad libitum fed TMR (37.5% corn silage, 12.5% grass silage, 50% concentrate; CP, OM, NDF and starch concentrations of 146, 937, 428 and 202 g/kg DM respectively) fed twice daily (CONT2), or the same TMR fed ad libitum with added protein (Amino Green, SCA Nutec, Thirsk, UK) to increase CP concentration (177 g/kg DM), fed once

(PS1), twice (PS2) or 4 times (PS4) daily. Data were analyzed using the Mixed procedure of SAS with period and treatment as fixed effects and cow as a random effect. Mean DMI (18.7 ± 0.45 kg/d), milk yield (27.8 ± 0.78 kg/d) and milk fat, protein and lactose concentrations were unaffected ($P > 0.167$) by treatment. Temporal distribution of eating behavior was affected ($P < 0.001$) by treatment (eating behavior occurring between 10.00 and 16.00 was 43.2, 65.5, 50.8, and 23.9% of 24 h total for CONT2, PS1, PS2 and PS4 respectively) but total time spent eating (mean 305 ± 26.5 min/d) was unaffected ($P = 0.798$). Although number of meals/d (mean 12.1 ± 1.2) did not differ ($P = 0.188$), meal length decreased ($P = 0.008$) as feeding frequency increased (27.9, 31.4, 24.3 and 20.2 min for CONT2, PS1, PS2 and PS4 respectively). Total methane production was lowest in PS1 and highest in PS4 (571, 524, 566 and 576 l/d for CONT2, PS1, PS2 and PS4 respectively, $P = 0.048$). Methane production tended ($P = 0.063$) to be lowest in PS1 and PS2 when expressed as MJ/MJ milk (0.256, 0.223, 0.227 and 0.231 for CONT2, PS1, PS2 and PS4 respectively) but there was no treatment effect ($P > 0.233$) when expressed as L/kg DMI (mean = 29.9 ± 1.1) or L/kg milk (mean 21.0 ± 1.0). Increasing dietary CP concentrations or increasing feeding frequency to encourage animals to distribute feed intake more evenly are not effective strategies to decrease methane yield (L/kg DMI) of lactating dairy cows.

Key words: protein supplementation, feeding frequency, methane

W275 Withdrawn

W276 Effect of Quebracho-chestnut tannin extracts at two forage levels on dairy cow lactation performance and emission of methane and ammonia. M. J. Aguerre*[1], M. C. Capozzolo[1], M. A. Wattiaux[1], and J. M. Powell[2], *[1]University of Wisconsin-Madison, Madison, [2]U.S. Dairy Forage Research Center, Madison, WI.*

Our objective was to determine the effects of a tannin mix on lactating cow performance and emission of methane (CH_4) and ammonia-nitrogen (NH_3-N), and whether any responses were affected by dietary forage to concentrate (F:C) ratio. Sixteen multiparous Holstein cows (626 ± 60 kg BW; 120 ± 28 DIM) were randomly assigned to one of 4 air-flow controlled chambers, constructed to fit 4 cows each. Chambers were assigned to dietary treatments sequences in 4 × 4 Latin square designs with 2x2 factorial arrangements of treatments. Dietary treatments, fed as total mixed rations, included the following F:C ratio: 47:53 and 61:39 (DM basis, alfalfa silage and corn silage in a 1:1 ratio) without or with 0.45% tannin (diet DM). Air samples entering and exiting each chamber were analyzed with a photo-acoustic gas monitor. There was no tannin by F:C ratio interaction for any of the measured variables. Overall, DMI (28.5 kg/d), milk fat yield (1.67 kg/d) and MUN (10.6 mg/dL) were not affected by tannin. However, relative to the control, inclusion of tannin reduced ($P < 0.05$) energy corrected milk yield (ECM; 44.6 vs.43.4 kg/d) and true protein yield (1.32 vs.1.28 kg/d). Increasing F:C ratio reduced ($P < 0.05$) DMI (29.5 vs. 27.5 kg/d), ECM (45.5 vs. 42.2 kg/d), milk true protein (1.37 vs. 1.23 kg/d) and fat yield (1.71 vs. 1.63 kg/d), but did not affect MUN. Emission of CH_4 was not affected by tannin (693 g/d), but increased from 15.1 to 17.1 g/kg ECM ($P = 0.03$) relative to control. Although tannin tended to decrease N intake (667 vs. 684, $P = 0.08$), it did not affect NH_3-N emission (28.1 g/d). Increasing the F:C ratio tended to increase CH_4 emission (672 vs. 714 g/d; $P < 0.08$), increased CH_4 per unit of ECM (15.5 vs. 16.7 g/kg, $P < 0.01$), decreased N intake (711 vs. 640 g/d, $P < 0.01$), but increased NH_3-N emission per unit of N intake (3.9 vs. 4.6 g/g, $P = 0.04$). In this study, adding tannin to the diet had negative effects on performance and increased CH_4 emission per unit of milk by 8%, regardless of the dietary content of forage. In addition, F:C ratio altered manure NH_3-N emission and CH_4 emission.

Key words: methane, ammonia, dairy

W277 Effect of fiber on greenhouse gas emissions from stored manure. Q. Huang[1], K. Perano*[2], M. Tenuta[1], C. M. Nyachoti[1], A. Strathe[2], and E. Kebreab[2], *[1]University of Manitoba, Winnipeg, MB, Canada, [2]University of California, Davis, Davis.*

Lagoons from livestock operations emit greenhouse gases (GHG), particularly methane (CH_4) and carbon dioxide (CO_2). Methane emissions result from anaerobic breakdown of volatile solids in livestock excreta during storage in the lagoon. The purpose of the study was to explore the effects of fiber content in the manure on the amount of GHG emitted from pig manure in an anaerobic digester. Pigs were fed 3 different diets (NDF = 12%, 16%, and 20%) to manipulate the amount of fiber in excreta. Manure from the treatments was collected and stored in anaerobic digesters in triplicate for 139 d. The solids concentration was adjusted weekly to keep it at 3%. Each week, 1 L of manure was added and 0.25 L taken out and analyzed for the solids concentration. The resulting increase in volume of the manure in the digester was 0.75 L/wk. The CH_4 and CO_2 emitted by the digesters were collected for each digester daily. A first order model was derived describing the concentration of volatile solids (S) as [dS/dt = (inflow*0.03*0.80 – outflow*S–k*S*V)/V], where k is the rate constant and V is volume. The Arrhenius relationship [CH_4 = k*S*exp(log(A)–E/R*T)] was used to model rate of formation of CH_4 over time. Here A is the Arrhenius constant and E, R and T represent the activation energy, gas constant and temperature, respectively. The parameters k and A were estimated from the time-series using generalized nonlinear least squares. The ANOVA analysis of k and log (A) showed no difference between the 3 treatments ($P = 0.63$). Cumulative emissions over 139 d showed a trend toward higher GHG production as NDF content increases, but it was not statistically significant ($P = 0.55$). Similarly, analysis based on CO_2-equivalent emissions did not show a difference between treatments ($P = 0.55$). Part of the reason for lack of detecting a difference between treatments was the high variation of observed emission values within a treatment. Increased replications per treatment are required to overcome within-treatment variation. Alternatively, GHG emissions from stored manure could mostly be a function of total carbon and may not depend on NDF levels.

Key words: methane, manure, fiber

W278 Evaluation of SF_6 emission for determination of methane in ruminants. A. C. Ruggieri*, N. C. Meister, I. P. Carvalho de Carvalho, N. L. Santos, V. Costa e Silva, F. de Oliveira Alari, and K. T. de Resende, *UNESP-Universidade Estadual Paulista, Jaboticabal, São Paulo, Brazil.*

One requirement of using the technique of inert traced gas sulfur hexafluoride (SF_6) to measure the emission of methane is the determination of emission rate or permeation of gas through the membrane. The aim of this study was to evaluate 2 different thicknesses of membrane permeation (Teflon), and the influence of the use of the washer. We used a factorial (2x3), with 2 thicknesses of film (0.2mm and 0.3mm) and 3 type of assemble: 1- with washer 5mm bore hole (i.d.); 2- with washer 2.5mm bore hole (i.d.); 3- without washer, totalizing 6 treatments with

10 replication each. The capsules were made of brass with the following measures outside diameter (o.d.) 11.1 mm (7 / 16 inch) and 4.76 mm bore role (i.d.), with nut length (Swagelok), were charged with approximately 500mg of SF_6. Compact stick (nylon 6.6) was used to make a washer with 0.8 mm thick. The following capsules were kept at 39°C in the laboratory. They were weighed weekly for 8 consecutive weeks and discarding the first to review the weighing according to the methodology for methane emission from rumen adapted to Brazil. The experimental data were analyzed by SAS statistical software. Analyses of variance were performed using PROC MIXED with repeated measures. The averages of the treatment were compared by Tukey test at 5% probability. The use of film 3 mm resulted in lower emissions ($P < 0.05$) of SF_6 over 2 mm. The emission of SF_6 capsules with or without washer did not different ($P > 0.05$), and they were higher when compared with the capsules inside area with washer lower in 2 thicknesses of film. However the use of the capsules was higher when the washer was used, whereas use of a capsule with emission from 500 to 2000 ng/min.

Key words: membrane permeation, size washer, emission rate

W279 Effect of dietary protein level on ammonia and greenhouse gas emissions from dairy manure. C. Lee*[1], A. N. Hristov[1], C. J. Dell[2], G. W. Feyereisen[3], J. Kaye[1], and D. Beegle[1], *[1]Pennsylvania State University, University Park, [2]USDA-ARS-PSWMRU, University Park, PA, [3]USDA-ARS-SWMRU, St. Paul, MN.*

Experiments were conducted to investigate the effect of dietary crude protein (CP) concentration on ammonia (NH_3) and greenhouse gas (GHG; CH_4, N_2O, and CO_2) emissions from dairy manure in simulated storage (Exp. 1) and from manure-amended soil in lysimeters (Exp. 2). Twenty 4 lactating Holstein cows were grouped and offered randomly one of the following diets: 16.3% CP (HighCP), or 13.5% CP (LowCP). Feces and urine were separately collected from each cow and manure was prepared by mixing feces and urine in a 1.7:1 ratio. Total N concentration and the proportion of ammonium– and urea–N in total N were greater ($P < 0.001$) for HighCP manure compared with LowCP manure (4.4 vs. 2.8% and 51.6 vs. 30.8%, respectively). In Exp. 1, manure was incubated in laboratory conditions for 122 h. The cumulative NH_3 emission from LowCP manure was lower (by 47%, $P < 0.001$) compared with HighCP manure. The emission rates and cumulative emissions of GHG were not affected by type of manure. In Exp. 2, manure was applied to lysimeters (61 × 61 × 61cm; Hagerstown silt loam; fine, mixed, mesic Typic Hapludalf) at 9.5 and 9.1 g N and 1,653 and 2,356 g fresh manure per lysimeter (HighCP and LowCP, respectively). The emission rate of NH_3 was 49% greater (1.53 vs. 1.03 mg/m^2 per min; $P < 0.001$) for HighCP than for LowCP manure. In contrary, the emission rates of CH_4 and CO_2 were greater ($P < 0.001$ and 0.01, respectively) for LowCP compared with HighCP manure, which was explained by the increased manure application rate with LowCP (to achieve similar N application rate). Emissions of N_2O were not affected by treatment. In conclusion, LowCP manure significantly decreased NH_3 emission in simulated storage conditions and from manure-amended soil and increased, due to greater application rate, CH_4 and CO_2 emissions from manure-amended soil compared with HighCP manure.

Key words: dietary protein, gas emission, dairy manure

W280 Use of an activity monitoring system as part of the Cal Poly dairy breeding protocol. T. Nutcher* and S. Henderson, *Department of Dairy Science, California Polytechnic State University, San Luis Obispo.*

Dairy herd reproductive efficiencies have dropped in the past 40 years. Increased milk production, and genetic pull toward more milk production, has led to reproductive rates declining. An advanced breeding program is needed to become more efficient in this area and many options exist such as synchronization programs, pedometers, and other electronic detection aids. The objective of this study was to determine the effectiveness of an activity monitoring system, Heatime by MICRO Dairy Logic, as an integral part of the Cal Poly Dairy breeding protocol. Once installed, the program was kept up to date with the herd, including: pen moves, fresh events, bred events, dry-off events, and collar movements. This was done at least 4 times per week to ensure current information. Pregnancy checks were done every other week to obtain results of previous bred events and were then entered into the system. Pregnancy rates derived by this data were compared with the previous history of the herd. The results of this study yielded a well functioning breeding program. The system continuously monitored activity, stored records, and generated user defined reports with activity and rumination graphs. The system used this data to flag cows to be bred, checked for sickness, or pregnancy checked. Concerns arose with the system being abandoned once the Senior Project was complete. These have been resolved as seen by the breeders and herdsmen having adapted to the new technology smoothly, and using it as an integral part of their management protocol. The system has been established and in use for 5 mo. The pregnancy rates before the system averaged 14.3% compared with the system at 22.5%, which increased the pregnancy rate to a combined 15.3% (12/26/09 – 11/06/10). In conclusion, the Heatime system has shown to be an effective addition to the Cal Poly breeding program; however, further observation is needed to determine effectiveness and consistency over the long-term.

Key words: activity, rumination, estrus

W281 Seasonal and diel changes of air emissions from cross-ventilated dairy freestall barns in Midwestern United States. F. Y. Ayadi*[1], E. L. Cortus[1], L. D. Jacobsen[2], B. P. Hetchler[2], and A. J. Heber[3], *[1]South Dakota State University, Brookings, [2]University of Minnesota, St. Paul, [3]Purdue University, West Lafayette, IN.*

A design feature of the National Air Emissions Monitoring Study was to investigate climate and facility management influence on gaseous and particulate matter (PM) emissions. One monitored site consisted of 2 mechanically cross-ventilated freestall dairy barns in Wisconsin with capacities of approx. 275 and 375 cows. In yr 1, pens were flushed 3 times daily with recycled lagoon effluent; in yr 2, barn floors were scraped with a tractor. The objective of this analysis was to determine variations in ammonia (NH_3), hydrogen sulfide (H_2S), carbon dioxide (CO_2), and PM_{10} attributed to season and time of day over a 2-yr period. Because change in manure removal method had a significant effect on emissions, season and time of day effects were evaluated separately for each yr. Seasons were defined as spring (March–May), summer (June–Aug), fall (Sept-Nov), and winter (Dec-Feb). Time of day influence was evaluated using averages from day (9 a.m.-4 p.m.) and night (10 p.m.-5 a.m.) periods. Yearly ave. values for NH_3 emission were 3.4 g/m^2/d (SE = 0.01) and ranged between 3.5 and 4.4 g/m^2/d during day and 2.8–3.4 g/m^2/d during night. All NH_3 emissions were significantly lower at night ($P < 0.05$). Mean H_2S emission (646 mg/m^2/d, SE = 8.3) during yr 1 was significantly higher than during yr 2 (37.4 mg/m^2/d, SE = 0.5) and showed only minor variations related to season. However, in yr 2, H_2S emissions showed significant differ-

ences based on season; H_2S emissions were highest in summer (63.2 mg/m^2/d, SE = 1.1) and lowest in winter (16.7 mg/m^2/d, SE = 0.2). Differences between years for H_2S were most likely related to the different manure removal systems; a time of day effect on H_2S emissions was not evident. Conversely, PM_{10} emission was significantly lower in yr 1 (121 mg/m^2/d, SE = 3.3) than in yr 2 (187 mg/m^2/d, SE = 3.7 mg/m^2/d) and was significantly higher during the day, most likely as a result of different scraping systems. Emission rates for CO_2 varied due to season and were highest in the winter (1.5–2.1 kg/m^2/d, SE = 0.01). This study demonstrated that season influenced H_2S, and PM_{10} emissions and time of day affected NH_3 and PM_{10} emission.

Key words: manure, cross-ventilated barn, emission

Ruminant Nutrition: Beef Cattle

W282 Effect of oat maturity and variety on yield and nutritive value for grazing cattle. M. L. Drewery*[1], L. A. Redmon[2], and T. A. Wickersham[1], *[1]Texas A&M University, College Station, [2]Texas AgriLife Extension, College Station.*

Oats (*Avena sativa*) often provide earlier grazing, later maturity, and greater forage production during warm weather than wheat or rye, but are often more sensitive to cold stress. Therefore, in warmer climates, oats are often used as a forage resource. However, data are limited on production and nutritive value for many oat varieties when used as a forage source. Accordingly, the objective of this study was to determine the yield and nutritive value of 4 oat varieties (TAMO 405, Harrison, BOB, and Exp 1) at 6 maturities. A prepared seedbed was divided into 4 blocks with each variety randomly assigned to a plot within each block. Plots were established on Oct 20, 2009 in Burleson County, Texas, and were provided with 167 kg/ha of 16–20–0 fertilizer at planting and top dressed with 43 kg N/ha (N-32) on Feb 18, 2010. Samples were clipped from each plot using 0.09 m^2 square on Dec 10, Jan 11, Feb 15, Mar 11, Apr 14, and May 10. All samples were dried at 60°C for 72h, ground to pass a 1-mm screen and subsequently analyzed for OM, N, and NDF. In vitro true digestibility (IVTD) was determined on all samples, except those collected in Dec. Statistical analysis was completed using SAS with variety and maturity in the model and using block as the random term. Maturity linearly ($P < 0.01$) increased DM production while CP content linearly ($P < 0.01$) decreased from 27% in Dec to 8% in May. The largest decrease in CP, from Mar to Apr, corresponded with the greatest increases in DM yield. Nitrogen yield (kg N/ha) increased quadratically ($P < 0.01$), with a plateau occurring at the Mar sampling. Through the Feb sample, NDF content was <29%, then increased rapidly to above 57% for samples collected in Apr and May. Samples collected in Jan and Feb had IVTD above 93%, then linearly decreased ($P < 0.01$) with advancing maturity to <59% in May. There was a tendency ($P = 0.07$) for variety to effect IVTD. Digestible DM kg/ha increased linearly ($P < 0.01$) with advancing maturity from <660 kg in Jan to 2,481 kg in May. Variety did not significantly affect yield or nutritive value. Maturity was the primary driver of forage production, which increased with advancing maturity, while nutritive value declined.

Key words: grazing, oats

W283 Replacing grain and silage with wheat distiller grains: effects on feed intake, daily gain, carcass characteristics, and blood metabolites in finishing beef cattle. W. Z. Yang*[1], T. A. McAllister[1], J. J. McKinnon[2], and K. A. Beauchemin[1], *[1]Agriculture and Agri-Food Canada, Research Centre, Lethbridge, AB, Canada, [2]Department of Animal & Poultry Science, University of Saskatchewan, Saskatoon, SK, Canada.*

A study was conducted to evaluate DMI, daily gain, carcass quality and blood metabolites in feedlot beef steers fed diets that varied in proportion of wheat dried distillers grains with solubles (DDGS) with DDGS replacing barley grain or silage. Two hundred crossbred steers (489 ± 30 kg) were blocked by weight and randomly allotted to 20 pens (5 pens per treatment). Steers were fed one of 4 diets: control, low (25DDGS), medium (30DDGS), and high (35DDGS) wheat DDGS (DM basis). The control diet consisted of 15% barley silage and 85% barley concentrate; the 3 DDGS diets were formulated by substituting 20% barley grain and 5, 10 and 15% silage, respectively, with 25, 30 and 35% wheat DDGS so that the 35DDGS diet contained no silage. Steers were weighed at the start and end and every 21 d during the experiment. In comparing with the control, DMI (10.9 vs. 11.6 kg/d) of calves fed 25DDGS was greater ($P < 0.01$), but final BW tended ($P < 0.06$) to be lower (635 vs. 621 kg), so they were less efficient (130 vs. 113 g gain/kg DMI; $P < 0.01$). With substitution of DDGS for silage, DMI linearly ($P < 0.01$) decreased from 11.6 to 10.7 kg/d without changing final BW or ADG, consequently, feed efficiency linearly ($P < 0.02$) improved from 113 to 128 g/kg DMI. Overall, carcass characteristics were not different among the 4 diets. Plasma glucose averaged 1.0 g/L and was not affected by diet, whereas plasma urea N was doubled from control (95 mg/L) with DDGS diets (195 mg/L). Results indicate that partially replacing barley grain and silage with wheat DDGS in high-grain diets reduces growth and feed efficiency. However, further substitution of wheat DDGS for silage such that the diets contained minimal or no silage did not adversely impact cattle growth or feed efficiency.

Key words: feedlot beef cattle, growth performance, wheat DDGS

W284 Effects of restricted versus conventional dietary adaptation over periods of 14 and 21 days on feedlot performance and carcass characteristics of Nellore cattle. D. D. Millen*[2,3], F. S. Parra[1], J. R. Ronchesel[1], M. D. B. Arrigoni[1], C. L. Martins[1], R. S. Barducci[1], L. M. N. Sarti[1], R. D. L. Pacheco[1], L. C. Vieira Júnior[1], M. C. S. Franzói[1], R. Espigolan[1], J. M. P. Silva[1], M. F. Val[1], F. P. Luiz[1], E. A. Chacon Filho[1], *[1]São Paulo State University (UNESP), Botucatu, São Paulo, Brazil, [2]São Paulo State University (UNESP), Dracena, São Paulo, Brazil, [3]Supported by FAPESP, São Paulo, São Paulo, Brazil.*

This study, conducted at the São Paulo State University feedlot, Botucatu Campus, Brazil, was designed to determine effects of restricting intake of the final finishing diet (REST) as a means of dietary adaptation compared with diets increasing in concentrate (STEPUP) over periods of 14-d and 21-d on overall feedlot performance and carcass characteristics. The experiment was designed as a completely randomized block with a 2 × 2 factorial arrangement, replicated 6 times (5 bullocks/pen), in which 120 18-mo-old yearling Nellore bulls (372.2 ± 21.5 kg) were fed in 24 pens for 84-d according to the treatments: STEPUP for 14-d, STEPUP for 21-d, REST for 14-d, and REST for 21-d. The STEPUP program consisted of ad libitum feeding of 3 adaptation diets over periods of 14-d or 21-d with concentrate level increasing from 55% to 85% of diet DM. The REST program consisted of restricted intake of the final diet (85% concentrate) with programmed increases in feed offered until yearling bulls reached ad libitum access over periods of 14-d or 21-d. No significant ($P > 0.10$) protocols and days main effects were observed for any of the feedlot performance parameters analyzed: final BW, ADG in kg (STEPUP = 1.554, REST = 1.545; 14-d = 1.556, 21-d = 1.539), G:F ratio (STEPUP = 0.147, REST = 0.149; 14-d = 0.148, 21-d = 0.148) and DMI in kg, however a interaction was found ($P < 0.05$) for DMI in % of BW. Animals in STEPUP for 21-d treatment presented greater DMI (% of BW) than yearling bulls in REST for 21-d (2.43% vs. 2.34%). With respect to carcass characteristics, no significant ($P > 0.10$) protocols and days main effects were observed for LM area, 12th rib fat thickness and kidney-pelvic fat, however, yearling bulls in treatments that lasted 14-d presented heavier ($P < 0.05$) HCW (285.61 kg vs. 278.72 kg) and increased ($P < 0.05$) dressing percentage (56.76% vs. 56.13%) when compared with animals allocated in protocols that lasted 21-d. The adaptation in 14-d did not negatively affect feedlot performance of

Nellore cattle and improved HCW and dressing percentage regardless of adaptation protocol.

Key words: adaptation, feedlot, Nellore

W285 Effect of three diets on carcass quantitative traits in cattle Nellore and crossbreed F1 Nellore × Brahman. I. S. Silva*, F. A. Barbosa, S. L. S. Cabral Filho, R. A. Mandarino, and P. C. A. C. Alves, *Faculty of Agronomy and Veterinary Medicine, University of Brasília-UnB, Brasília/DF, Brazil.*

The experiment evaluates the characteristics of carcass in fattening cattle, divided into 2 genetic groups and submitted to 3 diets in a feedlot. The herd was composed of 42 bulls with an average age of 23 mo, 21 were Nellore (NEL) and 21 crossbreed Nellore x Brahman (NBR). Each genetic group was divided and allotted to 3 diets, with 7 animals each. The experimental groups were: 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 pellets diet; GRN-whole grain corn and pellets diet. The experiment was conducted in a 2x3 factorial, completely randomized design. After slaughter, were evaluated at the half carcass the rib-eye area (REA) and the subcutaneous fat thickness (SFT), and the body composition (muscle, bone and fat) of the section HH (between the 9th and 11th rib). There was no difference to the SFT in comparison of genetics or diets ($P > 0.05$). The REA was similar for the different diets, but differ among the genetic groups ($P < 0.05$), with values 69.25 and 77.15 cm^2 for NEL and NBR. The percentage of bone was not different for diets or genetic groups. The percentage of muscle was similar to the genetic groups but was different for the diets. On the diet PEL the proportion of muscle was higher than in SIL and GRN, 60.43, 55.25 and 57.03%, respectively ($P < 0.05$). The percentage of fat was different for both genetic groups and diets ($P < 0.05$). The NEL was 17.48% while NBR obtained 14.72%. The SIL diet had a high proportion of fat (19.60%), compared with the diets PEL and GRN, 12.98 and 15.96% respectively ($P < 0.05$). The genetic groups did not influence the SFT, or the percentage of bone and muscle in the section HH. The diets did not affect REA, SFT and the percentage of bone in section HH. The REA was higher in NBR in comparison with the NEL. The percentage of fat in the HH section was higher for the NEL compared with NBR. The results indicate that PEL showed a higher percentage of muscle in the HH section between diets, while the SIL and NEL had a greater percentage of fat.

Key words: beef cattle, feedlot, genetic group

W286 Effects of supplementing an exogenous proteolytic enzyme on growth performance in finishing beef steers. J. M. Vera*[1], C. T. Noviandi[1], A.-H. Smith[2], D. R. ZoBell[1], and J.-S. Eun[1], *[1]Department of Animal, Dairy, and Veterinary Sciences, Utah State University, Logan, [2]Danisco USA, Inc., Waukesha, WI.*

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 supplementing EPE, 48 Angus crossbred finishing beef steers (473 ± 37.3 kg BW) were used to assess the growth performance when fed a DDGS-based TMR without (control) or with an EPE supplementation in a completely randomized design. The finishing TMR consisted of 5% alfalfa hay, 20% corn silage, 40% barley grain, 30% DDGS, and 5% feedlot supplement (DM basis). The EPE contained 38,622 U/g protease activity with negligible fibrolytic activities. The EPE was diluted with warm water and added at a rate of 0.52 g/kg DM TMR. Four animals were placed in each pen, and 6 pens allocated to each treatment (n = 6). Prior to starting the trial, all steers were adapted to the TMR for a 3-wk period. 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 d at the beginning of trial and wk 4, 8, and 12. The experiment lasted 84 d, and data were analyzed using the MIXED procedure of SAS. There were no differences ($P > 0.15$) on BW gain (123 vs. 131 kg) and G:F ratio (0.141 vs. 0.148) between control and EPE treatment, respectively. Intake of DM (12.8 vs. 13.3 kg/d, $P = 0.13$) and ADG (1.75 vs. 1.96 kg/d, $P = 0.11$) tended to increase with EPE supplementation. The positive effects of supplementing EPE on DMI and ADG may have resulted from beneficial modification of ruminal fermentation by EPE. Further investigation is needed to understand if supplementing EPE influences ruminal metabolism of finishing beef steers fed DDGS at relatively high inclusion rate.

Key words: exogenous proteolytic enzyme, finishing beef steers, growth performance

W287 Effects of supplementing an exogenous proteolytic enzyme in beef finishing diets on ruminal fermentation in continuous cultures. J. M. Vera[1], T. Astuti[2], A.-H. Smith[3], D. R. ZoBell[1], and J.-S. Eun*[1], *[1]Department of Animal, Dairy, and Veterinary Sciences, Utah State University, Logan, [2]Faculty of Animal Science, Andalas University, Padang, West Sumatra, Indonesia, [3]Danisco USA, Inc., Waukesha, WI.*

We investigated whether supplementing an exogenous proteolytic enzyme (EPE) would be beneficial on in vitro ruminal fermentation characteristics when supplemented in beef finishing diets without or with dried distillers grains with solubles (DDGS). The finishing TMR consisted of 70% barley grain without DDGS (BT) or 40% barley grain and 30% DDGS (DT) on DM basis. A dual-flow continuous culture system consisting of 4 fermentors was used in a 4 × 4 Latin square designed study with dietary treatment arranged as a 2 × 2 factorial. The 4 treatments were: 1) BT without EPE; 2) BT with EPE; 3) DT without EPE; and 4) DT with EPE. Filtered ruminal contents were allowed 6 d of adaptation to the treatments followed by 3 d of data collection. The EPE contained 38,622 U/g protease activity with negligible fibrolytic activities. The EPE was diluted with warm water and added at a rate of 0.52 g/kg DM TMR. Feeding BT decreased culture pH compared with DT (6.01 vs. 5.82; $P < 0.01$), but supplementing EPE had no effect on culture pH regardless of TMR. Total VFA concentration increased by feeding DT ($P = 0.03$), but EPE supplementation had no effect on the total VFA concentration. While feeding DT increased ($P = 0.03$) or tended to increase ($P = 0.07$) acetate or propionate concentration, respectively, EPE supplementation tended to increase ($P = 0.11$) propionate concentration regardless of TMR. Methane production tended to increase ($P = 0.10$) by feeding DT compared with BT, whereas EPE supplementation increased methane production in BT, but not in DT, resulting in a TMR × EPE interaction ($P = 0.04$). The increased propionate concentration due to EPE supplementation in beef finishing diets may affect growth performance of finishing steers by providing more glucogenic precursor.

Key words: exogenous proteolytic enzyme, ruminal fermentation, continuous cultures

W288 Fecal and urinary excretion of N, P and S with increasing feeding wheat distillers dried grains with solubles (DDGS) in finishing beef heifers. Y. L. Li[1,2], C. Li*[1,3], 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, [3]College of Animal Science, Inner Mongolia Agricultural University, Hohhot, Inner Mongolia, China.*

A study was conducted to determine the fecal and urinary excretion of N, P and S with increasing inclusion of wheat DDGS in finishing diet fed to growing beef heifers. Eight ruminally fistulated Angus heifers were assigned to a replicated 4 × 4 Latin square design with treatments: control, low (25%), medium (30%) and high (35%) DDGS. 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 for ad libitum intake. Total collection of feces and urine were conducted for 5 d in each period. Intakes of N were higher ($P < 0.01$) for the DDGS diets (averaged 327 g/d) than for the control (186 g/d). Consequently, total excretion of N was greater ($P < 0.01$) for DDGS (264 g/d) than for control (164 g/d), which were primarily excreted through urine (control vs. DDGS; 104 vs. 185 g/d) and less in feces (control vs. DDGS; 60 vs. 79 g/d). Intake of P quadratically increased ($P < 0.01$) with increasing DDGS in the diets (38, 49, 49 and 43 g/d for control, low, medium and high DDGS, respectively) without affecting P retention. Fecal P excretion quadratically changed (24, 30, 29 and 23 g/d; $P < 0.05$), whereas urinary P linearly increased (3, 10, 11 and 14 g/d; $P < 0.01$) with increasing DDGS from 0 to 35% in the diets. Feeding DDGS diets increased ($P < 0.01$) S intake (control vs. DDGS; 17 vs. 42 g/d), whereas S retention was not affected (2 g/d) by diets. Increased S consumption proportionally increased urinary S excretion (53 to 80% intake) but reduced fecal S excretion (38 to 22% S intake). Results indicate that inclusion 25 to 35% wheat DDGS in finishing diets substantially increased the intakes of N and S, which were then primarily excreted through urine. Influence on intake and excretion of P were relatively small by feeding DDGS.

Key words: wheat DDGS, balance of N, P and S, beef cattle

W289 Effect of Optaflexx when fed as a topdress on performance and carcass traits of finishing steers. G. J. Vogel*, R. L. Botts, J. W. Homm, N. A. Pyatt, and G. D. Hufstedler, *Elanco Animal Health, Greenfield, IN.*

Two-thousand nine hundred forty-nine steers (581 kg) were allotted to 32 pens in a randomized complete block design of 4 treatments with 8 replications to evaluate the effects of differing methods of Optaflexx administration on growth performance. Experimental treatments included: 1) Non-medicated control (Cont); 2) Optaflexx fed continuously (200-C); 3) Optaflexx fed once daily in 0.45 kg topdress pellet (200-P); and 4) Optaflexx fed once daily in 1.8 kg of finisher ration as a topdress (200-FR). Optaflexx was fed at 200 mg hd^{-1} d^{-1} during the final 28 d before slaughter. All cattle were fed their respective basal diets twice daily at 0700 and 1300 h. The basal ration contained Rumensin at 36.7 mg/kg and Tylan at 11.2 mg/kg of the diet DM. Cattle in treatments 200-P and 200-FR were fed their respective medicated topdress, containing the entire daily dose of Optaflexx approximately 30 m after the am feeding. Data were analyzed using a mixed model with treatments fixed and blocks random. Feeding Optaflexx as a topdress resulted in similar live performance ($P > 0.21$) and carcass traits ($P > 0.22$) when compared with feeding Optaflexx continuously. Compared with control, Optaflexx increased ($P < 0.01$) daily gain 0.22 kg/d, live weight gain 6.1 kg/hd, and carcass weight 6.0 kg/hd and improved ($P < 0.01$) feed to gain 12.2%. These data indicate that feeding Optaflexx in a topdress feed once daily is equivalent to feeding Optaflexx continuously in the ration. Feeding Optaflexx increased daily gain, improved feed efficiency and increased carcass weight.

Table 1. Effect of Optaflexx fed as a topdress

	Treatments					
Item	Cont	200-C	200-P	200-FR	SEM	*P*-value
Final BW, kg	623.8[a]	630.5[b]	630.9[b]	628.4[b]	1.2	< 0.01
DM Intake, kg	9.47	9.40	9.58	9.45	0.11	0.54
Daily Gain, kg/d	1.54[a]	1.78[b]	1.79[b]	1.70[b]	0.04	< 0.01
Feed / Gain	6.17[a]	5.31[b]	5.36[b]	5.59[b]	0.11	< 0.01
Carcass weight, kg	397.2[a]	402.9[b]	403.7[b]	402.9[b]	0.6	< 0.01
Dressing percent	63.7[a]	63.9[ab]	64.0[b]	64.1[b]	0.1	0.03
Marbling score	small[02]	slight[96]	small[00]	slight[89]	2.9	0.11

[ab]Within a row, means without a common superscript differ ($P < 0.05$).

Key words: ractopamine, Optaflexx, topdress

W290 Effects of crude glycerin on in vitro gas production dry matter disappearance, VFA profiles, and composition of fermentative gasses. E. H. C. B. van Cleef*[2], S. Uwituze[1], and J. S. Drouillard[1], *[1]Kansas State University, Manhattan, [2]São Paulo State University, Jaboticabal, São Paulo, Brazil.*

Two studies were conducted to evaluate effects of glycerin on in vitro fermentation parameters and substrate DM disappearance. Ruminal fluid was collected from 4 fistulated steers fed finishing diets (90% concentrate) of rolled corn, 35% wet corn gluten feed, 20% soybean hulls, 4% supplement, 0 or 15% crude glycerin (2 steers/level), and the balance as dry-rolled corn. Buffered ruminal fluid (150 mL) was placed into 250-mL flasks equipped with pressure monitors. Substrates were added at 1.5 g DM/flask, and consisted of the same ingredient mixture fed to donor steers. The study was arranged as a 2 × 2 factorial, with factor 1 being the diet to which steers were adapted, and factor 2 being type of substrate added to cultures. Gas production, VFA profiles, and composition of head-space gas from each flask were determined after 24 h of incubation, and repeated for 2 d. Data were analyzed using the Mixed procedure of SAS. Study 2 used the same treatments, but measured DM disappearance of substrates using 50-mL in vitro tubes containing 30 mL buffered ruminal fluid and 0.5 g substrate. In study 1, there was an interaction between substrate and diet of the donor steers ($P \leq 0.01$). Differences in gas production for substrates with and without glycerin were negligible when added to cultures containing ruminal fluid from unadapted animals, but were greater for substrate with 15 compared with substrate with 0% glycerin for cultures containing ruminal fluid from steers adapted to glycerin. Prior adaptation of steers to glycerin resulted in greater methane production ($P \leq 0.01$). Adding glycerin as substrate ($P \leq 0.01$), but not as a component of donor diets ($P \geq 0.10$), increased propionate, butyrate, isobutryate, valerate, and isovalerate. In experiment 2, there was a tendency for interacation between substrate and donor steer diet ($P = 0.06$). Glycerin used in conjunction with ruminal fluid from unadapted

animals depressed digestion, but increased it when added to ruminal fluid from adapted animals. These studies suggest that prior microbial adaptation is needed to optimize fermentation of crude glycerin.

Key words: fermentation, glycerin, methane

W291 Effects of ginger root (*Zingiber officinale*) on blood oxidative stability of beef cattle. M. J. Liu*, Z. B. Yang, and W. R. Yang, *Shandong Agricultural University, Shandong, Taian, China.*

Four Lu-xi beef cattle (BW = 420 ± 20 kg) were used to evaluate the effects of different levels of ginger root (*Zingiber officinale*) on serum oxidative stability. The beef cattle were randomly allocated into individual pens and assigned to a 4 × 4 Latin square with the following feeding diets: 1) basal diet (Control), 2) Control diet + 0.5 g/kg ginger powders, 3) Control diet + 1.0 g/kg ginger powders, 4) Control diet + 1.5 g/kg ginger powders. The basal diet was formulated to meet nutrient requirement of NRC (2001). Twenty-milliliter blood samples were obtained from each cattle via jugular vein on d 1, 7 , 14, and 21, subsequently centrifuged at 3,000 r/min for 5 min, and the serum was stored in 1.5 mL Eppendorf tubes at −20°C and analyzed with Assay Kits made by Nanjing Jiancheng. The results showed that supplementation of ginger powder did not affect ($P > 0.05$) total superoxide dismutase (T-SOD) activity on d 1, but reduced ($P < 0.05$) activity on d 7 by addition of 0.5 g/kg ginger powder. Addition of ginger powder at the level up to 1.5 g/kg increased ($P < 0.05$) serum T-SOD activity. Glutathione peroxidase (GSH-Px) activity was significantly decreased ($P < 0.05$) by 0.5 g/kg ginger powder on d 7. Regardless of addition rate, ginger root reduced ($P < 0.05$) MDA content in the serum. Supplemented with ginger powders were not significantly affected ($P > 0.05$) total antioxidant capacities (T-AOC) among treatments ($P > 0.05$). Adding ginger can decline the oxidative stability in serum of beef cattle.

Key words: ginger, oxidative stability, beef cattle

W292 Oro-sensorial preferences for mixtures of protein and energetic 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., Montornés del Vallés, Barcelona, Spain, [3]ICREA, Barcelona, Spain.*

In previous studies with weaned calves, it was determined that soybean meal (SBM) and wheat were the preferred ingredients among 6 protein and 8 energetic ingredients, respectively. On contrary, corn gluten meal (CGM) and corn gluten feed (CGF) were the least desired. The objective of this study was to determine whether these oro-sensorial preferences remain the same when ingredients are part of a mixture. A total of 6 assays involving 60 calves (62 ± 1.3 d of age) were conducted to rank calf oro-sensorial preferences for 4 mixtures at 50%: SBM-CGF, SBM-Wheat, CGM-CGF and CGM-Wheat. To minimize potential interferences with feed texture, all ingredients were ground at 3 mm. In each assay, 20 naive calves were offered a choice ad libitum of 2 mixtures and feed consumption was recorded during 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 mixture. Oro-sensorial preference was calculated as a percentage of total feed consumption ((consumption of one mixture / total consumption) x100). Preference data were subjected to one-sample comparison *t*-test using 50% as a reference value (i.e., lack of preference). The most preferred mixture was SBM-Wheat. It was preferred in all assays (Table 1). The CGF-CGM mixture was the least preferred in all assays. No differences were observed between SBM-CGF and CGM-Wheat mixtures. Results indicate that SBM and wheat are still preferred when offered as a part of a mixture. For this reason SBM and wheat could be used to improve starter acceptability by calves. On the other hand, CGF and CGM should be avoided when attempting to improve palatability of starters for calves.

Table 1. Oro-sensorial preferences of weaned calves for different mixtures (50:50%)

Mixture A	Mixture B	Oro-sensorial preferences (%)[1]	SE	*P*-values[2]
SBM-Wheat	CGM-CGF	95.7	2.66	<0.001
SBM-Wheat	CGM-Wheat	83.1	11.37	<0.001
SBM-Wheat	SBM-CGF	80.2	11.42	<0.001
SBM-CGF	CGM-CGF	81.5	5.82	<0.001
SBM-CGF	CGM-Wheat	58.6	11.34	0.130
CGM-Wheat	CGM-CGF	81.8	8.1	<0.001

[1]Percentage of consumption (Mixture A / (Mixture A + Mixture B)) x 100.

[2]Tests whether the relative consumption of mixture A differs from 50%.

Key words: palatability, preferences, intake

W293 Evaluation of cotton ginning by-product value added feed as a supplement for grazing beef cattle. J. D. Rivera*, L. W. Fitzgerald, M. L. Gipson, K. L. Odom, and R. G. Gipson, *South MS Branch Experiment Station, Poplarville, MS.*

A cotton ginning by-product (CPM) was evaluated as a supplemental feedstuff for beef cattle (n = 52, BW = 321 kg ± 15.1 kg) grazing dormant warm-season mixed grass pastures during a 70 d period in 2010. The CPM product was packaged as a 226 kg bale and is a mixture of cotton-gin trash, added protein, molasses and a complete mineral package. These bales are designed to be a self fed complete feed for pasture cattle. In this study, CPM was compared with a limit fed diet (DIET) of soybean hull pellets, dried distillers grains with solubles and a mineral package in a randomized complete design using pasture as the experimental unit. There were 4 pastures per treatment and each pasture was approximately 2.83 ha in area and consisted of dormant warm-season grass mix: bahiagrass (*Paspalum notatum*), bermudagrass (*Cynodon dactylon*), and crabgrass (*Digitaria sanguinalis*), all clipped to uniform height, and were stocked with either 6 or 7 head of predominantly English crossbred steers. Treatments were CPM fed ad libitum and DIET limit fed at the rate of 1.5% of BW and was formulated to be similar in nutrient profile to the CPM bale. At the initiation of the study, cattle were stratified by BW and assigned to pastures, and pastures were randomly allotted to treatment. Data were analyzed with PROC GLM of SAS. Pasture was the experimental unit, and means were separated using the PDFIF option. Cattle fed CPM had greater feed intake compared with cattle limit fed DIET (6.49 kg vs. 4.69 kg, respectively, $P < 0.10$). Nonetheless, cattle fed DIET had greater ADG ($P < 0.05$) compared with cattle fed CPM (0.76 kg vs 0.60 kg, respectively, $P < 0.05$). Additionally, cattle fed DIET had more efficient supplement only feed conversion ($P < 0.05$). Nonetheless, due to the by-product nature of CPM it was less expensive resulting in a cost of gain ($P > 0.10$) that was not different compared with DIET. Results of the study indicated that limit feeding a mixed ration yielded greater daily gain and efficiency, however, did not result in a greater cost of gain in cattle grazing dormant warm-season pastures.

Key words: beef cattle, supplements, pasture

W294 Influence of addition of tannins-extract in low concentration of dietary dry matter on feedlot-performance of bulls. R. Barajas*[1], B. J. Cervantes[2], A. Camacho[1], M. Verdugo[1], M. A. Espino[1], L. R. Flores[1], J. A. Romo[1], E. A. Velazquez[1], and J. J. Lomeli[1], *[1]FMVZ-Universidad Autonóma de Sinaloa, Culiacán, Sinaloa, México, [2]Ganadera Los Migueles S.A. de C.V., Culiacán, Sinaloa, México.*

A 226-d experiment was conducted to determine the influence of addition of tannins-extract in low concentration of dietary dry matter on feedlot-performance of bulls. Forty *Bos indicus* x *Bos taurus* bull-calves (184 ± SE 0.22 kg) were used. The experiment was conducted as a complete randomized block design. Bull-calves were blocked by initial weight and in groups of 5 were placed in 6 × 12 m ground floor pens. Treatments were: 1) Feedlot diets based in dry-ground corn, canola meal and dry distiller grain without additional tannins (CTRL); and 2) Diet similar to CTRL added with 0.32% (DM basis) of a tannins-extract (TE). The tannins-extract was obtained from a commercial blend that contains extracts of condensed-tannins and soluble-tannins (Silvafeed-Bypro; Silvateam-Inudor S.A., Argentina). The final weight of bull-calves fed TE treatment was 7% higher ($P = 0.04$) than CTRL (529.2 vs. 492.4 kg). Average daily gain was improved 11% ($P = 0.04$) by the inclusion of TE in the diet means were 1.37 vs. 1.53 kg/d for CTRL and TE treatments, respectively. Dry matter intake was increased 6% ($P < 0.01$) by TE (8.446 vs. 8.994 kg/d). Feed efficiency was not affected by treatments ($P > 0.15$). Bull-calves that received TE showed a tendency ($P = 0.10$) for best using of dietary NEm, Net energy observed/expected ratio were 0.93 and 0.98 for CTRL and TE, respectively. Hot carcass weight was improved ($P = 0.05$) by TE addition (313.1 vs. 338.6 kg for CTRL and TE, respectively). In blood samples taken at 161-d PUN was 15% lower ($P < 0.01$) in bulls fed tannins (12.79 vs. 10.85 mg/dL for CTRL and TE, respectively). It is concluded, that 0.3% (DM basis) of extract tannins-supplementation in the diet improves feedlot performance of bull-calves.

Key words: feedlot-performance, bull-calves, tannins

W295 Influence of addition of tannins-extract in low concentration of dietary dry matter on carcass characteristics of bull-calves. A. Camacho*[1], B. J. Cervantes[2], M. A. Espino[1], M. Verdugo[1], L. R. Flores[1], J. A. Romo[1], and R. Barajas[1], *[1]FMVZ-Universidad Autonóma de Sinaloa, Culiacán, Sinaloa, México, [2]Ganadera Los Migueles S.A. de C.V., Culiacán, Sinaloa, México.*

Forty *Bos indicus* x *Bos taurus* bull-calves (184 ± 0.22 kg SE) were used to determine the influence of tannins-extract addition in low concentration to dietary dry matter on carcass characteristics of bull-calves. The experiment was conducted as a complete randomized block design. Bull-calves were blocked by initial weight and located in groups of 5 in ground floor pens (6 × 12 m). Treatments were: 1) Feedlot diets based in dry-ground corn, canola meal and dry distilled grain without additional tannins (CTRL); 2) Feeding with a diet similar to CTRL added with the 0.32% (DM basis) of a tannins-extract (TE) from condensed and soluble tannins blend (Silvafeed-Bypro; Silvateam-Inudor S.A., Argentina), along the complete feedlot experiment. Upon the complete feedlot period, animals were sacrificed and carcass weight was measured. Carcasses were chilled during 24 h (0°C), and left half of carcass was cross-sectioned between 12th and 13th ribs to determine carcass traits. Hot carcass weight was improved ($P = 0.05$) by TE addition (313.1 vs. 338.6 kg for CTRL and TE, respectively). Carcass dressing (63.8 ± SE 0.38%) was not affected by treatments ($P = 0.18$). Rib eye area was enhanced ($P = 0.03$) by TE with means of 77.4 and 85.6 cm2 for CTRL and TE, respectively. Adjusted rib eye area (using final weight as co-variable) tended to be higher ($P = 0.09$) in carcass of cattle fed TE (minimum-squares means 79.4 vs. 82.8 cm2 for CTRL and TE, respectively). Back fat thickness (9.2 ± SE 0.54 mm) and KPH-fat (1.9 ± SE 0.11%) were similar between treatments ($P > 0.20$). Meat pH (6.23 ± SE 0.04) was not influenced by treatments ($P > 0.20$). It is concluded that, the addition of a tannins-extract in low concentration of dietary dry matter, enhanced carcass weight and rib eye area without affecting remainder traits of bull-calves carcass.

Key words: carcass-characteristics, bull-calves, tannins

W296 Effect of length feeding additional tannins-extract on feedlot-performance of finishing-bulls. R. Barajas*[1], B. J. Cervantes[2], S. C. Arechiga[1], M. A. Espino[1], L. R. Flores[1], A. Camacho[1], and J. A. Romo[1], *[1]FMVZ-Universidad Autonóma de Sinaloa, Culiacán, Sinaloa, México, [2]Ganadera Los Migueles S.A. de C.V., Culiacán, Sinaloa, México.*

Sixty *Bos indicus* x *Bos taurus* bulls (366 ± 0.39 kg) were used to determine the effect of length feeding additional tannins-extract on feedlot-performance of finishing-bulls. The experiment was conducted as a complete randomized block design. Animals were blocked by initial weight and allotted in groups of 5 in ground floor pens (6 × 12 m). Treatments were: 1) Feeding with a DDG-ground corn based 96% concentrate-finishing diet (12.6% CP, 2.052 Mcal of NEm/kg) without additional tannins during 98 d-complete finishing period (CTRL); 2) Diet similar to CTRL added with the equivalent of 0.32% DM of a tannins-extract (TE) of condensed and soluble tannins blend (Silvafeed-Bypro; Silvateam-Inudor S.A., Argentina), during first 67 d (68%) of finishing period (TE68); and 3) Diet similar to CTRL added with the equivalent of 0.32% DM of a TE during 98 d (100%) of complete finishing period (TE100). Final weight was increased linearly ($P < 0.01$) as length feeding TE was augmented (497.7, 507.1, and 512.6 kg for CTRL, TE68, and TE100, respectively). Average daily gain was increased linearly ($P = 0.02$) as time feeding TE was increasing with means of 1.345, 1.452, and 1.500 kg/day for CTRL, TE68, and TE100, respectively. DMI was not affected by treatments ($P > 0.30$). Gain/DMI ratio was increased linearly ($P < 0.01$) with the increment in days feeding TE (0.145, 0.153, and 0.160 kg gain/kg DMI for treatments CTRL, TE68, and TE100, respectively). Hot carcass weight increased linearly ($P = 0.02$) with the increment in days feeding TE (309.2, 316.4, and 320.1 kg for treatments CTRL, TE68, and TE100, respectively). TE intake reduced ($P = 0.04$) plasma urea nitrogen of bulls relative to no tannins treatment (6.06 vs. 5.25 mg/dL). It is concluded, that as increased the length of feeding additional tannins-extract, improves the feedlot performance of finishing-bulls.

Key words: feedlot-performance, finishing-bulls, tannins

W297 Effect of length feeding additional tannins-extract on carcass traits of finishing-bulls. S. C. Arechiga*[1], B. J. Cervantes[2], M. A. Espino[1], L. R. Flores[1], A. Camacho[1], J. A. Romo[1], and R. Barajas[1], *[1]FMVZ-Universidad Autonóma de Sinaloa, Culiacán, Sinaloa, México, [2]Ganadera Los Migueles S.A. de C.V., Culiacán, Sinaloa, México.*

Sixty *Bos indicus* x *Bos taurus* bulls (366 ± 0.39 kg) were used to determine the effect of length feeding additional tannins-extract on carcass traits of finishing-bulls. The experiment was conducted as a complete randomized block design. Treatments were: 1) Feeding with a DDG-ground corn based 96% concentrate-finishing diet (12.6% CP, 2.052 Mcal of NEm/kg) without additional tannins during 98 d-com-

plete finishing period (CTRL); 2) Diet similar to CTRL added with 0.32% (DM basis) of a tannins-extract (TE) during first 67 d (68%) of the finishing period (TE68); and 3) Diet similar to CTRL added with 0.32% (DM basis) of a TE during 98 d (100%) of the complete finishing period (TE100). TE was supplied as a condensed and soluble tannins extract-blend (Silvafeed-Bypro; Silvateam-Inudor S.A., Argentina). Hot carcass weight increased linearly ($P = 0.02$) with the increment in days feeding TE (309, 316, and 320 kg for treatments CTRL, TE68, and TE100, respectively). Rib eye area was higher ($P = 0.09$) in bulls fed tannins-extract relative to no TE fed-bulls (69.7 vs. 75.6 cm2). Back fat thickness was 13.7% lower ($P = 0.05$) in bulls consuming TE along the complete finishing period (TE100) in relationship to CTRL-bulls that did not received TE. Back fat thickness was decreasing linearly ($P = 0.05$) as time-length in TE was increasing, means were of 10.7, 10.1, and 9.3 mm for CTRL, TE68, and TE100, respectively. KPH values were decreasing linearly ($P = 0.06$) as time-length feeding tannins was augmenting, means were 2.1, 1.9, and 1.6% of carcass weight for CTRL, TE68, and TE100, respectively. Marbling score and muscle pH were not affected by treatments ($P > 0.20$). It is concluded, that feeding tannins-extract along complete finishing period increases carcass weight and decreases fat content in carcass of feedlot-bulls.

Key words: carcass traits, finishing-bulls, tannins

W298 Meta-analysis of the effects of the interaction between copper and molybdenum on weight gain and gain:feed ratio in growing cattle. R. Dias*[1], S. Lopez[2], Y. Montanholi[1], B. Smith[1], L. Haas[1], S. Miller[1], and J. France[1], *[1]University of Guelph, Guelph, Ontario, Canada, [2]Instituto de Ganadería de Montaña (IGM), Universidad de León, León, Spain.*

Copper and molybdenum are essential trace minerals for proper functioning of many biological systems in ruminants. A variety of disease conditions are caused by lack of copper in the feed or by excesses of other minerals such as molybdenum which bind to copper and make it unavailable. Adequate trace mineral supply favors animal performance by improving weight gain and feed efficiency. A meta-analysis was undertaken to summarize and evaluate available data relating to the effects of copper and molybdenum supplementation on weight gain and gain:feed ratio in growing cattle weighing between 120 and 320 kg using 22 studies. The mixed model was applied by considering each study as a random effect. The standard error of weight gain and gain:feed ratio were recorded to give a distinct weight for each study. According to the first model, the interaction between supplementation of copper and molybdenum together, and molybdenum supplemented individually are more influential ($P < 0.05$) to weight gain in growing cattle than copper supplemented individually and DM intake ($P > 0.05$). In contrast, the second model showed that gain:feed ratio was significantly affected by DM intake, copper and molybdenum supplemented individually in the diet, and the interaction between these minerals ($P < 0.05$). The level of copper in plasma and the effects of copper source and animal sex were not significant with either model ($P > 0.05$). The first model indicated that the negative effect of possible excessive molybdenum supplementation on weight gain is more relevant than the effect of copper supplementation. Interaction between copper and molybdenum seems to favor weight gain due to copper neutralizing the negative effect of molybdenum on this parameter. In the second model, gain:feed ratio was negatively affected by copper and molybdenum supplemented individually, but these minerals together favored the gain:feed ratio. The interactions between copper and molybdenum needs to be considered carefully when supplementing these trace minerals individually in diets for growing cattle.

Key words: copper, molybdenum, growing cattle

W299 Effects of restricted versus conventional dietary adaptation over periods of 14 and 21 days on rumen papillae of feedlot Nellore cattle. F. S. Parra[1,3], J. R. Ronchesel[1], M. D. B. Arrigoni[1], C. L. Martins[1], D. D. Millen*[2], R. D. L. Pacheco[1], R. S. Barducci[1], L. M. N. Sarti[1], L. C. Vieira Júnior[1], M. C. S. Franzói[1], R. Espigolan[1], J. M. P. Silva[1], D. Setten[1], F. P. Luiz[1], E. A. Chacon Filho[1], *[1]São Paulo State University (UNESP), Botucatu, São Paulo, Brazil, [2]São Paulo State University (UNESP), Dracena, São Paulo, Brazil, [3]Supported by FAPESP, São Paulo, São Paulo, Brazil.*

This study, conducted at the São Paulo State University feedlot, Botucatu Campus, Brazil, was designed to determine effects of restricting DMI of the final finishing diet (REST) as a means of dietary adaptation compared with diets increasing in concentrate (STEPUP) over periods of 14-d and 21-d on rumen wall absorptive surface area (RASA) of feedlot Nellore cattle. The experiment was designed as a completely randomized block with a 2 × 2 factorial arrangement with repeated measures over time, replicated 6 times (5 bullocks/pen), in which 120 18-mo-old yearling Nellore bulls (372.2 ± 21.5 kg) were fed in 24 pens for 84-d according to the treatments: STEPUP for 14-d and 21-d, REST for 14-d and 21-d. The STEPUP program consisted of ad libitum feeding of 3 adaptation diets over periods of 14-d or 21-d with concentrate level increasing from 55% to 85% of diet DM. The REST program consisted of restricted DMI of the final diet with programmed increases in feed offered until animals reached ad libitum access over periods of 14-d or 21-d. After adaptation one animal per pen was slaughtered for rumen papillae evaluations. The remaining 96 animals were harvested when achieved about 500 kg of BW. At harvest a 1-cm^2 fragment of each rumen was collected from ventral sac. Manually, the number of papillae per cm^2 of rumen wall (NOP) was determined and 12 papillae were randomly collected from each fragment; scanned, and mean papillae area (MPA) in cm^2 was measured by software for image analysis. RASA in cm^2 was calculated as follows: 1 + (NOP*MPA) – (NOP*0.002). No significant ($P > 0.10$) protocols or days main effects were observed for MPA and NOP. Animals in STEPUP protocol had greater ($P < 0.05$) RASA (24.98 vs. 20.52) than animals in REST protocol. A significant ($P < 0.05$) interaction was observed between days and harvesting dates. Animals adapted for 14-d had reduced RASA after adaptation than: 1) after finishing (16.20 vs. 25.58) and, 2) animals adapted for 21-d after adaptation (16.20 vs. 27.78). The STEPUP protocol and 21-d of adaptation led to greater RASA, which could indicate lesser extent of rumen lesions.

Key words: Zebu, papillae

W300 Feedlot performance and carcass traits of yearling bulls fed polyclonal antibody preparations, yeast or monensin. E. Rodrigues[1,3], F. S. Parra[1], M. D. B. Arrigoni[1], C. L. Martins[1], D. D. Millen*[2], R. D. L. Pacheco[1], C. R. M. Andrade[1], R. S. Barducci[1], L. M. N. Sarti[1], J. R. Ronchesel[1], A. L. Campanini[1], and D. Tomazella[1], *[1]São Paulo State University (UNESP), Botucatu, São Paulo, Brazil, [2]São Paulo State University (UNESP), Dracena, São Paulo, Brazil, [3]Supported by FAPESP, São Paulo, São Paulo, Brazil.*

This study, conducted at the São Paulo State University feedlot, Botucatu Campus, Brazil, was designed to test the effects of polyclonal antibody preparation (PAP) against lactate-producing rumen bacteria,

Saccharomyces cerevisiae yeast (YEA) or monensin (MO) on feedlot performance and carcass traits of Nellore yearling bulls fed high concentrate diets for 112-d. One-hundred 20-mo-old bullocks (323.3 ± 21.8 kg) were assigned to 25 pens (4 bullocks/pen) and used in a completely randomized design with a 2 × 2 + 1 factorial arrangement of treatments, replicated 5 times. Factors were inclusion or not of PAP or YEA, both at a dose of 450 mg•kg^{-1} of DM, and the additional treatment was MO at 30 mg•kg^{-1} of DM. Dunnett test was used to compare MO with other treatments. Yearling bulls were weighed every 28-d to calculate ADG and F:G ratio, and DMI was recorded every day. No significant ($P > 0.10$) MO effect was observed for DMI in kg from 0-d to 112-d, however feeding MO reduced ($P < 0.05$) DMI in % of BW from 0-d to 28-d when compared with the other treatments (2.19% vs. 2.29%). Feeding MO from 0-d to 112-d reduced ($P < 0.05$) cost to gain 1 kg of BW (CBW; $2.62 vs. $2.79) and led to greater ($P < 0.05$) amount of kidney-pelvic fat (4.74 kg vs. 4.15 kg) when compared with the other treatments. A significant ($P < 0.05$) YEA main effect was observed for ADG, F:G ratio, CBW and HCW. Feeding YEA from 0-d to 112-d reduced ADG (1.13 kg vs. 1.24 kg), and led to greater F:G ratio (7.16 vs. 6.74) and CBW ($2.88 vs. $2.82) and lighter HCW (252.77 kg vs. 258.46 kg). No significant ($P > 0.10$) PAP main effect was observed for any of the feedlot performance parameters analyzed throughout the study. In addition, no significant ($P > 0.10$) differences between PAP and MO were detected in terms of feedlot performance (ADG, DMI, F:G ratio and CBW) and carcass traits (HCW and dressing percentage) from 0-d to 112-d. Yearling bulls not fed YEA performed better than those animals fed YEA. Feeding PAP did not affect negatively feedlot performance and carcass traits. Thus, the potential of PAP to replace ionophores, such as MO, should be further investigated.

Key words: Nellore, PAP, yeast

W301 Rumen papillae alterations of feedlot yearling bulls fed polyclonal antibody preparations, yeast or monensin. E. Rodrigues[1,3], F. S. Parra[1], M. D. B. Arrigoni[1], C. L. Martins[1], D. D. Millen*[2], R. D. L. Pacheco[1], R. S. Barducci[1], L. M. N. Sarti[1], J. R. Ronchesel[1], C. R. M. Andrade[1], A. L. Campanini[1], and D. Tomazella[1], *[1]São Paulo State University (UNESP), Botucatu, São Paulo, Brazil, [2]São Paulo State University (UNESP), Dracena, São Paulo, Brazil, [3]Supported by FAPESP, São Paulo, São Paulo, Brazil.*

This study, conducted at the São Paulo State University feedlot, Botucatu Campus, Brazil, was designed to test the effects of polyclonal antibody preparation (PAP) against lactate-producing rumen bacteria, *Saccharomyces cerevisiae* yeast (YEA) or monensin (MO) on rumen papillae alterations of Nellore yearling bulls fed high concentrate diets for 112-d. One-hundred 20-mo-old bullocks (323.3 ± 21.8 kg) were assigned to 25 pens (4 bullocks/pen) and used in a completely randomized design with a 2 × 2 + 1 factorial arrangement of treatments, replicated 5 times. Factors were inclusion or not of PAP or YEA, both at a dose of 450 mg•kg^{-1} of DM, and the additional treatment was MO at 30 mg•kg^{-1} of DM. At harvest rumenitis incidence (RUM) was determined, on the entire washed rumen, using a scale of 0 (no lesions noted) to 10 (severe ulcerative RUM). A fragment of 1 cm^2 of each rumen was collected from ventral sac. Manually, the number of papillae per cm^2 of rumen wall (NOP) was determined and 12 papillae were randomly collected from each fragment; scanned, and mean papillae area (MPA) in cm^2 was measured using software for image analysis. Rumen wall absorptive surface area (RASA) in cm^2 was calculated as follows: 1 + (NOP*MPA) – (NOP*0.002). A significant ($P < 0.05$) PAP main effect was observed for RUM, NOP and RASA. Yearling bulls fed PAP presented lesser RUM (1.38 vs. 1.77) and greater NOP (56.42 vs. 44.45) and RASA (21.10 cm^2 vs. 17.30 cm^2) than those animals not fed PAP. Feeding YEA led to smaller ($P < 0.05$) MPA (0.36 cm^2 vs. 0.44 cm^2) and reduced ($P < 0.05$) NOP (48.05 vs. 52.66) and RASA (17.39 cm^2 vs. 21.02 cm^2). Feeding MON led to greater ($P < 0.05$) RASA (25.82 cm^2 vs. 15.99 cm^2) and NOP (57.98 vs. 43.20) when compared with animals fed YEA, but no significant ($P > 0.10$) differences were observed when compared with animals fed PAP. Yearling bulls not fed YEA presented greater development of ruminal epithelia than those animals fed YEA. Feeding PAP reduced RUM and led to greater development of ruminal epithelia. Thus, PAP presents a new technology to control rumen acidification with the potential to replace ionophores, such as MO.

Key words: Nellore, PAP, yeast

W302 Fatty acid profiles in adipose tissue of grazing and feedlot beef steers. C. T. Noviandi*[1], R. E. Ward[2], J.-S. Eun[1], D. R. ZoBell[1], R. D. Stott[1], T. Astuti[3], B. L. Waldron[4], and M. D. Peel[4], *[1]Department of Animal, Dairy, and Veterinary Sciences, [2]Department of Nutrition, Dietetics, and Food Sciences, Utah State University, Logan, [3]Faculty of Animal Science, Andalas University, Padang, West Sumatra, Indonesia, [4]Forage and Range Research Laboratory, USDA-ARS, Logan, UT.*

A livestock study was conducted to evaluate the effects of pasture finishing vs. feedlot finishing beef steers on subcutaneous adipose tissue fatty acid (FA) composition. Twenty-seven Angus crossbred steers were arranged on the following 3 treatments: grazing on tall fescue without N fertilizer (TF–NF), grazing on tall fescue with N fertilizer (TF+NF), and feeding TMR on feedlot (FLT). A total of 168 kg/ha N fertilizer was applied in 3 split applications of 56 kg/ha to the TF+NF. The treatments were arranged in a randomized complete block design with 3 replicates and 3 steers per replicate. The pasture-finished steers grazed on replicated 0.47-ha paddocks from May through September 2010 for total of 16 wk. The steers on FLT were housed in 3 group pens with 3 animals per pen and fed a typical finishing diet containing 83% barley grain. Adipose tissue biopsies were obtained on wk 4, 12, and 16. There were no effects of time and treatment × time interaction on FA composition ($P > 0.10$). Fertilizing N did not affect FA composition, except for C18:1 trans-11 being higher in TF+NF compared with TF–NF ($P = 0.03$). Concentration of C18:2 cis-9, cis-12 tended to increase ($P = 0.09$) in TF–NF compared with TF+NF. Concentrations of C18:3 cis-9, cis-12, cis-15 and C18:2 cis-9, trans-11 were higher in grazing steers compared with those in FLT (0.41 vs. 0.20 and 0.48 vs. 0.25 g/100 g FA, respectively; $P < 0.01$), whereas concentrations of C18:1 cis-9 and C18:1 cis-11 were higher in FLT than grazing treatments. Overall results from this study indicate that 4 wk of grazing resulted in remarkable changes in adipose tissue FA profiles in beef steers, but N fertilization had minor impacts on the FA composition. Grazing beef steers elicited increases in human beneficial FA concentrations compared with steers fed FLT.

Key words: fatty acids, feedlot finishing diet, grazing beef steers

W303 Chromium propionate supplementation on feedlot performance of bulls. M. A. Espino*[1], B. J. Cervantes[2], P. W. Rounds[3], F. Valdez[3], E. A. Velazquez[1], J. A. Romo[1], and R. Barajas[1], *[1]FMVZ-Universidad Autonóma de Sinaloa, Culiacán, Sinaloa, México, [2]Ganadera Los Migueles S.A. de C.V., Culiacán, Sinaloa, México, [3]Kemin Agrifoods, Des Moines, IA.*

With the objective of determine the influence of chromium propionate supplementation on feedlot performance of bulls, a 189 d experiment was conducted. Forty 5 bulls 228 ± 2.84 kg were used. Animals were blocked by initial weight and in groups of 5 were located in ground floor pens (6 × 12 m). The experiment was conducted as a complete randomized block design (CRBD). Treatments were: 1) Feedlot diets without additional chromium (CTRL); 2) Diets added with an equivalent of 0.15 ppm of chromium as Cr-propionate (Cr15); and 3) Diets added with an equivalent of 0.30 ppm of chromium as Cr-propionate (Cr30). Supplementary chromium was provided from Kemin Trace Cr premix (Kemin Agrifoods, Des Moines, IA). The experiment was analyzed by ANOVA for CRBD; CTRL vs. Cr-supplemented diets (Cr15 + Cr30) was compared by orthogonal contrasts; and quadratic trend was explored using polynomial contrasts. In a 189-d experiment, bulls receiving any additional Cr-level were 5% heavier than CTRL (P = 0.03). Ending weight showed a quadratic trend (P = 0.11) toward Cr-level; Cr15-bulls were the heaviest with values of 469.8, 495.9, and 492.2 kg for CTRL, Cr15, and Cr30 treatments, respectively. Average daily gain was improved 10.8% by supplementary Cr compared with CTRL (P = 0.03). Weight gain had a quadratic response to additional Cr-level (P = 0.05), with values of 1.27, 1.42, and 1.40 kg/d for CTRL, Cr15, and Cr30 treatments, respectively; the highest ADG was observed in bulls fed with 0.15 ppm additional Cr. DMI and gain/feed ratio were not affected by treatments (P > 0.20). Cr15 treatment, improved 5.2% hot carcass weight (P = 0.09) comparative to CTRL; carcass weight of Cr30-fed cattle was no different from remainder treatments (P > 0.20). Carcass traits and meat pH were similar across all treatments (P > 0.20). It is concluded, that chromium propionate supplementation improves feedlot performance of bulls, and dosage of 0.15 ppm would result in better response against not Cr addition or 0.30 ppm Cr supplementation

Key words: bulls, chromium, feedlot performance

W304 Creatinine to estimate the quantity of carcass muscle and crude protein in the empty body weight. L. F. Costa e Silva, S. de C. Valadares Filho, P. P. Rotta*, R. F. D. Valadares, and D. Zanetti, *Universidade Federal de Viçosa, Viçosa, Minas Gerais, Brazil.*

The creatinine production is due the protein turnover that occurs in animal muscle. It is possible to determine the muscle and crude protein quantity in carcass and the crude protein quantity in the empty body by the urinary creatinine excretion. The aim of this study was to estimate the urinary creatinine excretion by the body weight (BW) and the muscle quantity in carcass and crude protein quantity in carcass and in the empty body by the urinary creatinine excretion. 32 Nellore bulls with initial body weight of 259 kg and 14 mo were used in this experiment. Four bulls were fed at maintenance and the 28 animals were kept at ad libitum system with corn silage and 40% of diet with concentrate in dry matter. The animals were allocated in 4 groups, which each group was slaughtered in different times of feedlot (42, 84, 126 and 168 d). To estimate the urinary creatinine excretion, 14 animals were kept at Tie Stall system. The others animals were allocated at collective pens with electronic gates to evaluate the individual feed intake. Before each slaughter, collections of urine were realized during 3 consecutive days. From the slaughters the empty body weight and the body composition of the animals were determined. After the slaughter, the left carcass was separated in muscle, fat and bone. The carcass samples were dried and ground to determine the total nitrogen. In urine, the creatinine analyses followed the protocol to high performance liquid chromatography. The creatinine excretion (Y) can be obtained by the equation: $Y = 0.0276 \times BW^{0.9811}$, $r^2 = 0.9761$. The quantity of carcass muscle (Mcarc) and carcass crude protein (CPcarc) estimated by the creatinine (CRE) were: $Mcarc = 15.307 \times CRE^{0.9894}$, $r^2 = 0.9341$ and $CPcarc = 3.2756 \times CRE^{1.0683}$, $r^2 = 0.9312$. The crude protein in empty body weight (CPEBW), estimated by the CRE was: $CPEBW = 6.5563 \times CRE^{0.9502}$, $r^2 = 0.9427$. All the exponents of the equations were near from 1. It allows concluding that the urinary creatinine excretion and the quantity of carcass muscle and carcass and empty body crude protein present near relation.

Key words: excretion, turnover, urine

W305 Effect of glycerin on intake and digestion of bermudagrass hay in beef cattle. T. A. Wickersham*, K. M. Bodensteiner, M. L. Drewery, R. O. Dittmar, and J. E. Sawyer, *Texas A&M University, College Station.*

Glycerin is a byproduct of biodiesel production and has the potential to provide supplemental energy to cattle consuming forage diets; however, the effect of glycerin in these diets has not been determined. Our objective was to determine the effects of increasing levels of glycerin on bermudagrass hay utilization. Four Angus × Hereford steers (BW = 301 ± 18.5 kg) were used in a 3 × 3 Latin square with an additional column for steer. Steers were provided ad libitum access to bermudagrass hay (10.6% CP and 69.0% NDF) and supplemented with cottonseed meal (0.2% of BW per day; 42.5% CP). Treatments consisted of 3 levels of glycerin infusion (0, 0.1, and 0.2% BW). Glycerin was delivered directly into the rumen once daily. Experimental periods were 17d long. Intake was determined from d 11 through 14 to correspond with fecal grab samples collected from d 12 to d 15. Acid detergent insoluble ash was used as an internal marker to estimate fecal production. On d 16 of each period, ruminal fermentation profiles were evaluated. Increasing levels of glycerin resulted in a quadratic (P = 0.04) response in hay OM intake from 6.75 kg/d for 0% glycerin to 5.92 and 6.46 kg/d for 0.1 and 0.2% BW as glycerin, respectively. There was a correspondent quadratic (P = 0.05) response in total OM intake to glycerin provision (7.25, 6.72, and 7.56 kg/d for 0, 0.1, and 0.2%). However, there was no significant (P > 0.12) effect of glycerin on either OM digestion (54.2, 55.6, and 51.5% for 0, 0.1, and 0.2%, respectively) or NDF digestion. When measures of intake and digestion were combined as total digestible OM intake, there was no significant effect (P > 0.35) of increasing glycerin. Intake of total digestible OM was 3.95, 3.74, and 3.92 kg/d for 0, 0.1, and 0.2%. A treatment by time interaction (P = 0.03) occurred for ruminal pH. Increasing glycerin resulted in greater reductions in ruminal pH post feeding; however, all pH values were greater than 6.30. Further work is required to understand why glycerin negatively affected forage intake when provided at 0.1% of BW.

Key words: forage, glycerin, cattle

W306 Effect of methanol on intake and digestion in beef cattle. K. N. Winsco*, N. M. Kenney, R. O. Dittmar, J. A. Coverdale, J. E. Sawyer, and T. A. Wickersham, *Texas A&M University, College Station.*

Methanol is used in biodiesel production, is found in significant quantities in crude glycerin, and has adverse effects on non-ruminants. Currently, the maximum concentration allowed for methanol in ruminant feeds is 150 ppm, but there is little data describing the effects of methanol concentrations in excess of 150 ppm on ruminants. Our objective was to determine effects of methanol concentration on intake and digestion in cattle consuming a grain-based diet. Five ruminally cannulated Holstein steers (BW = 399 ± 34 kg) were used in a 4 × 4

Latin square with an additional column for steer, and provided ad libitum access to a grain-based diet (49% corn, 14.7% CP, 32.1% starch). Treatments consisted of 4 levels of methanol (0, 70, 140, and 210 g/d) infused directly into the rumen to prevent volatilization from feed. Experimental periods were 16 d, with 9 d of adaptation to treatment and 7 d of data collection. Determinations of intake were made on d 10 through 14 of each period to correspond with fecal grab samples collected from d 11 through 15. Titanium dioxide, dosed daily at 10 g/d, was used as an external marker to estimate fecal production. Ruminal fluid was collected on d 16. Methanol intake increased linearly ($P < 0.01$) from 0 to 6,563, 13,356, and 19,831 ppm diet for 0, 70, 140, and 210 g/d of methanol, respectively. Intake was not ($P > 0.71$) affected by methanol infusion (9.93, 9.93, 9.73, and 9.83 kg OM/d for 0, 70, 140, and 210 g/d of methanol). Methanol infusion did not affect ($P > 0.12$) OM or starch total tract digestion, which averaged 75.6 and 93.9%, respectively, across treatments. Our results indicate that levels of methanol consumption in excess of the current recommendation of 150 ppm did not have adverse effects on intake and digestion in cattle. These data suggest minimal risk in allowing ruminant diets to contain greater levels of methanol than non-ruminant diets.

Key words: methanol, glycerin, cattle

W307 Effects of purified lignin on growth performance of feedlot cattle. Y. Wang*[1], J. H. Lora[2], and T. A. McAllister[1], *[1]Agriculture and Agri-Food Canada, Lethbridge Research Centre, Lethbridge, Alberta, Canada, [2]GreenValue Enterprises LLC, Media, PA.*

A feedlot experiment was conducted to assess the effect of purified lignin recovered from wheat straw soda pulping (PL) on the growth performance of feedlot cattle. A total of 60 Hereford-Angus cross weaned calves were randomly divided into 4 groups. The cattle were individually fed a barley grain/barley silage based total mixed ration and randomly assigned to one of 4 diets containing increasing levels of PL (0, 4, 8 and 16 g/kg DM). Cattle were fed once daily for ad libitum intake and had free access to water during a 70-d growing period and a 121-d finishing period. Inclusion of PL in the diet tended to linearly reduce ($P = 0.090$) average daily gain (ADG) during the growing period, but not in the finishing period. Feed intake over the entire experimental period tended to be linearly reduced ($P = 0.100$). Feed efficiency was similar among groups of steers during growing period, but was quadratically improved ($P = 0.059$) during the finishing period with increasing PL in the diet. Supplementation of PL tended to increase ($P = 0.098$) the saleable meat yield, but had no effects on other carcass traits. The quadratic improvement in feed efficiency by adding PL to finishing diet (high grain diet) but not to growing diet is likely due to PL regulating ruminal microbial activity in digestion of starch, as well as modulation of the feed intake. Inclusion of PL at the level of about 8 g/kg DM in diet containing high grain may benefit the feedlot cattle in terms of improving feed efficiency.

Key words: feedlot cattle, purified lignin, growth

W308 Protein balance alters expression of key genes for protein and lysine catabolism in liver of lactating dairy cattle. H. A. Tucker*[1], S. L. Koser[1], P. H. Doane[2], and S. S. Donkin[1], *[1]Purdue University, West Lafayette, IN, [2]Archer Daniels Midland Company, Decatur, IL.*

Lysine supply is often limiting for milk protein production in dairy cattle. The availability of lysine for mammary protein synthesis is a function of metabolizable lysine supply and hepatic lysine catabolism. The objective of this experiment was to examine the effect of protein balance in early lactating dairy cattle on expression of aminoadipate semialdehyde synthase (AASS), a committing step in lysine catabolism by liver, and ornithine transcarbamoylase (OTC), a general indicator of protein utilization and ureagenesis. Thirty multiparous early lactation Holstein cows were fed diets containing either 16.0 or 17.5% crude protein for an 84 d period. Liver samples were collected via percutaneous liver biopsy on d 42 and 84 of the experiment for mRNA analysis. Blood samples were collected on d 42 and 84 and analyzed for blood urea nitrogen. Protein balance was determined for the week preceding sample collection and used to classify cows as either positive or negative with respect to MP balance. AASS expression differed ($P < 0.05$) for d 42 (0.37 ± 0.2 arbitrary units) and d 84 (0.88 ± 0.2 arbitrary units) of the experiment. OTC expression differed ($P < 0.05$) between d 42 (1.43 ± 0.2 arbitrary units) and d 84 (2.62 ± 0.2 arbitrary units). Expression of AASS tended ($P < 0.1$) to be lower in cows experiencing negative protein balance (0.39 ± 0.2 arbitrary units) and was elevated in cows in positive protein balance (0.85 ± 0.2 arbitrary units), while expression of OTC did not differ ($P > 0.05$) between groups. There were no interactions between protein sufficiency and day of experiment for either transcript. Expression of OTC on d 42 was correlated ($P > 0.05$) with metabolizable and rumen undegradable protein intake. Expression of AASS was correlated ($P > 0.05$) with milk urea nitrogen in cows in negative protein balance. No significant correlations between gene expression and positive protein balance were observed. These data indicate that expression of lysine catabolism and ureagenic genes in the liver are responsive to protein balance in early lactating dairy cattle and suggest enhanced sensitivity when protein is limiting.

Key words: lysine, protein balance, gene

W309 Effects of OmniGen-AF on performance and economics of a veal operation. O. Bewley*[1], J. D. Chapman[1], K. P. Zanzalari[1], Y. Q. Wang[2], and N. E. Forsberg[2], *[1]Prince Agri Products, Quincy, IL, [2]OmniGen Research, Corvallis, OR.*

The goal of this study was to evaluate the effects of OmniGen-AF (Prince Agri Products, Quincy, IL) on veal calf performance, immune parameters and economics of production. Two hundred Holstein calves were received at a commercial Pennsylvania veal operation within 48–72 after birth and assigned to 2 treatments: control-fed (n = 50) and OmniGen-AF-fed (n = 150). At trial start, animals on the OmniGen-AF treatment received 10 g OmniGen-AF/head/day. This was added to a commercial milk replacer. The amount of OmniGen-AF was thereafter increased to maintain a dose of 0.09g/kg BW/d. Duration of the study was 137d. Starting weights and final weights were recorded and gain calculated. Whole blood was sampled 4 times during the study (Day 0 and monthly thereafter). Blood RNA was purified with Trizol and used for assay of 2 immune markers: L-selectin mRNA and interleukin-8 receptor (IL8R) mRNA using quantitative reverse transcriptase PCR. Beta-actin mRNA concentration was also assessed to normalize expression of L-selectin and IL8R mRNAs. Treatments and treatment costs were also recorded and economic value of the supplementation program was calculated using on-farm medication costs. Data were analyzed with SAS using least squares means for unequal cell sizes. The Proc GLM procedure was used to compare means for main effects (ration). Mean final weights of control and OmniGen-AF-fed animals were 126.4 and 128.5 kg ($P > 0.05$), respectively. OmniGen-AF reduced ($P < 0.05$) treated calves ($P < 0.05$) from 29 treated calves/50 calves to 18, respectively. Treatment costs were thereby reduced from $2.58/calf to $1.46/calf, respectively. Numbers of calves experiencing severe infections was reduced from 8 to 5.6 severe infections/50 calves by feeding OmniGen-AF. Effects of the additive on blood immune markers were similar to those reported previously (Wang et al., 2007, 2009). Feeding OmniGen-AF tended to increase ($P > 0.05$) L-selectin mRNA and increased ($P < 0.05$) IL8R mRNA during the third and fourth months of the study. Veal calves responded to OmniGen-AF as have most other animal models; including adult dairy cattle, beef cattle, sheep, swine and rodents.

Key words: veal calves, immunity, OmniGen-AF

W310 Determining methionine bioavailability in commercial dairy herds. D. Stucker[1], J. R. Knapp*[2], and N. R. St-Pierre[3], *[1]Venture Milling, Salisbury, MD, [2]Fox Hollow Consulting LLC, Columbus, OH, [3]The Ohio State University, Columbus.*

Our objective was to determine the relative bioavailability of methionine in rumen-protected supplements under field conditions using the selenomethionine dilution approach of Weiss and St-Pierre (2009). Three commercial methionine supplements were fed to 3 pens of approximately 250 cows each in a commercial dairy herd, and methionine bioavailaibility compared with an unsupplemented control in a truncated Latin square design. The selenium yeast and methionine supplements were fed to provide 0.3ppm selenium and 15g methionine per cow per day, respectively. The herd was milked 3x per day, and milk was sampled from each pen during 6 milkings distributed over the last 3 d in each 10-d period. Milk was sampled via an in-line sampling device, mixed extensively, and sub-sampled. Milk components, somatic cell counts, and milk urea nitrogen levels were determined by NIR (DHI Cooperative, Inc.). Milk nitrogen and selenium were determined by micro-Kjeldahl analysis and fluorometry, respectively. Data were analyzed using a mixed model with period and treatment (methionine supplement) as fixed effects and pen and related interaction terms as random effects. Supplementation with selenium yeast increased milk selenium from 19.8 to 36.6 ng/g milk, and is typical of the response observed in previous research. Methionine supplementation increased milk crude protein 0.049% units ($P < 0.05$), decreased milk selenium 6.1 ng/g ($P < 0.0001$), and decreased milk selenium:nitrogen ratio ($P < 0.0001$). No differences were observed in these measurements among methionine supplements ($P > 0.20$). These results confirm that the selenomethionine dilution approach provides an excellent method to determine methionione bioavailability to the mammary glands. However, refinement of the method is required to allow detection of differences between methionine supplements. In this experiment, within-pen variances were larger than expected from prior research conducted on individual animals, indicating that further research is needed to separate components of variances that contribute

to the large within-pen variances, including analytical, sampling, day-to-day, and animal variances.

Key words: amino acid availability, amino acid supplement, methionine

W311 Effect of returned milk (Nutri-Gold) on performance of veal calves. D. Vermeire*, *Nouriche Nutrition Ltd., Lake St. Louis, MO.*

Calves were fed either control (CON) milk replacers (MR) produced with whey and whey protein concentrate or experimental (EXP) MR in which dried milk comprised 30% of the formula (w/w). CON and EXP MR were formulated to contain equal protein and fat concentrations. Dried milk (Nutri-Gold) was within-date returned milk from grocery stores, blended, and dried with drum dryers. Holstein calves (n = 196, 43.5 kg) were fed either CON or EXP pre-starter and starter MR (d 1–52), and either CON or EXP finisher MR (d 53–144) in a 2x2 factorial arrangement of treatments in a completely randomized experimental design. Calves were randomly assigned to individual stalls upon arrival. Calves in odd-numbered stalls were fed EXP while calves in even-numbered stalls were fed CON pre-starter and starter MR treatments, respectively. Calves in stalls 1 and 2, 5 and 6, 9 and 10, etc. were fed EXP while calves in stalls 3 and 4, 7 and 8, and 11 and 12, etc. were fed CON finisher treatments, respectively. All treatment combinations were represented in every 4 stalls throughout the room. Weight (WT) on day (d) 1 or d 52, and gain from d 1–52 were not different due to starter or finisher treatment. Gain from d 52–144 tended ($P = 0.056$) to be greater, and gain from d 1–144 tended ($P = 0.069$) to be greater for calves fed EXP vs CON starter MR. Carcass WT were heavier ($P = 0.023$, 120.9 ‡1.16 vs 117.1 ‡1.17 kg, respectively), and LD color was lighter ($P = 0.031$, 2.25 ‡0.05 vs 2.40 ‡0.05 VUSA score) for calves fed EXP vs CON starter MR, respectively. During the finishing phase, calves fed EXP were heavier on d 144 ($P = 0.002$, 201.0 ‡1.85 vs 192.8 ‡1.86 kg, respectively), had heavier carcass WT ($P = 0.002$, 121.5 ‡1.14 vs 116.4 ‡1.16 kg, respectively) and gained more WT from d 52–144 ($P = 0.002$, 126.7 ‡1.60 vs 119.7 ‡1.63 kg, respectively) than calves fed CON. LD color was not affected by finisher MR. Interaction of MR (CON vs EXP) and phase (starter vs finisher) was significant ($P < 0.001$) for WT on d 144, carcass weight, and gain from d 52–144 indicating that feeding drum-dried returned milk in either starter or finisher phase increased carcass WT, WT on d 144, and WT gain from d 1–144.

Key words: veal, dried milk, calves

W312 Antioxidant activity in milk of dairy cows fed diets containing propolis-based products. S. M. Cottica[1], S. C. de Aguiar[1], E. M. de Paula[1], R. B. Samensari[1], L. P. P. de Moura[1], S. L. Franco[1], J. V. Visentainer[1], G. T. dos Santos[1], R. Kazama[2], O. P. P. do Prado[1], F. J. Maia[1], and L. M. Zeoula*[1], *[1]Universidade Estadual de Maringá, Maringá, Paraná, Brazil, [2]Universidade Federal de Santa Catarina, Florianópolis, Santa Catarina, Brazil.*

The objective was to evaluate the effect of propolis-based products (PBP), which differ in the concentration of propolis, alcohol content, and concentration of flavonoids (PBP1, PBP2, PBP3) in the diets of dairy cows, to verify the antioxidant activity in the milk produced by these animals. Four Holstein cows, with 550 kg of body weight and 147 d of lactation were subjected to 2 daily milkings (0600h and 1500h) and randomly assigned to a 4x4 Latin Square. The diets were formulated with 60.27%:39.73% forage:concentrate to contain 16.9% of CP, 1.49 mcal/kg of NEL, 10.2% RDP and 38.2% NDF, differing with the inclusion or not of PBP, which are: control (no additives), PBP1, PBP2 and PBP3 (with 30.63, 71.88 and 78.45 mg of quercetin equivalents ($QE.g^{-1}$), respectively). The PBP1 and PBP2 differ only in the concentration of propolis and have the same ethanol content, while the PBP3 has the same propolis concentration of PBP2 and higher ethanol content. The PBP, a powder, were introduced into the rumen via ruminal cannula at the time of diets ministration. Analyses of antioxidant activity of milk samples were performed using the ORAC method - Oxigen Radical Absorbance Capacity with fluoresceíne (ORAC-FL), based in the capacity that the sample has to capture peroxyl radicals generated by thermal decomposition of 2.2-azobis (2-amidinopropane) dihydrochloride (AAPH). The results were expressed as mM of Trolox Equivalent (mM TE) and differed significantly between treatments. It was observed that PBP increased ($P = 0.000001$) the antioxidant activity of milk compared with control treatment. Milk samples resulting from treatments PBP2, PBP1 and PBP3 had antioxidant activity of 24.352, 23.640 and 16.075 mM TE, respectively, and the control treatment had antioxidant activity of 14.582 mM TE. It can be concluded that the PBP has antioxidant capacity and its addition in the diet of dairy cows can be positive, due to an increase transfer of antioxidant activity to the milk, preventing, therefore, their lipid oxidation, which will improve quality and lead benefits to consumer health.

Key words: antioxidant activity, milk, propolis ethanolic extracts

W313 Ruminal fermentation of acidosis induced cows treated with monensin or polyclonal antibodies against target ruminal bacteria. D. D. Millen*[2,3], R. D. L. Pacheco[1], C. T. Marino[4], J. P. S. T. Bastos[4], T. A. Barros[4], F. A. Ferreira[4], C. L. Martins[1], M. D. B. Arrigoni[1], and P. H. M. Rodrigues[4], *[1]São Paulo State University (UNESP), Botucatu, São Paulo, Brazil, [2]São Paulo State University (UNESP), Dracena, São Paulo, Brazil, [3]Supported by FAPESP, São Paulo, São Paulo, Brazil, [4]University of São Paulo (USP), Pirassununga, São Paulo, Brazil.*

This study was designed to evaluate the potential of a multivalent polyclonal antibody preparation (PAP) against target ruminal bacteria (*S. bovis*, *F. necrophorum* and *Lactobacillus* ssp.) or monensin (MO) as acidosis preventative feed additive for cattle switched abruptly to high concentrate diets. Nine cannulated cows (677 ± 98 kg of BW) were used in a completely randomized design in 2 periods of 20-d. Treatments were: control (CTL), PAP at a dose of 450 $mg•kg^{-1}$ of DM and MO at 30 $mg•kg^{-1}$ of DM. During first 5 d of each period, animals were fed a 100% forage diet (fresh chopped sugarcane). Ruminal acidosis was induced by abruptly introducing a 74% concentrate diet (based on high moisture corn) during 15-d. An interval of 15-d was considered between the 2 periods as ruminal washout. Ruminal acidosis evaluation parameters were: DMI, DMI fluctuations during the subsequent days after challenge, rumen pH, and VFA, lactate and NH_3-N concentrations. There was no treatment main effect ($P > 0.05$) for DMI. Higher pH was observed ($P < 0.01$) for MO fed cows (6.06) compared with those on PAP (5.89) and CTL treatments (5.91). Ruminal lactate concentration remained low (0.23 mM) and unchanged ($P > 0.05$) throughout the study. The NH_3-N concentration of cows on CTL treatment (11.20 $mg•dl^{-1}$) was lower ($P < 0.01$) compared with cows fed MO (14.74 $mg•dl^{-1}$) and PAP (13.64 $mg•dl^{-1}$). A day x treatment interaction ($P < 0.01$) for molar concentration of propionate was found, in which feeding MO increased propionate concentration during 4 d after challenge. Feeding MO also reduced ($P < 0.01$) acetate:propionate ratio during 3 d after challenge. Molar proportion of butyrate was reduced ($P < 0.01$) when cows were fed MO (15.42

mol•100mol^{-1}) and PAP (16.35 mol•100mol^{-1}) compared with cows on CTL treatment (18.43 mol•100mol^{-1}). The type of ruminal acidosis generated in the present study was not lactic and possibly did not promote adequate conditions for PAP control ruminal lactate-producing bacteria. Nevertheless, MO was effective in increasing rumen pH and improving ruminal fermentation of cows induced to ruminal acidosis.

Key words: acidosis, monensin, PAP

W314 Effect of a combined supplement of vitamin B12 and folic acid on vitamin B12 concentration in milk of dairy cows. M. Duplessis*[1], D. Pellerin[1], and C. L. Girard[2], *[1]Université Laval, Département des sciences animales, Québec, QC, Canada, [2]Agriculture and Agri-Food Canada, Sherbrooke, QC, Canada.*

Increasing folic acid supply could mask vitamin B12 deficiency until neurological damages are irreversible. Consequently, since folic acid fortification of flour became mandatory in many Western countries, there is a renewed interest for vitamin B12 status in human populations. The natural source of vitamin B12 in human diets comes from animal products, especially those from ruminants. Moreover, a recent study showed that vitamin B12 in cow′s milk is absorbed more efficiently than its synthetic form. The objective of this work was to evaluate the effect of a combined supplement of vitamin B12 and folic acid on vitamin B12 concentration in milk of dairy cows. Commercial dairy herds were involved in this study (n = 15). Every 2 mo and within each herd, from February to July 2010, cows (n = 309) were randomly assigned, based on parity, predicted 305d milk yield, and calving interval to weekly intramuscular injections of 5 mL of 1) saline 0.9% NaCl (C) or 2) 10 mg of vitamin B12 + 320 mg of folic acid (V). The treatments began 3 wk before the expected calving date until 8 wk after parturition. Milk samples were taken on average at 28.1 ± 3.9 (T1) and 55.6 ± 3.9 (T2) DIM. Data were analyzed using the MIXED procedure of SAS with block, herd, parity, treatment and time as main effects. Vitamin supplements increased ($P < 0.0001$) average milk concentration of vitamin B12 from 3.1 to 5.2 ± 0.1 ng/g. For V and S, vitamin B12 concentrations were 5.5 and 5.0 ± 0.1 ng/g and 3.1 and 3.2 ± 0.1 ng/g at T1 and T2, respectively (treatment × time, $P = 0.0005$). Vitamin B12 concentration in milk was not affected by parity ($P = 0.13$) but it differed among herds ($P < 0.05$); there was no interaction treatment × herd ($P = 0.23$). Weekly intramuscular injections of vitamin B12 and folic acid increased by 68% milk concentration of vitamin B12 in commercial dairy herds. A glass (250 mL) of milk from supplemented cows provides 54% of the recommended daily allowance (2.4 µg) for adults and children over 13 years of age.

Key words: vitamin B12, folic acid, dairy cow

W315 Effects of cornmeal or molasses supplemented with different protein sources on milk production and nitrogen utilization of organic dairy cows. S. Ross*[1], A. F. Brito[1], H. V. Petit[2], and K. J. Soder[3], *[1]University of New Hampshire, Durham, [2]Agriculture and Agri-Food Canada, Sherbrooke, QC, Canada, [3]USDA-Agricultural Research Service-Pasture Systems and Watershed Management Research Unit, University Park, PA.*

Sixteen lactating organic Jersey cows were assigned to 4 replicated 4 × 4 Latin squares with a 2 × 2 factorial arrangement of treatments to compare the effects of feeding cornmeal (CM) or molasses (MOL) with either flaxseed meal (Flax) or a protein mix [(PM = 11% soybean meal (SB) + 5% sunflower meal (SM)] on milk yield and N utilization. Cows were fed (% diet DM) grass baleage (70%), mineral pre-mix (2%), plus one of 4 concentrates (28% diet DM): 1) 12% CM plus 16% PM (CMP); 2) 12% CM plus 16% Flax (CMF); 3) 12% MOL plus 16% PM (MOLPM); or 4) 12% MOL plus 16% Flax (MOLF). Cows were fed twice a day with concentrates top-dressed on the baleage. Preplanned orthogonal contrasts were used to compare the main effects of: energy source (ES = CM vs. MOL) and protein source (PS = SB + SM vs. Flax), and the ES × PS interaction. A significant PS was observed for milk yield with cows fed Flax diets producing the lowest amounts. Cows fed MOL diets had the lowest ($P = 0.01$) feed efficiency while those fed PM diets the highest ($P < 0.001$). Significant PS effects were observed for yields and contents of milk fat and milk protein. A dilution effect possibly explains the reduced ($P < 0.01$) milk protein content in cows fed CMP and MOLP. A significant ES × PS interaction was found for MUN with cows fed CMF showing the highest and cows fed MOLF showing the lowest values, indicating enhanced N utilization in the latter diet. Cows fed MOL diets had the lowest PUN showing improved N utilization. Increased PUN with PM diets can be explained by their slightly greater CP compared with Flax diets. Overall, diets containing Flax reduced yields of milk and milk components while those containing MOL improved N utilization in organic cows.

Table 1. Performance and N utilization

	Diets					Contrasts		
	CMP	CMF	MOLP	MOLF	SED	ES	PS	ES × PS
DMI, kg/d	16.0	16.2	16.3	17.1	0.34	0.20	<0.001	NS
Milk yield, kg/d	14.0	13.0	14.0	12.3	0.34	NS	<0.001	NS
Milk: DMI	0.89	0.81	0.87	0.73	0.03	0.01	<0.001	0.10
Fat, %	4.58	4.43	4.56	4.29	0.11	NS	0.01	NS
Fat, kg/d	0.62	0.57	0.64	0.52	0.02	NS	<0.01	0.06
Protein, %	3.35	3.53	3.38	3.54	0.04	NS	<0.01	NS
Protein, kg/d	0.46	0.45	0.48	0.44	0.01	NS	0.01	0.09
MUN, mg/dL	15.7	17.4	15.6	14.9	0.44	<0.001	NS	<0.001
PUN, mg/dL	20.9	19.4	19.2	18.7	0.71	0.02	0.05	NS

SED=standard error of LSM difference; NS=not significant.

Key words: flaxseed meal, molasses, organic cows

W317 Effects of essential oils, yeast and enzyme additive to milk replacer and starter on dairy calf performance. A. D. Kmicikewycz*[1], H. T. Pervis[2], J. Hill[2], and N. B. Litherland[1], *[1]University of Minnesota, St. Paul, [2]Ralco Nutrition Inc., Marshall, MN.*

The objective of this study was to determine the effects of an essential oil blend, yeast cell wall extract, *B. subtilis*, and a source of digestible fiber in milk replacer (MRA) along with a digestible fiber, yeast cell wall extract, an essential oil blend, niacin and enzyme premix additive blend to starter (SA) on calf performance and health. Sixty multi-farm commingled male (n = 15) Holstein calves <7 d of age were randomly assigned to 1 of 4 treatments and balanced by initial body weight

(BW). The treatments (T) were as follows: T1) 20% CP:20% fat milk replacer (MR) and 18% CP texturized starter (control); T2) 20:20 MR with 10 g/d MRA and18% CP starter; T3) 20:20 MR and SA; T4) 20:20 MR with 10 g/d MRA and SA. All MR was non- medicated, reconstituted to 12.5% solids and fed at 1.5% of arrival BW. Calves were weaned on d 42. Water and starter were provided ad libitum from d 1 to 56. Weekly weight and structural measurements and daily starter intake and fecal scores (FS) were recorded. Data were analyzed using Proc Mixed in SAS as a completely randomized design with repeated measures. Starter and total DM intake was not different among treatments. There was a tendency ($P = 0.08$) for an increase in starter intake by week. Least squares means of starter intake (kg/d) from d 1 to 42 were 0.62 for T1, 0.59 for T2, 0.53 for T3, and 0.49 for T4. Average BW gain from d 1 to 42 (T1 = 15.4; T2 = 14.0; T3 = 13.0 and T4 = 10.7) was not different ($P = 0.40$) or was BW gain from d 1 to 56 ($P = 0.47$). Average daily gain (ADG) from d 1–56 was not different ($P = 0.47$) averaging 0.43, 0.36, 0.34 and 0.36 kg/d for T1, T2, T3, and T4. There was no significant T or T × wk interaction for hip width, hip height, wither height or heart girth. FS were not different ($P = 0.95$) between treatments and averaged 2.2. Feeding a combination of essential oils, microbial and enzyme additives did not increase calf daily gain or performance over the 56 d.

Key words: calf, milk replacer, essential oils

W318 Milk production responses of grazing cows to partial mixed rations. M. J. Auldist*, J. L. Jacobs, L. C. Marett, J. S. Greenwood, and W. J. Wales, *Department of Primary Industries, Ellinbank, Victoria, Australia.*

An experiment was conducted to measure milk production responses of grazing dairy cows in late lactation to supplements offered as partial mixed rations (PMR), or as grain in the dairy and forage in the paddock. Three groups of 72 multiparous spring-calving Holstein-Friesian cows had a common pasture intake of 8 kg DM /cow.d. Each group was randomly assigned to 1 of 3 rations to receive the balance of their nutrient intake. Rations were: (i) Control: barley grain in the dairy twice daily at milking times and pasture silage in the paddock. (ii). PMR1: a simple PMR of barley grain and pasture silage. (iii). PMR2: a PMR comprising maize silage, maize grain, barley grain and alfalfa hay. All rations were isoenergetic with grain:forage ratios of 75:25 (DM basis). Both PMRs were fed on a feed pad twice per day aftermilking. The 3 groups were further divided into 8 groups of 9 cows, and offered their supplements at one of 4 rates (6, 8, 10 or 12 kg DM supplement/cow.d) for 25 d. Milk yields measured daily and concentrations of fat and protein measured weekly were used to calculate yields of energy corrected milk (ECM). The ECM response to supplements between 6 and 12 kg DM/cow.d was linear ($P < 0.05$) for PMR2, but not for Control or PMR1. There was no difference between ECM yield of any group except at the highest rate, when cows fed PMR2 produced 1.9 kg/cow.d more ($P > 0.05$) than cows fed the Control and PMR1 diets. These data suggest that feeding grazing cows high rates of supplements as a PMR containing maize grain and maize silage may offer the opportunity to alleviate the diminishing or negative marginal response commonly observed when feeding high amounts of grain in the dairy.

Table 1. Yields of energy corrected milk (kg/cow.d) for cows offered different levels of supplements as a Control system or as one of two different partial mixed rations. Data are means for two groups of 9 cows offered each rate of each diet

Rate of feeding (kg DM/cow.d)	Control	PMR1	PMR2
6	17.5	15.8	16.5
8	19.6	18.1	19.5
10	21.4	20.3	21.0
12	20.1[a]	19.8[a]	22.0[b]

[a,b]Within rates of feeding, means with different superscripts are significantly different. Overall standard error of the difference between means was 1.09.

Key words: pasture, milk response, supplements

W319 Evaluation of a rumen protected carbohydrate supplement prototype feed with fresh lactation dairy cows. J. P. Russi*[1], P. F. Russi[1], J. M. Simondi[2], G. M. Bonetto[2], C. Nasser Marzo[2], J. A. Di Rienzo[3], and A. R. Castillo[4], *[1]Rusitec S.A., Buenos Aires, Argentina, [2]INTA, EEA Manfredi, Cordoba, Argentina, [3]University of Cordoba, School of Agriculture, Cordoba, Argentina, [4]University of California, Cooperative Extension, Merced, CA.*

The objective of this trial was to feed a prototype rumen protected carbohydrate supplement to fresh lactation cows to determine if a patent pending manufacturing product is effective in protecting simple carbohydrates against ruminal degradation. Twenty 7 cows were group fed the same basal diet from −21 d of expecting calving date to parturition. From calving to 28 DIM cows were assigned to 3 treatments in a randomized complete block design and fed a diet of (% DM): 31.4% corn silage, 19.4% alfalfa hay, 22.8% corn grain, 7.4% soybean seeds, 4% extruded soybean meal, 4.3% minerals and vitamins; and 10.7% basal supplement (58.9% solvent soybean meal, 37.4% glucose and 3.7% urea). The 3 treatments consisted on replacing 0% (T0), 50% (T1) and 100% (T2) of the basal supplement with the rumen protected carbohydrate prototype feed. The prototype feed had the same ingredients of the basal supplement. Body weight, BCS, and blood samples were taken once a week. Weekly samples of TMR were taken for feed analysis. Milk yield and milk composition per cow was measured 2 times per week on non-consecutive days. Energy corrected milk (ECM) was calculated based on milk fat, protein, and lactose contents and milk yield/cow/d. DMI and ECM were not different for T0, T1 and T2, averaging 19.0, 20.2 and 21.1 Kg/d. and 28.2, 25.7, and 26.6 Mcal/cow/d. Milk fat, 4.08, 4.06, 4.15% and protein 3.36, 3.47, and 3.48% were similar among T0, T1 and T2. Milk lactose (%) was higher for T1 (4.96) and T2 (4.88), compared with T0 (4.70). Milk ketone bodies were not different averaging 0.73, 0.36 and 0.57 mg/dl for T0, T1 and T2. Blood glucose (mg/dl) was higher for T1 (45.3) and T2 (42.5) vs. T0 (38.8). Body weight loss (kg) during wk 3 was higher for cows in T0 (20.5) compared with T1 (7.3) and T2 (5.7). Based on milk lactose content, blood glucose, and body weight changes, it was concluded that the rumen protected carbohydrate supplement prototype was effectively protected against rumen microbial degradation

Key words: rumen protected carbohydrate, fresh cows′ performance

W320 Effects of balancing for methionine and lysine in a lactation diet containing high concentrations of wet corn gluten feed. C. R. Mullins*[1], D. Weber[2], E. Block[2], J. F. Smith[1], M. J. Brouk[1], and B. J. Bradford[1], *[1]Kansas State University, Manhattan, [2]Arm & Hammer Animal Nutrition, Princeton, NJ.*

Primiparous (n = 33) and multiparous (n = 63) lactating Holstein cows (186 ± 51 DIM) were used to evaluate the effects of balancing for metabolizable amino acids using lysine in a matrix of Ca salts of fatty acids (Megamine-L, Arm & Hammer Animal Nutrition) and the isopropyl ester of 2-hydroxy-4-methylthio butanoic acid (HMBi; MetaSmart, Adisseo Inc.) in diets with high concentrations of wet corn gluten feed. Cows were blocked by production, parity, and pregnancy status, then randomly assigned to 1 of 8 pens and allowed a 7 d adaption period before receiving treatments. The study consisted of 2 28-d treatment phases, in which DMI and production were monitored daily and milk components analyzed 3 d/wk. Phase (P) 1 and 2 data were analyzed separately using mixed models with repeated measures. During P1, pens were offered 1 of 2 rations formulated to differ by amino acid content. The control diet had CPM-predicted values of 181 g/d of metabolizable lysine (6.05% of metabolizable protein [MP]) and 63 g/d of metabolizable methionine supply (2.11% of MP). The treatment diet was similar, with replacement of 190 g/cow per d of Ca salts of fatty acids (Megalac-R, Arm & Hammer Animal Nutrition) with the lysine product, and the addition of 14 g/cow per d of the HMBi product. This yielded CPM-predicted values of 197 g/d of metabolizable lysine (6.58% of MP) and 66 g/d of metabolizable methionine supply (2.20% of MP). No treatment effects were observed for any parameters in P1. For P2, cows remained in the same pens and dietary treatment groups; however, the treatment diet was modified to replace some wet corn gluten feed with corn silage, decrease dietary CP from 17.9% to 17.1% by removing expeller soybean meal, and further increase lysine and methionine supply. The resulting treatment diet had CPM-predicted values of 196 g/d of metabolizable lysine (7.10% of MP) and 69 g/d of metabolizable methionine supply (2.49% of MP). In P2, MUN was decreased in the treated group (10.8 vs. 12.5 ± 0.2 mg/dL, $P < 0.001$) without affecting milk production ($P = 0.51$). No differences were observed in any of the other parameters measured.

Key words: amino acid, dairy, by-product

W321 Effects of subacute ruminal acidosis (SARA) challenges on bacteria in the digestive tract of dairy cows. S. Li*, J. C. Plaizier, E. Khafipour, and D. O. Krause, *University of Manitoba, Winnipeg, MB, Canada.*

Effects of SARA challenges on bacterial populations in the rumen and cecum were determined in 6 nonlactating Holstein dairy cows with cannula in the rumen and in the cecum. A replicated 3 × 3 Latin square was used. During the first 3 wk of the 4 wk experimental periods, cows received a control diet containing 70% forage (DM basis). During wk 4, cows received one of the 3 diets: the control diet, a grain-based SARA challenge (GBSC) diet containing 64% concentrate including 34% wheat-barley pellets, or an alfalfa-pellet SARA challenge (APSC) diet with 56% of forage including 37% alfalfa pellets. Digesta samples were taken at 6 h after feed delivery in wk 4. The starch content in cecal digesta was 2.8, 2.6, and 7.4% of DM for the control, APSC, and GPSC treatments, respectively. Relative qPCR quantification was used to determine the relative changes of bacterial groups during SARA challenges compared with control. Both GBSC and APSC increased *P. bryantii* and *S. ruminantium*, but decreased *S. bovis* in the rumen. Only GBSC increased *M. elsdenii* in the rumen. *E. coli* was undetectable in the rumen. In the cecum, both GBSC and APSC increased *P. ruminicola*, whereas only GBSC increased lactobacillus and *E. coli*, and decreased *S. bovis*. Across treatments, all selected bacteria groups, with the exception of *M. elsdenii*, *S. bovis* and lactobacillus were higher in the rumen than in the cecum. Results indicate that the balance between lactate producers and lactate utilizers and increased *E. coli* numbers in the hindgut may play a role in the inflammatory response commonly associated with grain-based SARA.

Table 1. Relative change (log2) to control

	Rumen		Cecum	
	GBSC	APSC	GBSC	APSC
Prevotella bryantii	2.8*	1.6*	1.0	0.7
Prevotella ruminicola	0.2	−0.2	1.8*	1.9*
Ruminobacter amylophilus	1.8[a]	−0.8[b]	−0.1	2.5
Fibrobacter succinogenes	−0.02	1.0	2.0	2.2
Selenomonas ruminantium	2.5*	1.9*	0.1	0.8
Lactobacillus	0.7	0.2	2.1 *[b]	−0.2[a]
Streptococcus bovis	−2.2*	−1.3*	−1.5 *[a]	0.03[b]
Megasphaera elsdenii	3.1*	1.7	1.9	0.2
Escherichia coli	nd	nd	2.1*	1.6

Nd= not detected; [a,b]means within site differ ($P < 0.05$);*significant change ($P < 0.05$).

Key words: SARA, bacteria, digestive tract

W322 Interactions between mild protein imbalance and taste preference in young ruminants. A. Bach*[1], J. J. Villalba[2], and I. R. Ipharraguerre[3], *[1]ICREA and Ruminant Production-IRTA, Barcelona, Spain, [2]Utah State University, Logan, [3]Lucta, S.A., Barcelona, Spain.*

Thirty-two crossbred lambs (BW = 31.2 ± 4.7 kg) distributed in individual pens were used to determine whether an imbalanced protein supply would alter preferences for feeds containing flavors designed to elicit either umami (U) or a mix (33.3:33.3:33.3%) of umami, sweet, and bitter (M) taste. Lambs were randomly allocated to either a low (LP; 10.9% CP) or a high (HP; 20.4% CP) protein diet for 21 d. Afterward, lambs were presented during 21 d with a choice of the same LP or HP diet unflavored (LPC or HPC) or flavored either with U (LPU or HPU) or M (LPM or HPM) at 0.1% as fed in a 2× 2 factorial design with 8 replicates per treatment. Diets were offered ad libitum and intake was recorded daily. Blood samples were drawn on d 14 to assess blood urea N (BUN). Data were analyzed using a mixed-effects model for repeated measures accounting for random effect of animal within treatment and the fixed effects of treatment, time, and their interaction. During the first 21 d of study, feeding LP decreased ($P < 0.05$) DMI, ADG, and feed efficiency compared with HP. The restricted intake of CP caused by LP was further evidenced by the lesser ($P < 0.001$) BUN concentrations in LP lambs (7.63 ± 1.07 mg/dl) compared with HP lambs (18.81 ± 1.07 mg/dl). When offered a choice, all lambs showed a preference for the unflavored diet except for LP lambs which clearly ($P < 0.001$) preferred LPU (72% of total DMI) over LPC. However, preference for LPU progressively decreased ($P < 0.05$) as time of exposure to the choice increased. In summary, protein-restricted lambs were able to differentiate the umami-flavored feed and increase preference for and consumption of such feed probably in an attempt to fulfill their protein requirements. However, the increase in preference and consumption of the umami-flavored low-CP diet disappeared over time. This response was most likely a consequence of the overriding effects of metabolic control of intake elicited by the absence of a concomitant dietary supply of protein.

Key words: diet selection, sheep, flavor

W323 Evaluation of RumeNext-D and monensin in early lactation diets for dairy cattle. J. P. McNamara*[1], G. Duncan[1], R. Bose[1], S. Rocco[1], J. Kay[1], P. Doane[2], and K. L. Perfield[3], *[1]Washington State University, Pullman, [2]ADM Research, Des Moines, IA, [3]Elanco Animal Health, Indianapolis, IN.*

The plant botanicals eugenol and cinnamaldehyde (RumeNext-D), as well as the ionophore monensin, have been shown to positively affect performance of early lactation dairy cows. To test the effects of RumeNext-D (RND), monensin (MON) and the combination of the 2 (BOTH), on lactation performance of dairy cattle in early lactation as well as the relationship of productive responses and body compositional changes to estimate overall efficiency we used randomized complete block with parity (1 and 2) and genetic merit as blocks, with treatments (n = 15): 1) Control (CTL), 2) RND, 3) MON and, 4)BOTH. Alfalfa and triticale silage based diets with a corn, barley, peas and SBM based grain mix began at 21 DIM and continued to 111 DIM (d 13 through d 20 postpartum were used as a covariate). Monensin was mixed in the TMR at 14 g/ton (targeted 400 mg/d) and RND was included at 600 mg/d into the grain mix of the TMR. There was an effect of parity such that feed intake, milk yield and BW were all greater in 2nd parity animals. For most variables, there was a random effect of the covariate period. Dry matter intake (DMI) was 20.5, 21.0, 22.1 and 20.9 (SEM = 0.4) for the 4 treatments, respectively, 1.5 kg/d greater for the MON group versus CTL and 0.4 kg/d greater than control for RND or BOTH fed groups. However, with the covariate included, there was no significant effect of treatment on DMI. Milk yields were 34.2, 34.2, 36.5 and 34.9 kg/d (SEM = 1.1 kg/d) for the 4 treatments, respectively. Monensin increased ($P < 0.04$) milk yield 2.3 kg/d over the 3 mo experimental period and MON significantly ($P < 0.01$) increased milk protein yield by 0.15 kg/d over the CTL group. There was no effect of any treatment on milk fat or milk protein content or milk fat yield. Rumen pH (22 h after feeding) was approximately 6.2 and declined slightly as lactation progressed, there were no differences among treatments. Body weight and BCS did not change among treatments Monensin increased milk yield and milk protein yield, as previously demonstrated, however there did not appear to be an effect of the plant botanicals eugenol and cinnamaldehyde.

Key words: efficiency, monensin, plant botanicals

W324 Comparing a 40-d dry period with a single close-up diet with a 60-d dry period with far-off and close-up diets on glucose, lactate, and calcium in the blood plasma of dairy cows. H. Khazanehei*, S. Li, D. O. Krause, M. L. Connor, L. Lippins, and J. C. Plaizier, *University of Manitoba, Winnipeg, MB, Canada.*

Effects of a 40-d dry period with a single close-up diet (40-d) with a 60-d dry period with far-off and close-up diets (60-d) on glucose, lactate, and calcium in blood plasma were compared. Twenty-six multiparous Holstein cows were paired based on the expected calving date and within pairs randomly assigned to 1 of 2 treatments. The 60-d dry period was divided into a 39-d far-off period and a 21-d close-up period. The far-off diet contained (DM basis) 1.29 Mcal/kg NEL, 12.0% CP, 38.7% NDF, and 0.79% Ca. The close-up diet contained 1.43 Mcal/kg NEL, 14.7% CP, 34.0% NDF, and 0.78% Ca. After calving, all cows received a diet containing 1.71 Mcal/kg, 17.6% CP, 29.7% NDF, and 0.97% Ca. Blood samples were taken weekly from wk 3 prepartum to wk 9 postpartum. Blood plasma was analyzed for glucose, lactate, and Ca. Data were analyzed as repeated measures under a randomized block design using the MIXED procedure of SAS. Cows on the 40-d treatment had higher blood glucose at 3 wk before calving, and at 1 wk and 5 wk after calving. Cows on the 40-d treatment also had higher blood lactate at 1 wk after calving and higher blood calcium at 3 wk before and 2 wk after calving. The treatment differences at 3 wk before calving may be explained by the switch in diet that cows on the 60-d treatment, but not cows on the 40 d treatment made at that time. Treatment differences at wk 1 and 2 may have been due to the lower milk yields of the cows on the 40-d treatment.

Table 1. Concentrations of glucose, lactate, and calcium in the blood of dairy cows

Relative to Calving	Glucose (mg/dL)			Lactate (mmol/L)			Calcium (mmol/L)		
Week	40-d	60-d	*P*-value	40-d	60-d	*P*-value	40-d	60-d	*P*-value
−3	86	71	0.03	2.51	2.06	0.28	1.06	0.97	0.04
−2	87	79	0.19	1.62	1.29	0.17	1.06	1.03	0.42
−1	82	80	0.76	1.55	1.38	0.7	1.04	1.03	0.63
1	77	59	<0.01	2.38	0.92	<0.01	1.07	1.02	0.12
2	71	65	0.17	1.13	1.18	0.54	1.12	1.05	0.04
3	73	66	0.21	1.82	1.25	0.41	1.08	1.05	0.33
5	77	67	0.05	1.29	1.35	0.73	1.07	1.06	0.72
7	74	72	0.71	1.05	1.00	0.73	1.03	1.05	0.66
9	74	73	0.71	1.85	1.23	0.36	1.06	1.08	0.79

Key words: dry period, nutrition, dairy cows

W325 A meta-analysis on the effects of supplementing exogenous fibrolytic enzyme products in dairy diets on productive performance in early lactation. J.-S. Eun*[1], C. M. Williams[2], and A. J. Young[1], *[1]Department of Animal, Dairy, and Veterinary Sciences, Utah State University, Logan, [2]Department of Soil and Crop Sciences, Colorado State University, Fort Collins.*

There have been several studies to examine the effects of exogenous fibrolytic enzyme (EFE) products on milk production of dairy cows. When viewed across all studies the variability in response is high, as a range of different enzyme products and experimental conditions were used. Thus, we performed a meta-analysis to assess production responses when EFE were supplemented in early lactation dairy diets. Supplementing EFE is likely to be more beneficial to early lactating cows than mid- to late lactating cows. Therefore, a database was developed from 10 studies recently published in the J. Dairy Sci. using early lactating dairy cows. In addition, the best responding treatment was chosen if an individual study tested various enzyme treatments, because efficacy of EFE depends on rate of dose, method of providing enzymes, and diet composition. A mixed model regression analysis with random study effect was used to evaluate relationships between supplementation of EFE and lactational performance parameters. Supplementing EFE increased DMI ($P = 0.05$), milk yield ($P < 0.01$), and ECM yield ($P = 0.04$) by 0.5 (2.2% increase), 2.3 (6.6% increase), and 1.7 kg (4.7% increase) units, respectively, but did not affect milk fat ($P = 0.27$) and protein ($P = 0.82$) concentrations. While milk fat yield was not affected by EFE supplementation, milk protein yield increased by 0.06 kg unit (5.5% increase; $P = 0.02$). Milk production efficiency (milk yield/DMI) was improved by 0.07 units (4.6% increase; $P = 0.01$). Although the meta-analysis data set only included 10 studies, it is evident from the positive animal responses that EFE additives can be an effective means to improve productive performance of early lactating dairy cows. A better understanding of the factors affecting animal response to EFE supplementation will help ensure cost-effective use of these additives on-farm.

Key words: early lactating dairy cows, exogenous fibrolytic enzymes, meta-analysis

W326 Evaluation of dietary fat from dried distillers grains in the diet Holstein heifers on growth and dry matter intake. J. L. Anderson*, K. F. Kalscheur, A. R. Hippen, and D. J. Schingoethe, *South Dakota State University, Brookings.*

The objective of this study was to determine how increased dietary fat from dried distillers grains with solubles (DDGS) in diets of growing heifers affects DMI, ADG, and growth. Thirty-three Holstein heifers (133 ± 18 d old) were used in a 24-wk randomized complete block design. Treatments were: 1) control (C) containing ground corn (15.9% of DM) and soybean products (17.9%), 2) low-fat (LF) containing low-fat, high-protein DDGS (21.9%) and ground corn (11.9%), and 3) high-fat (HF) with traditional DDGS (33.8%). All diets contained 39.8% grass hay, 24.8% corn silage, and 1.5% vitamins and minerals. Diets were formulated for 16.3% CP (DM basis) 9.8% RDP and 6.5% RUP. The HF diet contained 4.8% fat compared with 2.8% in the C and LF diets, which were greater in NFC. Diets were 1.0 Mcal/kg of DM and limit-fed at 2.45% of BW. Heifers were weighed every 2 wk and rations adjusted accordingly. Every 2 wk, heart girth, hip height, wither height, body length, and BCS were recorded. No treatment × time interactions were found. Dry matter intakes were similar, averaging 7.01, 7.01 and 6.89 kg/d (SEM = 0.26) for C, LF, and HF, respectively. Body weights were similar among treatments (248.4, 243.9, 244.2 kg, SEM = 8.06), as were ADG (0.92, 0.90, 0.91 kg/d, SEM = 0.07). Heart girth was similar among treatments (137.7, 138.2, 144.7 cm, SEM = 3.51). Hip height was less ($P < 0.01$) for heifers fed HF (118.3 cm) compared with those fed C (119.7) and LF (119.3, SEM = 1.18). Wither height was greater ($P = 0.02$) for heifers fed LF (115.3 cm) compared with HF (114.4), and tended ($P = 0.09$) to be greater compared with heifers fed C (114.6), but C and HF were similar (SEM = 1.01). Body length was longest ($P < 0.01$) for heifers fed C (105.0 cm), shortest for HF (102.6), with LF (103.7) in between (SEM = 1.47). Overall BCS were similar for heifers fed C and LF (3.05), but greater ($P = 0.04$) for HF (3.09, SEM = 0.02). Despite similar BW, ADG, and DMI, feeding diets with additional fat from including DDGS compared with diets with low-fat DDGS or corn and soybean products to growing heifers may result in slightly greater BCS and slightly smaller body frame sizes.

Key words: distillers grains, heifers

W327 Bee pollen and its polysaccharides, the new feed additives in milk replacer of preruminant calves. Y. Tu*, G.-F. Zhang, N.-F. Zhang, C.-G. Jiang, and Q.-Y. Diao, *Key Laboratory of Feed Biotechnology of Ministry of Agriculture/Feed Research Institute, Chinese Academy of Agricultural Sciences, Beijing, P.R. China.*

The experiment investigated the influence of lotus bee pollen and polysaccharides extracted from lotus bee pollen on growth performance and nutrient digestibility in preruminant calves. Twenty-five neonatal Chinese Holstein female calves were randomly allotted to 5 groups, and each group was offered a milk replacer (MR) supplemented with 0 (control, C), 10 (10BP), 25 (25BP) or 50 g (50BP) lotus bee pollen/kg MR, or 5 g (5PS) polysaccharides/kg MR for 63 d. The MR, containing 20.41 MJ digestible energy/kg, 26.16% crude protein (CP) and 15.62% ether extract (EE), was fed at 11.0% of live weight of the calves, and a starter ration was offered ad libitum from 28 d thereafter. Average daily gain (ADG), average daily feed intake (ADFI) and feed/gain ratio (F/G) were measured fortnightly. A 3-d digestion trial by total collection of feed refusals, feces, and urine was conducted from 26 to 28 d and from 47 to 49 d, respectively. The apparent digestibility of dry matter (DM), CP, EE, Ca and total P was calculated. Data were analyzed by GLM procedure of SAS® software. The results showed that, compared with group C, ADG was significantly higher in the calves from group 25BP or group 5PS (656.6 vs 808.7 or 797.5 g/d, $P < 0.05$); F/G was decreased by 12.85% in the calves from group 25BP (1.79 vs 1.56, $P < 0.05$); there was no significant differences in ADFI among the groups. The apparent digestibility of DM during 26 to 28 d was increased by 8.38% and 7.66% respectively in the calves from groups 25BP and 5PS (79.02% vs 85.64% and 85.07%, $P < 0.05$); the apparent digestibility of CP was increased by 18.63% in the calves from group 25BP (66.35% vs 78.71%, $P < 0.05$). No differences in the apparent digestibility of the nutrients were detected among the groups during 47 to 49 d ($P > 0.05$). In conclusion, supplementation of bee pollen or its polysaccharides at 25 or 5 g/kg MR, respectively, improved ADG, F/G and apparent digestibility of DM and CP in preruminant calves.

Key words: bee pollen, calves, growth and apparent digestibility

W328 Effect of lipopolysaccharides on immune parameters and nitrogen metabolism in preruminant calves. N.-F. Zhang, H. Li, Y. Tu*, C.-G. Jiang, and Q.-Y. Diao, *Feed Research Institute, Chinese Academy of Agricultural Sciences, Beijing, P.R. China.*

This study investigated the effect of immunological stress on immune parameters and nitrogen metabolism in preruminant calves. Forty male Chinese Holstein calves of 24 d old were randomly divided into 2 groups with 20 calves each, and one group was injected intraperitoneally with 2.5 μg *E. coli* lipopolysaccharides (LPS)/kg BW at 24, 26 and 28 d of age, and the other was injected with an equivalent volume of sterile saline. Rectal temperature was measured at 30, 90, 150 and 210 min after injection. A total collection of feces and urine was conducted between 25 and 27 d for analysis of nitrogen metabolism. Plasma samples were collected 60, 120 and 180 min after injection for analysis of urea nitrogen, interleukin-1β (IL-1β), tumor necrosis factor-α (TNF-α), complement C3, interleukin-2 (IL-2) and interleukin-4 (IL-4). The body temperature was elevated significantly 150 and 210 min after the challenge of LPS ($P < 0.05$). The plasma concentration of IL-1β and TNF-α was increased significantly 120 and 180 min after the challenge of LPS ($P < 0.05$), the plasma complement C3 was decreased significantly 120 min after the challenge of LPS ($P < 0.05$), and the plasma IL-2 (Th1 type cytokine) ($P < 0.05$), IL-4 (Th2 type cytokine) and the ratio of IL-2 to IL-4 were increased following the challenge of LPS. The plasma urea nitrogen was increased significantly 120 min postinjection of LPS ($P < 0.05$). The urinary concentration of nitrogen was higher ($P < 0.05$), but the nitrogen retention and apparently biological value of nitrogen were lower in the LPS-challenged calves than control. The results suggested that the immunological stress induced inflammatory responses, activated immune responses, and shifted immune responses from Th2 type to Th1 type, and then suppressed the nitrogen retention and decreased the utilization efficiency of nitrogen in the calves.

Key words: immunological stress, nitrogen metabolism, calves

W329 Partially replacing barley grain with wheat factory sewage in the dairy cow diets did not affect digestion and milk production. M. Khorvash[1], S. Kargar[1], G. R. Ghorbani[1], M. Borou-

mand-Jari[2], A. Ghaempour[1], and W. Z. Yang*[3], *[1]Isfahan University of Technology, Isfahan, Iran, [2]Jahad-Agriculture Institute of Scientific-Applied Higher Education, Isfahan, Iran, [3]Agriculture and Agri-Food Canada, Research Centre, Lethbridge, Alberta, Canada.*

The objective of this study was to evaluate whether wheat factory sewage (WFS) could partially replace barley grain in the diet of dairy cows without adversely affecting DMI, rumen fermentation, digestibility, and milk production of dairy cows. Eight multiparous (60 ± 3 DIM) Holstein cows were used in a replicated 4 × 4 Latin square designed experiment with 4 21-d periods. The basal diet was formulated with 22% corn silage, 22% alfalfa hay and 56% barley grain-based concentrate (DM basis); barley grain was partially replaced with 0% WFS (WFS0), 4% (WFS26), 6% (WFS39) or 8% WFS (WFS52). Data were analyzed using the MIXED model procedure of SAS to account for diet as fixed effect and square, cows within square and period within square as random effect. DM content of diets linearly ($P < 0.01$) decreased from 65, 59, and 57 to 54% with increasing the inclusion of WFS due to high water content of WFS (80%). DMI was quadratically changed ($P < 0.04$) to be higher for WFS26 (23 kg/d) than for other 3 diets which were similar (21 kg/d). Rumen total VFA (100 to 103 mM), molar proportion of acetate (65 to 67%), propionate (24 to 25%), and ratio of acetate to propionate (2.68 to 2.89) were not affected with increasing the replacement of barley grain by WFS. Apparent total-tract digestibilities of DM (67%), CP (68%) and NDF (54%) were not different among treatments. Milk yield (averaged 40 kg/d) and milk composition were not affected by the diets. Results showed that partially replacing 26, 39 and 52% of barley grain with WFS in dairy cow diets decreased DM content but had no adverse effects on DMI, rumen fermentation, digestibility, and milk production responses. It suggests that WFS can be used as alternative to grain to feed dairy cattle.

Key words: barley grain, wheat factory sewage, dairy cow

W330 Effects of dietary crude protein level on eating pattern and performance of Holstein calves. G. Araujo[1], M. Devant[1], A. Mereu[2,1], I. Ipharraguerre[2], and A. Bach*[3,1], *[1]Deparment of Ruminant Production, Institut de Recerca i Tecnologia Agroalimentàries (IRTA), Barcelona, Spain, [2]Lucta, S.A., Barcelona, Spain, [3]Institució Catalana de Recerca i Estudis Avançats (ICREA), Barcelona, Spain.*

The objective of this study was to evaluate changes in eating pattern and performance of calves fed 2 isoenergetic concentrates differing in CP concentration. Seventy 5 male Holstein calves (initial BW 246 ± 29 kg and 211 ± 24 d of age) were housed in 4 homogenized groups of 18 to 20 animals each according to ages and weights. One dietary treatment consisted on a concentrate containing 18% CP on DM basis (HP) and the other contained 16% CP on a DM basis (LP). In addition to concentrates, calves had ad libitum access to barley straw on a separate feeder. Animals were weighed on d 0, 14, and 28 of study and individual concentrate intake was monitored daily using an electronic feeding system. Data were analyzed with a mixed-effects model with pen as a random effect and treatment and day as fixed effects, with time entering the model as a repeated measure. Calves receiving HP spent more ($P < 0.05$) time eating concentrate (42 ± 0.7 min/d) than those receiving LP (38 ± 0.7 min/d). However, the number of meals per day was similar for both treatments (9.0 meals/d for HP and 9.3 meals/d for LP) and average meal interval of HP calves (168.1 ± 2.8 min) was longer ($P < 0.01$) than that of LP (161.5 ± 2.8 min). This was mainly due to the greater ($P < 0.001$) meal length observed with HP (5.3 ± 0.1 min/meal) than with LP calves (4.5 ± 0.1 min/meal). Meal size was also greater ($P < 0.001$) in HP (845.4 ± 19.2 g/meal) than in LP (790 ± 19 g/meal) calves. Furthermore, eating rate of HP calves (163 ± 4 g/min) was slower ($P < 0.001$) compared with calves consuming the LP concentrate (185 ± 4 g/min). Although concentrate intake did not differ between both treatments (6.7 kg/d), HP calves tended ($P = 0.05$) to grow more (1.67 ± 0.02 kg/d) than LP (1.56 ± 0.02 kg/d) calves, and as a consequence HP calves were numerically ($P = 0.35$) more efficient (26.6 ± 0.9%) than LP calves (24.9 ± 0.9%) converting consumed nutrients into gain. In conclusion, concentrates containing 18% CP tend to result in improved ADG compared with 16% CP levels due to increased CP supply and changes in eating pattern, mainly increased meal size and length and decreased eating rate, but not due to changes in DMI.

Key words: feeding behavior, intake regulation, efficiency

W331 Feeding distiller′s grains as an energy source to gestating and lactating heifers: Impact on calving and pre-weaning progeny performance. P. J. Gunn*[1], J. P. Schoonmaker[1], R. P. Lemenager[1], and G. A. Bridges[2], *[1]Purdue University, West Lafayette, IN, [2]University of Minnesota, Grand Rapids*.

Angus-cross beef heifers pregnant to a single sire (n = 80; BCS = 5.1 ± 0.03; BW = 518 ± 6 kg) were used to determine the effects of feeding dried distiller′s grains with solubles (DDGS) as an energy source during the late gestation and early lactation on calving parameters and offspring growth through weaning. At 192 d in gestation, heifers were allotted by BW within BCS to receive either a control diet of corn silage and haylage (CON; 10% CP prepartum; 11.8% CP postpartum) or corn residue and DDGS, where DDGS were fed at 1.2% of BW per d (DG; 15.7% CP). Diets were formulated to be isocaloric (1.0 Mcal/kg NEg). Dietary treatments concluded and cattle were commingled 30 d after timed-AI (118 ± 0.1 d postpartum; DPP). Heifer BW and BCS (1–9) were assessed every 28 d. Calving score (1 = no assistance; 5 = C-section) and calf vigor at birth (1 = nursed on own; 4 = died after birth) was evaluated. Calf weights were taken at birth and at weaning (191 ± 0.6 d of age). Milk production was assessed via weigh-suckle-weigh procedure at 66 ± 0.6 DPP. Heifer BW never differed between treatments ($P \geq 0.33$), but BCS was greater before calving (5.8 vs. 5.3; $P < 0.01$) and at conclusion of dietary treatments (5.6 vs. 5.4; $P < 0.01$) for CON than DG heifers, respectively. Gestation length was greater ($P = 0.03$) for DG (278 ± 0.7 d) than CON (276 ± 0.6 d) heifers. Sex ratio and vigor of calves did not differ ($P \geq 0.69$). Birth weight (36.7 ± 0.7 vs. 32.5 ± 0.7 kg) and rate of dystocia (59 vs. 24%) was greater ($P < 0.01$) in DG than CON progeny, respectively. Although dam milk production did not differ between treatments ($P = 0.86$), weaning weight was greater ($P = 0.05$) for DG progeny (244 ± 3.6 kg) than CON (234 ± 3.7 kg). In summary, feeding DDGS at 1.2% of BW per d to gestating heifers resulted in greater birth weights, dystocia rates and weaning weights of the DG progeny without altering milk production, suggesting this dietary strategy induced developmental programming changes that increased progeny pre-weaning performance.

Key words: beef heifers, DDGS, developmental programming

W332 Feeding distillers grains as an energy source to gestating and lactating heifers: Impact on milk production, composition, and fatty acid profile. P. J. Gunn*[1], J. P. Schoonmaker[1], R. P. Lemenager[1], and G. A. Bridges[2], *[1]Purdue University, West Lafayette, IN, [2]University of Minnesota, Grand Rapids.*

Angus-cross beef heifers pregnant to a single sire (n = 80; BCS = 5.1 ± 0.03; BW = 518 ± 6 kg) were used to determine the effects of feeding dried distillers grains with solubles (DDGS) as an energy source during late gestation and early lactation on milk production, composition, and fatty acid profile. At 192 d in gestation, heifers were allotted by BW within BCS to receive either a control diet of corn silage and haylage (CON; 10% CP prepartum; 11.8% CP postpartum) or corn residue and DDGS, where DDGS were fed at 1.2% of BW per d (DG; 15.7% CP). Diets were formulated to be isocaloric (1.0 Mcal/kg NEg). Dietary treatments concluded and cattle were commingled 30 d after timed-AI (118 ± 0.1 d postpartum; DPP). BW and BCS were assessed every 28 d during treatment and did not differ during milk data collection. At 65 ± 0.6 DPP, milk samples were collected to determine composition and fatty acid profile. The following day, milk production was assessed via 24 h weigh-suckle-weigh. Total milk production (8.8 ± 0.4 kg/d), milk protein, and lactose content did not differ ($P \geq 0.38$). However, milk fat (223 ± 15 vs. 121 ± 14 g/d), total solids (1084 ± 44 vs. 951 ± 40 g/d), and energy corrected milk production (7.8 ± 0.4 vs. 6.5 ± 0.3 kg/d) was greater ($P \leq 0.03$) in CON than DG, respectively. Milk urea N (MUN) was greater in DG (16.4 ± 0.5 mg/dL) than CON (7.1 ± 0.6 mg/dL; $P < 0.01$). Short- (3.7 ± 0.2 vs. 2.3 ± 0.2 g/100 g) and medium-chain fatty acids, (17.3 ± 0.4 vs. 10.1 ± 0.4 g/100 g) and SFA (64.3 ± 1.1 vs. 47.5 ± 0.9 g/100 g) content was greater ($P < 0.01$) in CON than DG, respectively. In contrast, long chain fatty acids (87.7 ± 0.5 vs. 79.0 ± 0.6 g/100 g), MUFA (44.7 ± 0.9 vs. 32.0 ± 1.0 g/100 g), PUFA (7.8 ± 0.2 vs. 3.6 ± 0.2 g/100 g), and CLA (3.4 ± 0.1 vs. 0.9 ± 0.1 g/100 g) content was greater ($P < 0.01$) in DG than CON, respectively. In summary, feeding DDGS at 1.2% of BW per d to first-parity heifers resulted in decreased milk fat, milk solids, and energy corrected milk production, but greater MUN, long chain fatty acids, CLA, MUFA, and PUFA in the milk produced.

Key words: beef heifer, DDGS, milk

W333 Effect of extruded flax products on dairy cow milk and steer tissue fatty acid composition. D. A. Christensen*, P. Yu, J. J. McKinnon, and A. Foth, *University of Saskatchewan, Saskatoon, SK, Canada.*

Several benefits have been attributed to omega-3 content of milk and ruminant products. The objective of this research was to determine the effect of extruded flax products on fatty acid content of milk, organs and meat. To determine effect on milk 6 early lactation Holstein cows were fed a barley silage, alfalfa hay, barley grain, canola meal, SBM based ration for 28 d, then 5.8% of DM of an extruded product (Oleet Processing, Regina SK) replacing concentrate for 28 d followed by a second control period of 28 d. The extruded product contained 54% flax, 38% pea grain, 8% alfalfa meal, vitamin E and ethoxyquin. Extrusion temperature was 143°C. Six large frame crossbred steers were fed a similar product as 18% of ration DM which contained 36% flax seed and 20% canola seed for 70 d before slaughter. Three additional steers were fed a control barley grain, barley silage finishing ration. Milk yield in the test feeding period averaged 46.6 kg and 3.36% fat. Milk C18:3n3 (ALA) increased from 0.49% of fatty acid methyl esters (FAME) to 0.83% ($P < 0.01$) in the test period and declined to 0.46 in the second control period. C18:2 c9-t11 (CLA) increased from 0.30 to 0.60 ($P = 0.07$) then declined to 0.32% of FAME in the second control period. EPA, DPA and DHA were 0.07% of FAME or less. Total milk omega-3 fatty acids increased from 0.59 to 1.04% then declined to 0.60% of FAME 28 d after the extruded product was withdrawn. In steer liver ALA increased from 0.71% to 2.28% ($P < 0.01$). Liver EPA increased from 0.71 to 1.61% of FAME ($P = 0.03$). The increase in DHA from 1.74 to 2.04% of FAME was not significant ($P = 0.29$). Total liver omega-3 increased from 7.36 to 12.9% of FAME. Ribeye (L. dorsi) ALA increased from 0.25% to 0.78% of FAME ($P < 0.01$) with no other significant effects. Fatty acids in loin, shoulder and chuck meat samples showed a similar pattern to ribeye with the main effect being an increase in ALA. Substantial extruded product effects on ALA content of liver, milk, and meat samples were observed.

Key words: milk, meat and organ, fatty acids

W334 Grain source and alfalfa hay particle size effects on fecal fermentability and particle size in midlactation Holsteins. A. Nikkhah*[1], S. M. Nasrollahi[2], M. Khorvash[2], and G. R. Ghorbani[2], *[1]University of Zanjan, Zanjan, Iran, [2]Isfahan University of Technology, Isfahan, Iran.*

The objective was to determine independent and interactive effects of alfalfa hay particle size and grain source on fecal fermentability and particle size. Eight Holstein cows (175 d in milk) in a replicated 4 × 4 Latin square design with four 21-d periods were fed 4 diets with either finer (FA) or coarser (CA) chopped alfalfa hay, with either ground barley (GB) or a 50:50 ratio of ground barley and corn grains (BC). Diets were offered ad libitum as mixed rations with forage to concentrate ratio of 40:60 (DM based). Geometric mean particle size was 4.33 and 3.43 mm for CA and FA, respectively; and 3.8, 3.6, 3.7, and 3.4 mm for CAGB, FAGB, CABC, and FABC, respectively. Feces were sampled for 5 d directly from rectum before morning feeding. Acid insoluble ash was used as an internal marker to estimate fecal outputs. Wet sieving was utilized to measure feces particle size. Feed and fecal potential fermentability was measured after 48 h of rumen incubation in situ through cannula. Data were analyzed using Mixed Procedures of SAS with linear models consisting of fixed period, grain source, hay particle size, and grain source × hay particle size effects, plus cow and residuals random effects. Feed potential fermentability was similar among CAGB (84.35%), FAGB (84.33%), CABS (84.35%), and FABC (84.46%). However, fecal fermentability was greater for BC vs. GB (67.8 vs. 64.4%, $P < 0.01$). Fecal fermentable DM as % of DMI was similar among CAGB (33.9), FAGB (34.1), CABC (33.3), and FABC (32.0). Fecal fineness was not significantly different. Rumen pH was higher for CA vs. FA (6.45 vs. 6.27, $P < 0.05$), while similar for GB vs. BC (6.36 vs. 6.37). Data suggest that greater amount of partially digested organic matter escaped the gastrointestinal tract digestion for BC vs. GB, that agrees with greater DMI for BC vs. GB (25.6 vs. 24.3 kg/d, $P < 0.05$). Hay particle size and grain source interactions did not affect fecal properties. Results suggest that dietary grain source and not hay particle size can affect fecal fermentability in midlactation dairy cows.

Key words: fecal fermentability, grain source, alfalfa hay

W335 Textured versus ground starter effects on Holstein calves chewing behavior. A. Nikkhah*[1], S. M. Nasrollahi[2], B. Raad[2], S. Khorsandi[2], M. Forootan[2], and S. P. Emami Panaah[2], *[1]University of Zanjan, Zanjan, Iran, [2]Foeka Agriculture and Dairy Corporation, Isfahan, Iran.*

The objective was to determine effect of calf starter physical form on chewing activity. Thirty-two Holstein calves (16 males and 16 females, 41 ± 2.8 kg body weight) were offered from 4-d of age until weaning an either textured (T) (with steam flaked grains plus peletted non-grains) or fully ground (G) starter feed. Each treatment had 8 male and 8 female calves. Feed composition and calf management were

exactly the same for both groups. On d-60 of age, eating, ruminating and resting times were recorded visually every 5 min. Each activity was assumed to persist for the entire 5-min if occurred. Accordingly, meal size and eating rate per kg of dry mater intake and per minute of eating were calculated. Data were analyzed using Mixed Procedures of SAS as linear completely randomized models with fixed effect of starter physical form, and random effects of calf within treatment plus residuals. Daily starter intake (1.67 vs. 1.55 kg), duration of eating (126.7 vs. 117.0 min/d), ruminating (325.3 vs. 324.6 min/d), and resting (981.5 vs. 991.8 min/d), and per kg starter intake of eating (76.5 vs. 74.3 min) and ruminating (199 vs. 186 min) activities were not significantly different between T and G, respectively. Daily number of eating (24.3 vs. 24.4) and ruminating (15.3 vs. 13.7) bouts, mean eating bout size (68 vs. 64 g), and average bout length of eating (5.5 vs. 5.2 min) and ruminating (21.8 vs. 23.6 min) were also similar for T vs. G, respectively. In summary, results suggest that whether starter is textured or finely ground may not affect young calf eating and chewing behaviors.

Key words: calf chewing, physical form, starter

W336 Changes in long-chain polyunsaturated fatty acid status of dairy cows during the periparturient period based on erythrocyte-membrane fatty acids. C. L. Preseault[1], H. M. Dann[2], and A. L. Lock*[1], *[1]Michigan State University, East Lansing, [2]William H. Miner Agricultural Research Institute, Chazy, NY.*

This study examined shifts in long-chain polyunsaturated fatty acid (LCPUFA) status of dairy cows during the periparturient period using erythrocyte membrane (EM) FA profiles. It was hypothesized that EM FA could be used to assess LCPUFA changes in dairy cows because they have been used previously in human studies to assess long-term FA status. Two groups of cows (11/treatment) were fed a low-energy, high-straw diet during a 40 d dry period, and then fed either a low-starch (22%) diet, or a high-starch (26%) diet for the first 91 DIM. Blood samples were collected at −14 d before projected calving date (DRY), at 21 DIM (EARLY), and at 90 DIM (MID). Data was analyzed as repeated measures using SAS proc mixed. There was no effect of dietary treatment at any time point on EM FA. Sampling time did not affect EM concentrations of total saturated or cis PUFA (47.6 and 22.6 g/100 g FA, respectively). Total cis MUFA concentration was 26.6, 27.7, and 24.9 g/100 g FA for DRY, EARLY and MID, respectively ($P < 0.05$). The ratio of n-6/n-3 FA was 9.9, 9.1, and 11.2 for DRY, EARLY and MID, respectively ($P < 0.01$). There was a trend for total n-6 FA to be lower in EARLY ($P = 0.08$) whereas total n-3 FA were not different across time. EM concentrations of individual n-6 FA were consistently lower at EARLY, whereas individual n-3 FA were consistently lower at MID compared with the other times. Comparing EARLY to MID, the EM concentration of C18:2 n-6 was 11% lower ($P < 0.1$), C20:2 n-6 31% lower ($P < 0.001$), C20:3 n-6 37% lower ($P < 0.001$), and C22:4 n-6 38% lower ($P < 0.001$). Comparing MID to EARLY, the EM concentration of C18:3 n-3 was 11% lower ($P < 0.05$), and C20:3 n-3 30% lower ($P < 0.05$). Neither C20:5 n-3 nor C22:5 n-3 were different across time; 22:6 n-3 was not detected in cow EM. Total trans C18:1 was 19% higher in EARLY and MID compared with DRY ($P < 0.001$). Results demonstrate potential differences in LCPUFA status of cows during the periparturient period. Whether EM FA profiles provide a robust measure of LCPUFA status and if these changes affect animal production and health remain to be determined.

Key words: erythrocyte membrane, long-chain PUFA, transition cows

W337 A 40-d dry period with a single close-up diet and a 60-d dry period with far-off and close-up diets differ in their effects on lipolysis and liver triacylglycerol. H. Khazanehei*, S. Li, D. O. Krause, M. L. Connor, L. Lippins, and J. C. Plaizier, *University of Manitoba, Winnipeg, MB, Canada.*

Effects of a 40-d dry period with a single close-up diet (40-d) with a 60-d dry period with far-off and close-up diets (60-d) on β-hydroxybutyrate (BHBA) and nonesterified fatty acids (NEFA) in blood plasma and triacylglycerol (TAG) in liver samples were compared. Twenty 6 multiparous Holstein cows were paired based on their expected calving date. Cows within pairs randomly were assigned to 2 treatments. The 60-d dry period was divided into a 39-d far-off period and a 21-d close-up period. The far-off diet contained (DM basis) 1.29 Mcal/kg NEL, 12.0% CP, and 38.7% NDF. The close-up diet contained 1.43 Mcal/kg NEL, 14.7% CP, and 34.0% NDF. After calving, all cows received a diet containing 1.71 Mcal/kg, 17.6% CP, and 29.7% NDF. Blood samples were taken weekly from wk 3 prepartum to wk 9 postpartum, and were analyzed for BHBA and NEFA. Liver biopsies were obtained at wk 3 prepartum, and at wk 1 and wk 4 postpartum, and were analyzed for TAG. For both treatments TAG was low at 3 wk before calving, increased at 1 wk after calving, and remained high at 4 wk after calving. At 1 wk after calving cows on the 40-d treatment had higher TAG than cows on the 60-d treatment. NEFA were higher at 1 wk after calving than at 3 wk before calving. Cows on the 40-d treatment had higher NEFA at 1, 2, and 3 wk after calving than cows on the 60-d treatment. BHBA was not affected by treatments on any week before or after calving. The NEFA results mirrored the TAG results. Results suggest that during the 3 wk after calving, cows on the 40-d treatment had a deeper negative energy balance, which caused more intensive lipolysis and the accumulation of a greater amount of TAG in the liver. Results also suggest moderate fatty liver and high lipolysis in early lactation in cows on both treatments.

Table 1. Concentrations of liver TAG, and NEFA and BHBA in blood plasma

Week relative to calving	TAG (% wet weight)			NEFA (mmol/L)			BHBA (mg/dl)		
	60-d	*P*-value	40-d	60-d	*P*-value	40-d	40-d	60-d	*P*-value
−3	0.3	0.24	0.97	0.10	0.14	0.53	11.4	9.5	0.11
−2	ND	ND		0.18	0.18	0.94	10.6	11.0	0.91
−1	ND	ND		0.35	0.20	0.28	11.7	9.0	0.26
1	10.81	6.46	0.04	0.96	0.53	<0.01	19.0	18.4	0.98
2	ND	ND		0.62	0.29	0.05	20.1	15.8	0.98
3	ND	ND		0.42	0.28	0.05	23.8	16.1	0.45
4	9.36	9.22	0.88	ND	ND		ND	ND	
5	ND	ND		0.23	0.19	0.40	16.7	20.6	0.55
7	ND	ND		0.15	0.20	0.68	13.8	13.8	0.49
9	ND	ND		0.13	0.13	0.95	17.4	12.2	0.10

ND = not determined.

Key words: dry period, lipolysis, dairy cows

W338 Reduced protein for late-lactation dairy cows. A. B. D. Pereira*[1], L. K. Zeringue[1], C. Leonardi[2], M. E. McCormick[1], and V. R. Moreira[1], *[1]Louisiana State University Agricultural Center, Baton Rouge, [2]Louisiana State University - Health Sciences Center, New Orleans.*

Excess protein in dairy cattle diets unnecessarily increases the cost of production and may contribute to environmental pollution. The objective of this experiment was to determine the effect of feeding dairy cows with 2 levels of dietary protein on milk production and manure

characteristics. The experiment was carried out with 24 lactating dairy cows (334 ± 43 DIM and 22.2 ± 3.79 kg milk yield). Cows were randomized to 4 pens in a free-stall barn equipped with Calan gates for individual TMR feeding. Control TMR (HP) was estimated to contain 16.5% CP with soybean meal as the main protein supplement. Treatment TMR (LP; 13.5% CP) was prepared using dry distillers grains plus solubles (DDGS) and rumen protected Lys (AminoShure-L, Balchem) and Met (Metasmart, Adisseo) to offset AA deficiencies in the diet. Rations contained nearly 55% forage as corn silage and Bermudagrass hay. Manure (feces and urine) samples were collected for the last 3 d of each sampling period, twice daily while cows were milked. The experiment was analyzed as a crossover design using the MIXED procedure of SAS with pen as the experimental unit. No significant difference was observed between treatments in DMI (21.0 kg/cow/d for HP and 20.4 kg/cow/d for LP; $P = 0.46$), milk yield (20.7 kg/cow/d for HP and 20.5 kg/cow/d for LP; $P = 0.91$), body weight gain (38.2 kg/cow/period for HP and 37.2 kg/cow/period for LP; $P = 0.91$) and body condition score (0.14 units/period for HP and 0.10 units/period for LP; $P = 0.91$). Water intake tended to be higher (5 L/cow/d; $P = 0.09$) for HP. Percentages of milk components were 4.18 vs. 4.25 (HP vs. LP), 3.73 vs. 3.71, 4.53 vs. 4.55, and 9.18 vs. 9.12, respectively for fat, protein, lactose, and solids non-fat ($P > 0.60$). Milk urea nitrogen decreased ($P < 0.001$) from 17.2 mg/dL with HP to 9.93 mg/dL with LP. Manure pH was significantly higher for HP than LP (7.87 for HP and 7.53 for LP, $P < 0.05$). Both, MUN and manure pH, are indicative of less nitrogen loss to the environment when cows were fed LP. This experiment suggests that performance of late-lactation dairy cows can be maintained with low-protein diets based on DDGS and supplemented with Lys and Met.

Key words: dairy cows, protein, amino acids

W339 Comparison of in vivo and in vitro NDF digestibility data in dairy cows. S. Colombini*, G. Galassi, L. Rapetti, and G. M. Crovetto, *University of Milan, Department of Animal Science, Milano, Italy.*

Aim of the study was to determine, in dairy cows, the relationship between total tract in vivo NDF digestibility (NDFD) and the NDFD predicted by CNCPS model, using the k_d determined in vitro. Six lactating Italian Friesian cows were fed in a Latin square design 3 diets with a different silage basis: corn (CS), sorghum grain (SG) and sorghum forage (SF). Diets were formulated with the CNCPS model and balanced to have a content (% DM) of 11.0, 36.0 and 26.0 of metabolizable protein, NDF and starch, respectively. Due to the different fiber contents, forages were included in the diets in different proportions (41.5, 36.7 and 28.0% on DM for CS, SG and SF diet, respectively). Cows were housed in individual metabolic chambers to allow total collection of feces. TMRs were analyzed for NDF in vitro digestibility (Ankom Daisy Incubator) to predict the k_d according to Van Amburgh et al. (2003). Rumen NDF digestibility was predicted with the model of Waldo et al. (1972) with the k_p calculated according to Seo et al. (2006). According to CNCPS, intestinal NDF digestibility was supposed to be 20% of the NDF which enters the duodenum. The content of NDF was 39.5, 45.2 and 62.5 for corn, sorghum grain and sorghum forage silages. DMI (kg/d) was lower for SF (18.2) than CS and SG (20.0 for both diets) (P=0.07). Milk yield (kg/d) was higher for CS (25.4), intermediate for SG (24.6) and lower for SF (23.6) (P=0.05). In vivo NDFD was higher for SF than SG and SF (table). The predicted NDFD was slightly higher than the in vivo values but with the same rank. The relationship between in vivo and predicted NDFD was: $y = 0.543x + 23.5$ ($r^2 = 0.45$; n = 18).

Table 1. In vivo and in vitro NDF digestibility of TMRs

Diet	CS	SG	SF	SE	P
NDFD 6h[1], %	19.8	15.3	19.2	1.61	0.16
NDFD 24h[2], %	43.0	37.8	44.7	2.25	0.14
k_d[3], /h	0.035	0.032	0.042	0.004	0.21
NDFD vivo, %	51.4	48.6	54.1	0.94	0.01
NDFD predicted, %	53.4[b]	51.8[b]	57.4[a]	1.78	0.15

[1]Rumen NDF digestibility after 6 h of incubation.
[2]Rumen NDF digestibility after 24 h of incubation.
[3]Rate of degradation determined from the in vitro NDFD values.
[a,b]LS means with different superscript are different ($P = 0.05$).

Key words: NDF digestibility, CNCPS, sorghum silage

W340 Effect of two different non-forage fiber sources on performance and feeding behavior of Holstein calves. L. l. Castells*[1], A. Bach[1,2], G. A. Pirisino[1], 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 2 different non-forage fiber sources on performance and feeding behavior of Holstein calves. Fifty-nine male Holstein calves (initial BW = 44.5 ± 5.47 kg) were randomly assigned to 1 of 3 different dietary treatments that consisted on a starter (21% CP, 15% NDF) without any other supplementation (CTR) or with an additional bucket with soybean hulls (SBH) or dehydrated citrus pulp (DCP). 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). Intakes of starter, MR, and fiber sources were recorded daily and BW was recorded weekly. Calves were individually housed and bedded with wood shavings. Performance data were analyzed with an ANOVA with repeated measures, and behavior data were analyzed with a Poisson regression analysis. There were no differences in ADG and gain-to-feed ratio among treatments. Animals in the CTR treatment consumed (830 ± 44 g/d) more ($P < 0.01$) starter than those receiving SBH (610 ± 44 g/d) or DCP (450 ± 44 g/d). Calves tended ($P = 0.08$) to consume more citrus pulp than soybean hulls (59 vs 25 g/d, respectively). Total DMI tended ($P = 0.08$) to be greater in CTR and SBH than in DCP animals after weaning. Calves in DCP treatment were devoted 17% less ($P < 0.01$) time to eat starter than CTR calves, and 5% less ($P < 0.05$) time to eat non-forage fiber than those in SBH. Animals in the SBH treatment were 13.7 times more ($P < 0.05$) likely to ruminate than those in CTR, and DCP calves were 11% less ($P < 0.05$) likely to develop non-nutritive oral behaviors than CTR calves. In conclusion, providing a choice of a non-forage fiber source in the diet of young calves stimulates rumination and reduces non-nutritive oral behavior, but it reduces starter intake and tends to reduce DMI.

Key words: calves, non-forage fiber, performance

W341 Morphology of the rumen of dairy cows fed high or low grain content diets before parturition. T. S. Teófilo, J. C. Resende Júnior*, S. F. Costa, M. B. Moreira, R. F. Lima, D. O. R. B. Santoro, G. P. Lenzi, P. P. Bueno, T. M. França, and T. A. Dell Vale, *Universidade Federal de Lavras.*

Dairy cows after parturition are fed diets rich in rapidly fermentable carbohydrates in reticulorumen leading to production of VFA at high speed which can to induce ruminal acidosis (RA). A high-energy diet

before parturition is able to induce the proliferation of ruminal epithelium, but some experiments have found conflicting results raising questions about the effectiveness of transition diet. The aim of this study was to examine whether transition diet given in the last weeks of gestation could contribute effectively to the control of RA in the postpartum of dairy cows. Six Holstein cows with cannula in the dorsal sac of the rumen, were allocated to 2 treatments in 3 blocks of 2 cows, defined by the date of the expected parturition. Six weeks before the expected calving, cows were fed a standard diet and 4 weeks before delivery were subjected to diets with high (HGC) or low (LGC) grain content. After delivery, all cows were fed a high energy lactation diet. Fragments of the rumen were collected by biopsy on days –42, –28, –14, –7, 2, 14, 28, 42 and 56 in relation to parturition. Cows that were fed HGC diet had higher ($P < 0.01$) dry matter intake and higher ($P < 0.01$) milk production. The HGC diet induced greater ($P < 0.01$) extension of the rumen absorptive surface than LGC diet. This supports the hypothesis that transition diet improves the ruminal ability to absorb VFA. The extent of the absorptive surface before parturition was lower than after calving, probably reflecting the effect of the highly energetic lactation diet. The provision of HGC diet before parturition may be a good alternative for the RA control after calving of dairy cows. This practice induces further development of the absorptive surface of the rumen avoiding the accumulation of VFA in this compartment. The greater dry matter intake and the greater milk production associated to HGC diet appear to have been a reflection of better physiological conditions of the rumen of these animals.

Key words: acidosis, ruminant stomach, transition diet

W343 Energy efficiency and performance of lactating dairy cows fed ethanol and acetic acid. J. L. P. Daniel*, L. G. Nussio, R. C. Amaral, A. Sá Neto, E. H. C. Garcia, A. W. Bispo, F. C. L. Oliveira, and I. F. Silva, *University of Sao Paulo, College of Agriculture "Luiz de Queiroz", Piracicaba, SP, Brazil.*

Ethanol and acetic acid are common end products from silages. The objective of this study was to determine whether ethanol and acetic acid affect performance and energy efficiency of high producing dairy cows. Heat of combustion from ethanol (kcal/g) is higher than either acetic acid or glucose, thus ethanol fed animals could be more efficient. Thirty lactating Holstein cows were grouped in 10 blocks and fed either: Control (33% Bermuda hay + 67% concentrates); Ethanol (control diet + 5% ethanol); or Acetic acid (control diet + 5% acetic acid, DM basis) diets, during 7 weeks. Ethanol and acetic acid were diluted in water (1:2) and sprayed onto total mixed ration twice daily before feeding. The same amount of solution was replaced with water in the control diet. During the 1st week the cows received half-dose of these chemical compounds. Dry matter intake (DMI) and milk yield were recorded every day and milk composition was determined once weekly. Data were analyzed as repeated measures using the MIXED procedure of SAS. Cows fed ethanol yielded more milk (37.9 kg/d) than those fed control (35.8 kg/d) or the acetic acid (35.3 kg/d) diets ($P = 0.04$), due to the higher DMI (23.7, 22.2, 21.6 kg/d, respectively). The significant diet*week interaction for DMI ($P = 0.02$), mainly during the 2nd and 3rd weeks (when the 5% acetic acid achieved the full dose) was related to the decrease in DMI of the acetic acid diet. Milk fat yield, milk urea-nitrogen and somatic cells counts were unaffected by diets, however protein and lactose yields were higher for ethanol diet, which agrees with the higher milk yield. Energy efficiency showed diet*week interaction ($P = 0.06$) and again, during 2nd and 3rd weeks the acetic acid diet increased NEl milk/DMI ratio due to the lower DMI and body weight loss. Otherwise, energy efficiency was similar across diets (1.1 Mcal NEl milk/kg DMI). Animal performance suggested similar energetic value from ethanol containing diet as compared with the other diets. Volatilization losses of ethanol at feed bunk and rumen conversion to acetate might be reasonable explanations to the deviation on the predicted energetic value.

Key words: volatile organic compounds, alcohol, intake

W344 Effect of an essential oil compound based product on ruminal disappearance of proteins, fiber and starch and fermentation parameters in dairy cow. D. Éclache, P. Etienne, and V. Noirot*, *Phodé Laboratories, Terssac, France.*

An in vivo study was carried out to evaluate the effect of Oleobiotec (Phodé Laboratories, France) containing carvacrol on ruminal disappearance of crude proteins-CP (soybean meal), starch (corn meal), fiber (alfalfa hay) and rumen fermentation parameters. Four non lactating dairy cows with ruminal cannulas were assigned to a 2 × 2 factorial arrangement in a 4 × 4 Latin square design. The product was given orally (0 or 1g/cow/day) and tested on 2 types of diet: one concentrated in fiber (F diet: 42% NDF, 20% starch) and the other in starch (S diet: 42% starch, 27% NDF). The ruminal disappearance of starch, CP and fiber was measured by the nylon bag method, after 4, 8 and 24 h, respectively. Each experimental period lasted 35 d with 15 d for adaptation, 12 d for the treatment and measures and 8 d without additive. A mixed linear model was used for statistical treatment (SPSS). Oleobiotec increased ADF disappearance with the S diet (+6,1 pts, $P < 0.05$) and decreased CP disappearance when associated with F diet (−6.0 pts, $P < 0.05$). There was no significant effect on starch disappearance and total volatile fatty acids concentration on either diet. The proportion of acetate increased with the S diet ($P < 0.05$) and that of propionate tended to increase with the F diet and to decrease with the S diet($P < 0.10$). N-NH_3 concentration decreased with the S diet ($P < 0.05$). Oleobiotec seems to improve fiber utilization with high starch diet and lower CP rumen utilization with high fiber diet.

Table 1.

	F		S		
	Control	Oleobiotec	Control	Oleobiotec	SEM
Disappearance, %					
ADF	28.2^{c}	28.0^{c}	19.3^{a}	25.4^{b}	1.6
CP	40.1^{c}	34.1^{a}	36.1^{b}	37.3^{b}	2.2
Starch	50.7	50.5	51.1	51.2	2.3
Fermentation parameters					
Total VFA, mmol	80.2^{a}	82.2^{a}	97.5^{b}	100.8^{b}	2.4
Acetate, %	70.2^{c}	70.2^{c}	63.9^{a}	65.7^{b}	0.5
Propionate, %	15.9^{x}	16.5^{y}	17.8^{z}	16.9^{y}	0.3
N-NH_3, mg/L	166.1^{a}	160.1^{a}	272.7^{c}	223.0^{b}	16.7

$^{a-c}$Within a row means without a common superscript letter differ, $P < 0.05$; $^{x-z}P < 0.10$.

Key words: essential oil, dairy cow, rumen

W345 Milk fatty acid profile from dairy cows fed tropical forage-based TMR containing increasing levels of sunflower oil. M. A. S. Gama*[1], C. G. S. Ribeiro[4], F. C. F. Lopes[1], M. M. Almeida[2], E. F. Motta[1], M. T. Ribeiro[1], and J. M. Griinari[3], *[1]Brazilian Agricultural Research Corporation, Juiz de Fora, Minas Gerais, Brazil, [2]The Uni-*

versity of Juiz de Fora, Juiz de Fora, Minas Gerais, Brazil, [3]Swedish University of Agricultural Sciences, Uppsala, Sweden, [4]The University of Minas Gerais, Belo Horizonte, Minas Gerais, Brazil.

Due to health concerns associated with milk fat intakes, efforts have been made to decrease medium chain saturated fatty acids (C12 to C16) and increase oleic acid (cis-9 C18:1) as well as CLA (cis-9 trans-11 C18:2) in milk fat. Supplementation of the dairy cow diet with plant oils is a practical way to achieve this goal. Most studies published, thus far, have used temperate grasses or corn silage as forage. In this study, we evaluated the effects of increasing levels of sunflower oil (SO) on milk fatty acid profile in cows fed fresh Elephant grass (*Pennisetum purpureum*) - a tropical forage. Twelve primiparous Holstein cows (95 ± 25 DIM) were assigned to the following dietary treatments (level of SO inclusion, % of diet DM): Control (CTL): 0%; T1: 1.5%, T2: 3.0% and T3: 4.5%. The experimental design was a 4 × 4 Latin Square with 15 d treatment periods (last 5 d for data collection). Diet was fed as a TMR and it was composed of chopped Elephant grass and a concentrate mixture (65:35, DM basis) containing the SO. Milk yield, milk composition and DM intake were unaffected by the treatments. SO supplementation reduced the relative proportion of C12:0 to C16:0 fatty acids from 42.2% to 38.8, 27.8 and 26.8% for CTL, T1, T2 and T3, respectively ($P < 0.05$). C18:0 increased from 9.9% to 14.3, 15.7 and 16.7% ($P = 0.006$), cis-9 C18:1 increased from 21.7% to 24.8, 26.7 and 27.3% ($P = 0.0315$) and cis-9 trans-11 CLA increased from 0.88% to 1.26, 1.62 and 2.14% ($P < 0.0001$) for CTL, T1, T2 and T3, respectively. Interestingly, there was a linear decrease ($P < 0.05$) in desaturase indexes (14:1/14:0, 16:1/16:0, 18:1/18:0 and CLA/trans-11 C18:1) as the level of dietary SO increased. Concentration of C18:0 in milk fat was inversely associated with C18:1/C18:0 and CLA/trans-11 C18:1 ($r = -0.85$, $P < 0.0001$), and with C14:1/C14:0 ($r = -0.69$, $P < 0.0001$). These results suggest that extensive biohydrogenation of dietary PUFA has occurred in the rumen, leading to high levels of C18:0 in milk fat. High level of C18:0 in the preformed fatty acid supply to the mammary gland may have contributed to the observed reduction in desaturase indexes.

Key words: desaturase, milk fat, cows

W346 Effects of grinding or steam rolling of starter grains on nutrient digestibility of Holstein suckling calves. N. Jalali-Farahani, M. Dehghan-Banadaky*, K. Rezayazdi, and M. Ganjkhanlou, *Animal Science Department, Campus of Agriculture and Natural Resources, University of Tehran, Karaj, Tehran, Iran.*

This study conducted to evaluate the effects of grains processing (grinding versus steam rolling) in calf starter diet on nutrient digestibility of Holstein suckling calves. In present experiment, 60 Holstein calves (28 male and 32 female) with average 44 ± 5 kg birth weight were used from 3 until 120 d old. Calves randomly divided to 4 treatments included: 1) ground barley and corn, 2) steam rolled barley and ground corn, 3) ground barley and steam rolled corn, 4) steam rolled barley and corn. Calves were housed in individual hutch and had free access to water and starter diet. Calves weaned at 90 d old. In this experiment a complete blocks randomized design used with 4 treatment (diets) and 15 replicates (calves) and 2 blocks (sex). Feed and fecal were sampled at 90 and 120 d. Acid insoluble ash used as internal markers for nutrients digestibility study. Manure screening was done every other week for evaluation of grain digestion. In diet 1, undigested grain in fecal was significantly different from others treatments ($P < 0.05$). Apparent digestibility of dry matter, crude protein, neutral detergent fiber, organic matter, and ether extract between diets had not significant discrepancy. But apparent digestibility of non fibrous carbohydrates (NFC) was significantly different between treatments ($P < 0.05$). The results indicated that the treatment with grinding corn and grinding barley did the best performance for starter diet in Holstein claves.

Key words: calf starter, grinding, steam rolling

W347 Investigation of grinding or steam rolling of starter grains on growth performance of Holstein suckling calves. N. Jalali-Farahani, M. Dehghan-Banadaky*, K. Rezayazdi, and M. Ganjkhanlou, *Animal Science Department, Campus of Agriculture and Natural Resources, University of Tehran, Karaj, Tehran, Iran.*

This study conducted to evaluate the effects of grains processing (grinding versus steam rolling) in starter diet on growth performance of Holstein suckling calves. In present experiment, 60 Holstein calves (28 male and 32 female) with average 44 ± 5 kg birth weight were used from 3 until 120 d old. Calves randomly divided to 4 treatments include: 1) ground barley and corn, 2) steam rolled barley and ground corn, 3) ground barley and steam rolled corn, 4) steam rolled barley and corn. Calves were housed in individual hutch and had free access to water and starter diet. Calves weaned at 90 d old. In this experiment a block completely randomized design used with 4 treatment (diets) and 15 replicates (calves) and 2 blocks (sex). Measurements of shoulder height, hip width and hip height were recorded every 15 d. In diet 1, hip height and shoulder height were significantly more than other treatments ($P < 0.05$). Width hip between diets did not show any significant difference but hip width was a significant difference between sexes, female calves gad wide hip. Results indicate that the type of grain processing incorporated into calf starter can influence structural growth in suckling calves.

Table 1. Least squares means for structural growth measurements of Holstein calves fed for diet 1-4

	Diets					Sex		*P*-value	
	1	2	3	4	SEM	male	female	sex	treatment
Shoulder Height (cm)	89.9	86.1	88.3	87.8	1.16	88.5	87.6	NS	NS
Hip Height (cm)	92.8[a]	90.6[ab]	91.1[ab]	89.3[b]	1.01	90.4	90.0	NS	0.03
Hip Width (cm)	13.4	13.2	14.8	13.6	0.56	13.0[b]	14.5[a]	0.01	NS

Diets 1-4 included: 1) ground barley and corn, 2) steam rolled barley and ground corn, 3) ground barley and steam rolled corn, 4) steam rolled barley and corn.

Key words: grinding, steam rolling, calf starter

W348 Investigation of chewing activity in cows fed diet with different ratios of alfalfa hay and corn silage. A. Akbai, A. Zali, M. Ganjkhanlou, and M. Dehghan-Banadaky*, *Animal Science Department, Campus of Agriculture and Natural Resources, University of Tehran, Karaj, Tehran, Iran.*

In present study, chewing activity in cows fed total mixed ration based on alfalfa hay and corn silage evaluated. Fifteen Holstein cows (37 ± 10 DIM) were used in a completely randomized design with 3 treatments and 5 replicates during 9 weeks. Treatments included 3 levels of

hay and corn silage included: 1) 10% alfalfa −30% silage corn (CS), 2) 20% alfalfa −20% silage corn (CSAH) and 3) 30% alfalfa −10% silage corn (AH). The ratio of forage: concentrate was 40:60 in all treatments. Cows were fed the total mixed rations (TMR) twice daily. Individual dry matter intake and ort were measured daily. Chewing activity was recorded visual every 5 min during 24 h in 2 periods at 4 and 8 weeks. Eating and ruminating activities were monitored by 2 alternating individuals once every 5 min under the assumption that each activity would persist for the entire 5 min. Total time spent chewing was calculated as the time spent eating plus the time spent ruminating. Dry matter intake was higher when cows were fed CSAH (23.20 kg per day) compared with CS (22.95 kg per day) and AH (18.64 kg per day). Eating time (min/day) and (min/ kg DM, NDF intake) increased in CSAH group. Ruminating time (min/day) and (min/ kg DM, NDF intake) were not affected by treatment. Also, the total chewing time (min/day) decreased with increase alfalfa ratio. Resting time in AH group was more than CS and CSAH. Total pledges during the day and during each meal, ruminate and chewing activity did not significant difference between treatments.

Key words: alfalfa hay, corn silage, Holstein cows

W349 A non activated charcoal reduced diarrhea of calves subject to Escherichia coli compared to a conventional treatment after 9 days of treatment. C. Ionescu*[1], P. Ferretti[2], and D. M. Bravo[1], *[1]Pancosma, Geneva, Switzerland, [2]NanoAgro, Buenos Aires, Argentina.*

Calves post-weaning diarrhea is common in several areas. One of the diarrhea causes is the prevalence of *E. coli*. To treat diarrhea, veterinarian use conventional treatments including antibiotics (ANTIB). The objective of this trial was to check if a non activated charcoal (NAC: CARBOVET) could be used as an alternative, in case of *E. coli* diarrhea in calves. Twelve calves (34.9 ± 3.5 kg) were selected based on diarrhea diagnostic. *E. coli* presence was confirmed by microbiology counts in their feces. Calves were introduced in 2 groups for 20 d as following: NAC calves were given orally 20 g NAC per head per d for 6 d and 10 g NAC per head per d for the remaining 14 d; ANTIB calves were given: orally 30 mL Estreptocarbocaftiazol (ftalisulfatiazol, dihydroestreptomycin sulfate, coffee charcoal extract and dimethylpolyxyloxan) and 40 mL Brebaje (streptomycin sulfate, sodium sulfadimethylpyrimidine and gallotanic acid) for 3 d and injected 5 mL of Diafin (benzetimide hydrochloride and enrofloxacin), 6 mL of Terramycin (oxytetracyclin). Fecal score (FS) and average daily feed intake (ADFI) were measured daily; BW was measured on d 1/2, 5 and 20. Fecal scores were noted on a 5 points scale: 1 being normal to 5 being watery. Two calves died during the trial due to virosis. Data were analyzed using GLM procedure. ADFI was higher in NAC than in ANTIB during the first 4 d (25 vs. 0 g/d, $P \leq 0.05$, respectively). From d 5 to 20, no more differences in ADFI were observed. No differences in BWG were measured between groups. The FS for d 1 to 8 period was numerically higher in NAC than in ANTIB calves (3.47 vs. 2.77, $P = 0.20$) indicating a higher diarrhea intensity in NAC. For d 9 to 20 period, FS was lower in NAC group compared with ANTIB (1.04 vs. 1.63, $P \leq 0.05$, respectively). The percentage of calves relapsed in diarrhea (with FS values over 4) after 6 d where higher in ANTIB than in NAC (83.3% vs. 33.3%, $P = 0.09$,respectively). These results indicate that NAC could be beneficial for calves experiencing diarrhea caused by *E. coli*.

Key words: *E. coli*, charcoal, calves

W350 A new method for individually feeding a supplement to dairy cows in a free stall. E. M. Ramsing*[1], C. M. Shriver-Munsch[1], J. R. Males[1], W. K. Sanchez[2], I. Yoon[2], and G. Bobe[1], *[1]Department of Animal Science, Oregon State University, Corvallis, [2]Diamond V Mills, Cedar Rapids, IA.*

Previously, nutrition research on commercial farms was limited to treatments applied across entire pens or utilization of forced-intake techniques such as bolusing. Our hypothesis was to develop a reproducible, non-invasive procedure for individually feeding supplements to dairy cows on commercial dairy farms. Multiparous Holstein cows, housed in free-stall barns, received *Saccharomyces cerevisiae* fermentation product (Diamond V Original XP) as a top dressing during the morning feeding lock-up period. The supplement consisted of 0, 56, or 112 g of Original XP mixed with 84 g of molasses and 168, 112, or 56 g of corn meal, respectively. After creating an indentation (25 to 30 cm deep and 10 cm diameter) in front of each cow in the newly delivered TMR, the supplement was placed in the indentation so adjacent cows could not consume it. Intake of the supplement and other feed was monitored and given a score on a 5-point scale (0 = no supplement consumption, 1 to 4 = partial consumption, 5 = complete consumption). To prevent supplement consumption by other cows, leftovers of the supplements were removed after 15 min from the feed bunk. Cows accepted the new feeding method within 3 d. The greatest differences in feed consumption between cows were observed at calving (no supplement consumption: 25 cows; partial consumption: 5 cows; complete consumption: 66 cows). Using PROC GLM, complete supplement consumption on the day of calving was associated with lower serum β-hydroxybutyrate concentrations the following day ($P = 0.02$). The impact of the differing supplements on intake behavior is reported in companion abstracts presented at this meeting. In conclusion, the newly developed method is non-invasive to cows, requires minimal investment and no modification to existing facilities, and enables 3 technicians to feed and monitor up to 50 cows during a 30-min lockup period.

Key words: dairy, individual feeding, supplement

W351 Effect of quantity and frequency of colostrum feeding on passive transfer, health, and performance of pre-weaned and post-weaned dairy calves. B. Ozer*[1], M. Chahine[1], C. M. Matuk[1], and M. E. de Haro Martí[2], *[1]University of Idaho, Twin Falls, [2]University of Idaho, Gooding.*

The objective of this study was to determine the effect of quantity and frequency of colostrum feeding on serum IgG concentration, health parameters, and growth in Holstein calves. Two hundred 16 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 = 107) or maternal colostrum+milk (MCM, n = 106). The first feeding of colostrum (3.2 L) was administered to MC and MCM calves using an esophageal tube within 1 h of birth. A second feeding of colostrum (2 L) was administered 12 h following the first feeding to MC calves while MCM calves received 2 L of milk. Blood samples were collected at 24 ± 3 h of age and tested for total serum protein (TSP) and serum IgG concentration. Rectal body temperature was measured twice a week during the first 3 weeks of age. Health evaluations were conducted daily until calves were 3 mo of age. Fecal (FC), dehydration (DH) and respiratory (RS) scores were recorded during the first 4 weeks of age. Average daily gain was measured at 28 ± 1 d of age and at weaning (52 ± 3 d). Data were analyzed using a mixed model in SAS. TSP and IgG concentrations were significantly

greater ($P < 0.0001$) in calves fed MC (TSP = 5.74 ± 0.05 g/dL; IgG = 21.06 ± 0.53 g/L) compared with calves fed MCM (TSP = 5.17 ± 0.05 g/dL; IgG = 17.40 ± 0.53 g/L). Rectal body temperature did not differ between MC and MCM and averaged 38.8°C ± 0.01. No differences were detected in pneumonia or diarrhea incidence which averaged 70.4% and 10.3% respectively. MCM calves had a greater ($P < 0.05$) incidence of abnormal FC (75.0%) and DH (30.0%) compared with MC calves (30.3% and 12.1% respectively). MC calves had a greater ($P < 0.0001$) incidence of abnormal RS (69.7%) compared with MCM (20.0%). Average daily gain did not differ between MC and MCM and averaged 0.60 ± 0.01 kg. Results suggest that feeding Holstein calves 2 separate feedings of colostrum will improve passive transfer and might lead to some health benefits. The effect of colostrum feeding quantity and frequency on RS needs to be investigated further.

Key words: colostrum, immunoglobulin, calves

W352 Odd- and branched-chain fatty acid (OBCFA) composition of plasma in response to N underfeeding and energy source in dairy cows and their distribution among plasma lipid classes. R. Gervais*[1], B. Vlaeminck[2], A. Fanchone[3], P. Nozière[4], M. Doreau[4], and V. Fievez[2], *[1]Département des sciences animales, Université Laval, Québec, Québec, Canada, [2]Lanupro, Ghent University, Melle, Belgium, [3]Unité de Recherches Zootechniques, INRA, Petit Bourg, Guadeloupe, France, [4]Unité de Recherche sur les Herbivores, INRA, Theix, St-Genès-Champanelle, France.*

The objective of the current study was to evaluate the consequences of a strong decrease in dietary N supply in dairy cows and its interaction with the nature of energy on the OBCFA composition of plasma total lipids and to assess the distribution of these fatty acids (FA) among plasma lipid classes. Four Holstein cows (662 ± 62 kg; 71 ± 10 d in lactation), fitted with rumen, proximal duodenum, and terminal ileal cannulas, were used in a 4 × 4 Latin square design, with 28-d periods. Treatments were 2 N levels (low and high) combined with 2 energy sources rich in starch (barley, corn, and wheat) or fiber (soybean hulls and dehydrated beet pulp). The high level of N met 110% of N requirements expressed in the French protein digestible in the intestine (PDI) system from INRA, with an adequate supply in rumen degradable N, whereas the low level covered 80% of N requirements with a shortage in rumen degradable N. The 4 diets had a forage:concentrate ratio of 60:40 (DM basis) and were isoenergetic. A decrease in dietary N supplementation had no effect on total plasma concentration of iso, anteiso, and linear odd-chain FA. The total plasma concentration of iso FA was decreased when cows received starch compared with fiber-rich diets (1.07 vs. 1.25 g/100g FA; $P < 0.05$), whereas energy source had no effect on plasma concentrations of anteiso and linear odd-chain FA. No interaction between level of N supply and energy source on OBCFA plasma composition was observed. Regardless of treatments, proportions of iso and anteiso FA were higher ($P < 0.01$) in cholesterol esters (28.4 and 33.1 g/100g OBCFA, respectively) and triacylgycerols (28.0 and 31.7) compared with phospholipids (23.5 and 27.4) and free fatty acids (23.0 and 26.9). Phospholipids (49.2 g/100 g OBCFA) and free fatty acids (50.1) presented higher ($P < 0.01$) concentrations of linear-odd chain FA compared with cholesterol esters (38.5) and triacylglycerols (40.4). Results from the current study suggest the selective incorporation of OBCFA in different plasma lipid classes.

Key words: lipid class, OBCFA, plasma fatty acids

W353 Effect of dietary escape microbial protein (DEMP) and degradable protein level on fermentation, digestion, and N flow in rumen-simulating fermenters. G. A. Harrison*, M. D. Meyer, and K. A. Dawson, *Alltech Biotechnology, Nicholasville, KY.*

Dietary escape microbial protein (DEMP) is a yeast-derived protein source with a moderate ruminal degradation rate allowing supplementation of high quality protein similar to ruminally synthesized microbial protein. Effects of DEMP in diets differing in calculated ruminally degradable protein (RDP) were examined in single-flow rumen-simulating fermenter cultures. Twelve cultures were used in a 2 × 2 factorial design with 4 treatments and 3 replications per treatment. Cultures were fed 25 g twice daily for 6 d. Factors were DEMP at 0 or 2.64% (600 g/d equivalent at 22.7 kg DM intake) and RDP at 9.9 and 11.4% in diets balanced at 16.5% CP (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 analyses. Nitrogen flow measures were estimated by using purine to N ratios for effluent and bacteria. Data were analyzed for treatment effects using GLM procedure of SAS with factor effects determined by orthogonal contrasts. Culture fed higher RDP diets had higher molar proportions of acetate and isoacids (isobutyrate + isovalerate+ valerate) and lower molar proportion of propionate ($P < 0.05$). Ammonia concentration was higher in cultures fed more RDP ($P < 0.01$). Bacterial N yield was 10.3% greater in cultures fed higher RDP and efficiency of bacterial N production based on DM truly digested or fermentable carbohydrate greater ($P < 0.05$). Efficiency of bacterial N production based on DM truly digested tended to be higher in DEMP-fed cultures ($P < 0.10$). Bacterial N yield was numerically greater (+6.6%) in cultures fed DEMP ($P = 0.13$). Cultures fed DEMP and higher RDP degraded more protein and had a greater proportion of effluent N from bacteria but not when DEMP was fed with lower RDP (interaction; $P < 0.05$). DEMP fed at the equivalent of 600 g/d had no impact on fermentation. Interactions suggest that DEMP may have a more positive effect when fed in higher RDP diets.

Key words: dietary escape microbial protein, degradable protein, ruminal metabolism

W354 Effect of level of dietary escape microbial protein (DEMP) on fermentation, digestion, and N flow in rumen-simulating fermenters. G. A. Harrison*, M. D. Meyer, and K. A. Dawson, *Alltech Biotechnology, Nicholasville, KY.*

Dietary escape microbial protein (DEMP) is a yeast-derived protein source with a moderate ruminal degradation rate allowing supplementation of high quality protein similar to ruminally synthesized microbial protein. DEMP has a recommended feeding rate of 600 g/d for lactating dairy cows but effects of DEMP fed at higher levels on ruminal metabolism have not been evaluated. Diets were formulated at 16% CP with inclusion rates of DEMP at 0, 1.76, 2.64, 3.96, 5.95, and 8.92% DM or 0, 400, 600, 900, 1350, and 2025 g equivalent for 22.7 kg DM intake. DEMP primarily replaced soybean meal. Twelve single-flow rumen-simulating fermenter cultures were used in a completely randomized design with 6 dietary treatments, 2 replications per treatment, and 2 experimental runs. Cultures were fed 25 g twice daily for 6 d. 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. Culture diet did not affect fermentation pattern or extent of digestion ($P > 0.10$). Bacterial purine content was altered by diet. Bacteria isolated from cultures fed the 0 g DEMP diet had a higher purine concentration than those from all other treatments except the 400 g DEMP treatment. Bacteria from cultures fed the 900 g DEMP diet had a lower purine concentration than those from cultures fed 0, 400, and 2025 g DEMP diets ($P < 0.05$). Bacterial N yield and efficiencies of bacterial N yield production were not significantly affected by culture diet ($P > 0.10$). Numerical increases in bacterial N yield in cultures fed 600 to 2025 g DEMP compared with the 0 g DEMP diet (+6.1 to 8.2%) are in agreement with previous work with fermenter cultures. Inclusion of dietary escape microbial protein (DEMP) at equivalent feed rates of 400 to 2025 g/d did not affect ruminal fermentation.

Key words: dietary escape microbial protein, ruminal metabolism

W355 Effects of abomasal infusion of fish oil, sterculia foetida oil and conjugated linoleic acids on milk yield and composition, and mammary mRNA expression of stearoyl CoA desaturase in dairy cows. M.-P. Dallaire*[1,2], L. Ma[3], B. A. Corl[3], R. Gervais[1], Y. Lebeuf[1], F. J. Richard[1], and P. Y. Chouinard[1,2], *[1]Département des sciences animales, Université Laval, Québec, QC, G1V 0A6 Canada, [2]Institute of Nutraceuticals and Functional Foods (INAF), Québec, QC, Canada, [3]Department of Dairy Science, Virginia Tech, Blacksburg.*

Sterculic acid and t10c12 conjugated linoleic acid (CLA) are both inhibitors of stearoyl CoA desaturase (SCD). This enzyme is active in mammary gland of lactating cows where it plays a key role in the regulation of milk fat composition. The purpose of this study was to determine the effects of sterculic acid, CLA and fish oil (FO) on milk yield and composition and on the mammary expression of 2 isoforms of SCD (1 and 5). Eight multiparous Holstein cows (mean BW 635 ± 34 kg; mean DIM 69 ± 13 d) were used in a double 4 × 4 Latin square design with 28-d periods. For the first 14 d, cows received abomasal infusion of CTL) 406 g of saturated fatty acids (Energy Booster (EB); control); SFO) 7 g of sterculia fetida oil + 399 g of EB; CLA) 36 g of CLA (42% t10c12 CLA) + 370 g of EB; and FO) 406 g of fish oil. Contrasts were used to compare individual effects of SFO, CLA, and FO with CTL. On d 14 of infusion, mammary gland biopsies were harvested and analyzed for RNA transcripts of SCD1 and SCD5. Compared with CTL, SFO decreased milk yield from 38.0 to 33.0 kg/d, and increased milk fat and protein content from 3.79 to 4.45% and 3.30 to 3.63%, respectively ($P < 0.01$). Milk fat content was also decreased ($P < 0.01$) by CLA (2.23%) and FO (3.34%). Milk fat yield was not affected by SFO (1475 g/d) when compared with CTL (1431 g/d), but was decreased ($P < 0.01$) by CLA (774 g/d) and FO (1186 g/d). Compared with CTL, expression of SCD1 was increased ($P = 0.04$) by SFO (30%) and decreased ($P = 0.02$) by CLA (24%), while FO had no effect. The mRNA abundance of SCD5 was not affected by treatments. Results from the current study support the concept that SCD1 and SCD5 present differences in their regulation by dietary FA.

Key words: conjugated linoleic acids, stearoyl-CoA desaturase, sterculic acid

W356 Effect of corn silage inoculation with Sil-All and dietary protein on fermentation, digestion, and N flow in rumen-simulating fermenters. G. A. Harrison*, M. D. Meyer, M. S. Taylor, and K. A. Dawson, *Alltech Biotechnology, Nicholasville, KY.*

Effects of feeding corn silage treated with inoculant (Sil-All) on ruminal metabolism were evaluated in rumen-simulating fermenter cultures. Whole corn plants (CF 738; Caverndale Farms, Danville, KY) were harvested at 6 stages of maturity (90, 94, 98, 105, 108, and 111 d) and ensiled in 125 L black plastic bags. At each harvest date, 5 kg of wet forage was ensiled without treatment (control) and with Sil-All at 200,000 cfu/g (SA). After 35 d, silages were dried at 55o C and ground through a 4 mm screen. Twelve single-flow rumen-simulating fermenter cultures were used in a 2 X 2 factorial design with 4 treatments, 2 replications per treatment, and 6 experimental runs. For each run, diets were formulated at 15 or 18% CP (DM basis) with control or SA corn silage from a single maturity date. Diets consisted of 75–85% silage with soybean meal used to meet protein targets. Cultures were fed 20 g twice daily for 6 d. Fermentation samples were collected from cultures before morning feeding during the last 3 d. 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 factor effects determined by orthogonal contrasts. Culture pH was higher when either higher CP diets or SA corn silage were fed (6.40 vs. 6.46, $P < 0.05$). Higher protein diets resulted in higher molar proportions of isoacids (isobutyrate + isovalerate+ valerate) and greater culture ammonia ($P < 0.0001$). Digestion of OM and NDF were increased when cultures were fed more protein ($P < 0.05$). Bacterial N yield tended to be greater with higher protein diets (+3.4%, $P < 0.10$). Cultures fed SA silage produced 3.7% more bacterial N than cultures fed control silage ($P < 0.05$). Both higher protein and SA silage increased efficiency of bacterial N yield based on DM truly digested ($P < 0.05$). Diets based on Sil-All treated corn silage resulted in increased bacterial N production in fermenter cultures.

Key words: corn silage inoculation, ruminal metabolism

W357 Enhancing antioxidant properties of milk using a programmed, nutritional approach. G. A. Harrison*, M. S. Taylor, M. D. Meyer, and K. A. Dawson, *Alltech Biotechnology, Nicholasville, KY.*

The potential to enhance antioxidant capacity in milk was examined in a series of field trials. This programmed approach involved feeding a low inclusion rate pack of bundled, proprietary Alltech technology formulated to meet trace mineral and vitamin needs of lactating dairy cows. Six field trials were conducted using herds in SW Kentucky. Herds were selected on the basis of ability to follow trial protocols including replacement of current trace mineral and vitamin supplementation with an Alltech-Inside Dairy Pack (ATI) for 2–3 weeks and collection of individual milk samples from 12 cows before and during and ATI supplementation period. Bulk tank milk samples were also taken on collection days and approximately 3.5 L of milk was used in the production of mozzarella cheese. Herd was used as the experimental unit and response to ATI supplementation was evaluated using the GLM procedure of SAS. Milk and cheese samples were analyzed for selenium via hydride generation fluorescence (Millennium Excalibur 10.055, PS Analytical). Total antioxidant capacity was estimated by ferric reducing antioxidant power and radical scavenging ability by the DPPH assay (2,2-diphenyl-1-picryl hydrazyl). Se content of individual milk samples was 33% greater when cows were fed ATI Dairy Pack (32 vs. 42 ppb; $P < 0.05$). Total antioxidant capacity of individual milk samples was 9% greater when cows were fed ATI Dairy Pack (934 vs. 1021 μM Trolox equivalent; $P < 0.05$). Radical scavenging ability in milk from individual cows was similar comparing the 2 col-

lection periods (96 vs. 107 μM Trolox equivalent $P > 0.10$). Bulk milk samples collected during the ATI period had higher Se content (33 vs. 39 ppb; $P < 0.05$) and more radical scavenging ability (110 vs. 127 μM Trolox equivalent $P < 0.05$), but did not differ in total antioxidant capacity (1013 vs. 1099 μM Trolox equivalent $P > 0.10$). For mozzarella cheese, feeding the ATI pack resulted in higher Se content (178 vs. 294 ppb; $P < 0.05$) but did not alter in total antioxidant capacity and radical scavenging ability ($P > 0.10$). Antioxidant properties of milk can be enhanced through a programmed, nutritional approach.

Key words: milk, antioxidant capacity, selenium

W358 Mineral metabolism in pregnant dairy goats. C. J. Härter*[1], I. A. M. A. Teixeira[1], L. D. Lima[1], H. G. O. Silva[1], A. R. Rivera[1], D. S. Castagnino[1], K. T. Resende[1], and N. R. St-Pierre[2], *[1]Universidade Estadual Paulista, Jaboticabal, SP, Brasil, [2]Department of Animal Sciences, The Ohio State University, Columbus.*

Although mineral requirements are important to animal nutrition especially during pregnancy there are few studies on mineral metabolism of pregnant goats. Therefore the aim of this study was to determine calcium (Ca) and phosphorus (P) metabolism during pregnancy of dairy goats. After pregnancy confirmation, 32 female goats were distributed into treatments according to a block design in a 2 × 2 × 3 factorial as follows: 2 breeds (Oberhasli and Saanen), 2 types of pregnancy (single and twin) and 3 levels of feed restriction (0, 20 and 40% feed restriction). Blood samples were collected at 1, 35, 50, 65, 80, 95, 110, 125 and 140 d of gestation and serum samples were taken after centrifugation at 4°C for 20 min. at 1370 × g. Serum concentration of Ca, P, magnesium (Mg) and alkaline phosphatase (AP) activity were determined in these samples. Statistical analysis was performed in PROC MIXED using compound symmetry covariance structure. It was observed a significant decrease ($P < 0.05$) in serum concentration of Ca, P and AP activity after 80 d of pregnancy. Regardless the number of fetuses and the level of feed restriction Saanen goats presented higher levels of serum concentration of Ca and P and lower AP activity ($P < 0.01$). The serum concentration of Ca, P and AP activity decreased, and Mg raised as feed restriction increased ($P < 0.01$). Twin pregnant goats were found to have higher serum Ca ($P < 0.05$) than goats pregnant with one fetus . On the other hand, serum P concentration and AP activity ($P < 0.05$) were lower in twin pregant goats. These results show that the mineral demand increases as pregnancy advances, especially in twin pregnancy, and the higher mineral demand is met by calcium mobilization through bone resorption. Under feed restriction the animals might have attempted to meet Ca demand also by increasing intestinal absorption which is related to high ATPase activity and consequently higher Mg serum concentration (ATPase co-factor). (Fapesp project number 2009/10125–0).

Key words: dairy breeds, days of gestation, feed restriction

W359 Effect of various dosages of *Saccharomyces cerevisiae* fermentation product on milk production of multiparous dairy cows. E. M. Ramsing*[1], C. M. Shriver-Munsch[1], J. R. Males[1], W. K. Sanchez[2], I. Yoon[2], and G. Bobe[1], *[1]Department of Animal Science, Oregon State University, Corvallis, [2]Diamond V, Cedar Rapids, IA.*

Feeding 56 g/d of *Saccharomyces cerevisiae* fermentation product (Diamond V Original XP) to transition dairy cows increased milk production in most studies. Doubling feeding rates of Original XP was suggested during times of increased stress such as around parturition, which is an especially challenging time period for older cows. The objective of the current study was to evaluate whether greater dosages of Original XP than 56 g/d are beneficial during the transition period. Multiparous Holstein cows housed in the same pen were given a supplement containing either 0 (control; n = 32), 56 (n = 33); or 112 g (n = 31) of Original XP daily during morning lock-up as a top dressing to their TMR. The supplement consisted of 0, 56, or 112 g of Original XP mixed with 84 g of molasses and 168, 112, or 56 g of corn meal, respectively. Supplement feeding started 28 d before predicted calving date (at least 14 d prepartum) and ended 28 d postpartum. The study was conducted on a commercial dairy. Milk weights and samples were collected twice weekly from the afternoon milking on non-consecutive d and analyzed for milk fat, protein, lactose, and somatic cell counts. Overall, supplementation with Original XP did not significantly increase milk production, however, in second lactation Holstein cows (n = 25; 8 or 9 cows per group), Original XP supplementation, regardless of dosage, increased milk production by 5.5 kg/d ($P = 0.05$). Doubling feeding rates of Original XP (112 g/d) additionally benefitted milk production in the last supplementation wk in fourth or higher lactation Holstein cows (n = 27; 8 to 10 cows per group; +10.6 kg/d versus control, $P = 0.08$, and +9.8 kg/d versus 56 g Original XP; $P = 0.10$). Although there were several potential confounding factors that could not be controlled on the commercial dairy, our results support the original hypothesis that greater dosages of Original XP than 56 g/d may be required to support increased nutritional demands and milk production during time periods of increased stress.

Key words: dairy, milk, yeast culture

W360 Prediction of enteric methane output from milk fatty acid composition, intake and rumen fermentation parameters. R. Mohammed*, S. M. McGinn, and K. A. Beauchemin, *AAFC, Lethbridge Research Centre, Lethbridge, AB, Canada.*

Milk fatty acid (FA) composition has been suggested as a means of predicting enteric methane (CH_4) output in lactating dairy cattle. The objectives of this study were to: i) predict CH_4 from milk FA composition, intake and rumen fermentation parameters and ii) test the reliability of CH_4 prediction equations reported in previous studies. Sixteen lactating Holstein cows were used in a cross over design with four 28-d periods. All diets contained steam-rolled barley, a pelleted supplement and 45% barley silage and were supplemented with crushed oilseeds from sunflower, flax, canola and calcium salts of long chain FA to provide 3.3% added fat on dry matter basis. Methane (g/d) was measured in chambers (2 animals/chamber) on 3 consecutive days (d21–23). Total dry matter intake (DMI, kg/d; d21–23), forage DMI (kg/d; d21–23), milk FA composition (% total FA methyl esters; d18–21), volatile FA (mol/100 mol; d19–21) and protozoal counts (d19–21) were averaged by chamber before including in the model. Forage DMI (r = 0.52; n = 32), DMI (r = 0.52; n = 32) and rumen acetate:propionate (r = 0.66; n = 16) were positively related ($P < 0.01$) to CH_4 (g/d) whereas rumen propionate (r = 0.63; n = 16), milk c9–17:1 (r = 0.64; n = 32) and c11–18:1 (r = 0.64; n = 32) were negatively related ($P < 0.01$) to CH_4. The best regression equation was ($P < 0.001$; $R^2 = 0.90$; n = 16): CH_4 (g/d) = −910.8 (±156.7) x milk c9–17:1 + 331.2 (±88.8) x milk 16:0 iso + 0.0001 (±0.00) x total entodinomorphs + 242.5 (±39.7). Removing rumen parameters from the model also resulted in a reasonably good estimate ($P < 0.001$; $R^2 = 0.83$; n = 32) of CH_4. Step-wise regression analysis within diets resulted in greater R^2 and lower standard error values. Methane predicted using equations from previous studies resulted in a mean over-estimation ranging from 19 – 61% across studies. Thus, milk FA composition and intakes (DMI) can be used to estimate enteric CH_4 under field conditions. However, more accurate

predictions require equations specific to each diet. More studies are required to test the reliability of CH_4 prediction equations under varied feeding conditions.

Key words: methane, milk fatty acid composition, prediction equations

W361 Effect of dietary starch content in early lactation on the lactational performance of dairy cows. B. H. Nelson*[1,2], K. W. Cotanch[1], M. P. Carter[1], H. M. Gauthier[1], R. E. Clark[1], P. D. Krawczel[1], R. J. Grant[1], K. Yagi[3], K. Fujita[3], and H. M. Dann[1], *[1]William H. Miner Agricultural Research Institute, Chazy, NY, [2]Department of Animal Science, The University of Vermont, Burlington, [3]ZenNoh National Federation of Agricultural Cooperative Associations, Tokyo, Japan.*

Multiparous Holstein cows (n = 78) were used to evaluate the effect of dietary starch content in corn silage-based diets fed in early lactation on performance and blood metabolites. Dietary treatments were 1) a low-starch diet (L; 21.0%; 1.65 Mcal NE_L/kg) for the first 91 d in milk (DIM; LL), 2) a medium-starch diet (M; 23.2%; 1.67 Mcal NE_L/kg) for first 21 DIM and a high-starch diet (H; 25.5%; 1.68 Mcal NE_L/kg) for the next 70 DIM (MH), and 3) a high-starch diet (H; 25.5%; 1.68 Mcal NE_L/kg) for the first 91 DIM (HH). Corn meal was replaced partially with soyhulls and wheat middlings in the L and M diets. Cows were housed in sand bedded freestalls, fed in a Calan Broadbent feeding system and milked 3 × daily. Dry matter intake (DMI) and milk yield were measured daily. Milk composition was measured weekly starting at wk 2. Serum was collected every other day (1 to 21 DIM) and was analyzed for nonesterified fatty acids (NEFA) and β-hydroxybutyrate (BHBA). Data were analyzed as a completely randomized design by ANOVA with the MIXED procedure of SAS using treatment and time as fixed factors and cow within treatment as a random factor. Through the first 21 DIM (n = 78 cows), there was no treatment effect ($P > 0.10$) for DMI (20.3 ± 0.6 kg/d), milk yield (40.9 ± 1.6 kg/d), milk fat (4.34 ± 0.11%), milk protein (3.39 ± 0.05%), and serum BHBA (8.8 ± 1.1 mg/dL). Serum NEFA (μEq/L) was higher ($P = 0.02$; SEM = 39) for MH (578) than HH (437); LL was intermediate (452). Through the first 91 DIM (n = 72 cows; Table 1) treatment affected milk yield and milk urea nitrogen (MUN) and tended to affect DMI and milk fat. Diets containing ≤23% starch can be fed successfully to cows in early lactation when corn meal is partially replaced with nonforage fiber sources as long as energy density of the diet is maintained.

Table 1.

Item	LL	MH	HH	SE
DMI, kg/d	25.2^{x}	24.9^{xy}	23.7^{y}	0.5
Milk, kg/d	47.9^{ab}	49.9^{a}	44.2^{b}	1.6
3.5% FCM, kg/d	51.9	52.2	47.4	1.7
Fat, %	3.88^{x}	3.64^{y}	3.79^{xy}	0.08
True protein, %	2.90	2.92	2.97	0.04
MUN, mg/dL	15.2^{a}	12.7^{b}	11.9^{b}	0.31
FCM/DMI	2.04	2.07	1.97	0.06
Body weight, kg	681	682	682	12
Body condition score	3.13	3.04	3.16	0.07

^{ab} $P \leq 0.05$; ^{xy} $P \leq 0.10$.

Key words: lactation, starch, transition cow

W362 A fibrolytic enzyme additive for lactating dairy cow diets: ruminal fermentation, pH, bacterial populations and enteric methane emissions. Y.-H. Chung*[1], L. Holtshausen[1], T. W. Alexander[2], M. Oba[3], and K. A. Beauchemin[1], *[1]Agriculture and Agri-Food Canada, Research Centre, Lethbridge, AB, Canada, [2]Department of Animal Science, University of Vermont, Burlington, [3]Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada.*

The objective was to determine if supplementing a dairy cow diet with a fibrolytic enzyme product (Econase RDE; AB Vista, Marlborough, Wiltshire, UK) alters ruminal fermentation, pH, bacterial populations, the risk of ruminal acidosis or enteric methane (CH_4) emissions. In a companion study this enzyme product improved ($P < 0.05$) efficiency of fat-corrected milk production for early-lactation dairy cows in a dose-dependent manner up to 11.3%. Nine ruminally cannulated, lactating Holstein cows were used in a replicated 3 × 3 Latin Square design with 21-d periods. Dietary treatments were 0 (control), 0.5 (low) and 1.0 (high) mL enzyme/kg TMR DM. Rumen contents were collected on 2 d, ruminal pH was measured continuously for 6 d, and enteric CH_4 emissions were measured for 3 d. The enzyme additive did not alter volatile fatty acids or ruminal pH profiles. However population densities of certain bacteria, calculated as copy number of specific 16S rRNA genes, were affected by enzyme treatment. The ruminal fibrolytic bacterium, *Fibrobacter succinogenes* ($P = 0.11$), and non-fibrolytic bacteria, *Ruminobacter amylophilus* ($P = 0.04$) and *Selenomonas ruminantium* ($P = 0.03$), increased linearly with increasing levels of enzyme in the diet. Increasing the level of enzyme supplement in the diet also increased enteric CH_4 production, even when adjusted for feed intake or milk production (19.3, 20.8 and 21.7 g CH_4/kg DMI or 12.9, 13.6 and 15.1 g CH_4/kg milk for the control, low and high enzyme diet, respectively; $P \leq 0.05$). The improvement in feed conversion efficiency of fat-corrected milk production with this enzyme product was related to a shift in ruminal bacterial communities associated with improved fiber digestion, which resulted in an increase in enteric CH_4 emissions without a change in volatile fatty acids or pH profile of the rumen fluid.

Key words: fibrolytic enzyme, ruminal bacteria, enteric methane emission

W363 Nutritional and seasonal factors causes milk fat concentration variability in dairy cows. A. S. Atzori*[1], P. Carta[2], G. Gaspa[1], and A. Cannas[1], *[1]Dipartimento di Scienze Zootecniche, Università di Sassari, Sassari 07100, Italy, [2]Associazione Regionale Allevatori della Sardegna, Nuraxinieddu, OR, Italy.*

Many animal and dietary factors might affect milk fat concentration (MF) of dairy cows. In this work several of them were studied in cows kept in Mediterranean climatic conditions. From December 2009 to July 2010, 54 samples of different total mixed rations (TMR) and bulk milk were collected from 26 dairy Sardinian farms (Italy). Daily herd DMI intake and milk yield (MY) were also recorded at the day of sampling. TMR were analyzed for chemical composition and sieved with the Penn State Particle Separator (PSPS) to estimate their physical effectiveness (peNDF). In the studied farms MY was 27.3±2.8 kg/cow per d (mean±s.d.; range 20.0-33.3), MF was 3.79±0.26% (range 2.88-4.29), dietary NDF was 37±2.6% of DM (range 32.2-43.9), while peNDF was 31.1±3.0% of DM (range 24.8-38.4). Despite this large variability, no significant associations between MF and NDF, peNDF or DM in the PSPS sieves were found. MF was negatively associated with the DM of TMR ($r = -0.55$; $P < 0.001$) and positively associated

with the concentration of silage in the ration (r = 0.30; $P < 0.05$). MF was lower in hot than in cold seasons ($P = 0.03$). A multivariate factor analysis, which excluded MF, was applied to the dataset and 6 factors were extracted. They indicated: F1) diet energy content (linked to TDNm, NEL3m, apparent digestibility, ADL, lipids in diet), F2) forage to concentrate ratio (linked to starch, NFC, NDF, ADF), F3) silage effects (linked to middle and lower PSPS fractions, silage in diet, DM of TMR), F4) cow performances (linked to MY, DMI, upper PSPS fraction), F5) diet protein balance (related to CP and bottom pan of the PSPS) and F6) season effects (linked to cold and hot season). Silage and season effects were the only factors significantly correlated with MF (r = 0.40, $P < 0.01$ and −0.33, $P < 0.05$, for F3 and F6 respectively). F3 was positively related to MF, with a similar trend both in hot and cold seasons, highlighting the positive effects of silages in the nutritional supply. The results showed that in many instances other factors than peNDF affect MF of dairy cows.

Key words: factor analysis, PSPS, silage

W364 Replacing soybean meal with Upland cottonseed, Pima cottonseed or extruded Pima cottonseed cake on production of lactating dairy cows. G. A. Broderick*[1], T. M. Kerkman[2], H. M. Sullivan[2], M. K. Dowd[3], and P. A. Funk[4], *[1]U.S. Dairy Forage Research Center, Madison, WI, [2]EcoSol, Tucson, AZ, [3]USDA-ARS, New Orleans, LA, [4]USDA-ARS, Mesilla Park, NM.*

Pima cotton production is growing in the US Pima cottonseed contains more gossypol, a toxic compound, than Upland cottonseed; heating cottonseed reduces gossypol absorption. Forty lactating Holstein cows were blocked by DIM into 5 squares in an incomplete 8x8 Latin square. Diets were formulated to (DM basis) 30% alfalfa silage, 30% corn silage, 21–25% corn, 16% CP and fed as TMR for ad libitum intake. Dietary protein was from: 1) solvent soybean meal (SSBM) or SSBM plus equal CP from 2) Upland cottonseed (UCS), 3) cracked Pima cottonseed (PCS), 4) Pima cottonseed cake (PCSC; prepared using experimental extrusion), 5) UCS plus PCS, 6) UCS plus PCSC; or expeller soybean meal (ESBM) plus equal CP from 7) PCS, or 8) PCSC. Periods were 4-wk (total 16 wk); data were from the last 2 wk. Blood plasma was collected on d-28. Data were analyzed using Proc Mixed in SAS. LS-means are in the table. Diet affected DMI ($P = 0.05$), with greatest intake on diet 6 and lowest intake on diet 1. MUN ($P = 0.05$) was lowest on diets 3, 7 and 8. No other production trait was affected. Milk fat ranged from 3.78 to 4.25%, suggesting cottonseed oil had no adverse effects. Plasma gossypol was higher ($P < 0.001$) on PCS, and lower on PCSC, than on corresponding diets with UCS, indicating extrusion reduced gossypol absorption. Performance on all diets supplemented with cottonseed was comparable to that on SSBM.

Table 1. Results

	Diet no.								
	1	2	3	4	5	6	7	8	
Item	SSBM	SSBM + UCS	SSBM + PCS	SSBM + PCSC	SSBM + UCS + PCS	SSBM + UCS + PCSC	ESBM + PCS	ESBM + PCSC	P > F
DMI, kg/d	25.7^{c}	26.1^{bc}	25.9^{c}	26.9^{a}	26.0^{bc}	26.9^{a}	26.3^{abc}	26.9^{a}	0.05
Milk, kg/d	43.7	44.3	43.6	44.2	44.0	45.3	45.0	45.3	0.73
Fat, kg/d	1.61	1.70	1.74	1.67	1.72	1.73	1.64	1.83	0.13
Protein, kg/d	1.24	1.25	1.24	1.28	1.22	1.27	1.26	1.30	0.56
MUN, mg/dl	9.2^{ab}	9.2^{ab}	8.6^{b}	9.4^{a}	9.2^{ab}	9.5^{a}	8.9^{b}	8.9^{b}	0.05
Plasma (-)gossypol, µg/ml	0.3^{e}	0.9^{e}	2.2^{a}	0.5^{d}	1.6^{b}	0.8^{c}	1.9^{b}	0.5^{d}	<0.01
Total gossypol, µg/ml	0.5^{e}	1.4^{c}	3.3^{a}	0.8^{d}	2.5^{b}	1.3^{c}	2.8^{b}	0.7^{d}	<0.01

a-e ($P < 0.05$).

Key words: upland cottonseed, pima cottonseed, milk production

W365 The effects of feeding high-fiber byproduct feedstuff on productivity of dairy cows in early lactation. Y. Q. Sun* and M. Oba, *University of Alberta, Edmonton, Alberta, Canada.*

The objective of this study was to evaluate effects of a partial substitution of dietary grain with wheat DDGS on DMI, sorting activity, milk production and plasma metabolites of early-lactating dairy cows. Sixty-one Holstein cows were blocked by parity (22 primiparous and 39 mutliparous cows) and assigned to one of 2 experimental diets immediately after calving until 12 weeks in lactation. Experimental diets contained 43.1% barley silage, 21.6% rolled corn grain, and either steam-rolled barley grain (Control) or wheat DDGS (DDGS) at 17% of dietary DM. Both diets were formulated to contain 19.5% CP, 22.6% forage NDF, and 5.4% fat on a DM basis, but dietary NFC contents were 38.1% and 32.3% for Control and DDGS diet, respectively. Because excess fermentation in the rumen often decreases energy intake of ruminants, we hypothesized that reducing dietary NFC content by replacement of barley grain with DDGS would increase DMI and milk production. Cows fed DDGS diet sorted to a greater extent for long (104 vs. 102%, $P = 0.08$) and medium (94.7 vs. 91.4%, $P = 0.004$) particles, which retained on 19- and 8-mm screens of Penn State Particle Separator, respectively, compared with animals fed the control diet. Treatment did not affect body weight, BCS, or plasma concentrations of glucose, NEFA, BHBA, and plasma urea N. We observed parity-by-treatment interactions for DMI ($P = 0.08$), milk yield ($P = 0.05$), and milk protein concentration ($P = 0.05$). Feeding DDGS diet increased DMI (16.5 vs. 15.0 kg/d), milk yield (31.4 vs. 28.7 kg/d) but decreased milk protein concentration (2.71 vs. 2.78%) for primiparous cows. For multiparous cows, feeding DDGS decreased DMI (20.2 vs. 21.2 kg/d) and milk yield (39.1 vs. 41.8 kg/d) but increased milk protein concentration (2.85 vs. 2.77%). In conclusion, wheat DDGS can be used as a substitute for barley grain in the diets of dairy cows in early lactation, but the causes for different production responses between multiparous and primiparous cows warrant further investigation.

Key words: early-lactating cow, DDGS, barley grain

W366 Determination of the metabolizable methionine contributions of three different sources of lipid coated methionine. E. Devillard[1], F. Rouffineau[1], and B. Sloan*[2], *[1]Adisseo France, Commentry, France, [2]Adisseo North and Central America, Alpharetta, GA.*

Lysine and methionine (Met) are the most limiting amino acids (AA) for dairy cow production. To supply the required quantities of metabolizable lysine and Met, dairy rations often need to be supplemented with rumen-protected AA. This study aims at quantifying the metabolizable Met contribution of 3 different rumen-protected products: MethioPlus (Soda Feed Ingredients, protection by encapsulation), Mepron M85 (Evonik Degussa, protection by encapsulation) and Smartamine M (Adisseo, protection by pH-sensitive coating) and 2 experimental products that will not be discussed here. The methodology based on mathematically integrating the increases in blood plasma Met levels following a spot dose of product (50 g of Met), was as described by Graulet et al. (2005). The area under the curve (AUC) was thus used to determine the proportion of Met reaching the blood stream. Eight nonlactating Jersey cows were used in a replicated incomplete Latin square design (Cochran and Cox 1962), with 5 periods of one week. The total quantity of product was introduced in the rumen at 2 p.m. via the rumen cannula of cows receiving a diet composed of 75% hay and 25% concentrate. Blood samples were taken before and after the spot dose (at −22, −6, −3, 0, +6, +10, +14, +20, +24, +28, +32, +38, +48, +72 h) for quantification of Met concentration. An ANOVA with repeated measures was performed on the data using the PROC MIXED of SAS/STAT software. The maximum Met concentrations in plasma were observed 24h after the spot dose for Smartamine M (183 µmol/L) or Mepron M85 (49 µmol/L), and after only 14h (43 µmol/L) for MethioPlus, suggesting that product formulation characteristics influence rumen residence time, rate of release in the rumen and postruminally and Met absorption. From the AUC, the proportion of Met reaching the blood stream was calculated at 81% for Smartamine M, which was significantly higher ($P < 0.001$) than those of Mepron M85 and Methioplus, respectively 30% and 21%. These results suggest that products vary greatly in their ability to deliver metabolizable Met to meet requirements.

Key words: metabolizable methionine, rumen-protected amino acids

W367 In vitro degradation of melamine in rumen liquor. T. Calitz and C. W. Cruywagen*, *Stellenbosch University, Stellenbosch, South Africa.*

Melamine contains 667 g/kg N, which makes it an attractive protein adulterant, as it has the ability to inflate the crude protein content of feed- and foodstuffs artificially. Although melamine has been found to be a poor source of nitrogen for ruminants, its rumen degradability has not been determined previously. The current study was done to measure the in vitro degradability of melamine over time. For each of 5 repetitions, melamine (100 mg) was placed in Erlenmeyer flasks (n = 4/treatment) in a water bath at 39°C. Rumen liquor was collected from 4 ruminally cannulated dairy cows and volumes of 100 mL per cow were transferred to the respective flasks. Initial melamine concentrations were thus 1000 mg/L. Flasks were purged with CO2 and fitted with rubber stoppers equipped with one-way gas release valves. The flasks were then transferred to an incubator and samples were incubated for 6, 24 or 48 h at 39°C. Two control treatments were included where rumen fermentation was inhibited by either killing the microbes with the addition of 1 mL of 10% formaldehyde per 100 mL rumen liquor, or by exposing it to air while placing it on ice for 2 h. Erlenmeyer flasks in the control treatments were not incubated and served as a 0 h treatment and also to calculate the recovery rate of melamine after analysis. The total experimental sequence was repeated 5 times in different weeks in a randomized block design. A main effects ANOVA was done on the data with the aid of Statistica version 10. Main effects were treatment, cow and block. Melamine recovery from the control treatments was 91%. When the control treatments were adjusted to 100% recovery (1000 mg/L), melamine concentrations in the incubated samples were 993 mg/L (6 h), 1003 mg/L (24 h) and 1007 mg/L (48 h). Treatment means did not differ ($P = 0.981$). It was concluded that melamine is not degraded in rumen liquor up to 48 h of incubation.

Key words: degradation, melamine, rumen

W368 Characterization of lipase-producing bacteria in the presence of varying energy substrates in vitro. H. D. Edwards*[1], R. C. Anderson[2], R. K. Miller[1], T. M. Taylor[1], M. D. Hardin[3], S. B. Smith[1], N. A. Krueger[2], and D. J. Nisbet[2], *[1]Texas A&M University, College Station, [2]United States Department of Agriculture/Agricultural Research Service, Southern Plains Agricultural Research Center, College Station, TX, [3]IEH Laboratories & Consulting Group, Lake Forest Park, WA.*

Ruminal lipolysis has long been attributed mainly to *Anaerovibrio lipolyticus* and *Butyrivibrio fibrisolvens*. Conversely, *Propionibacterium* species *avidum* and *acnes* are also known to express lipase activity but little is known regarding the contribution of these prominent anaerobes to rumen lipolysis. To further characterize and understand the lipase activity of these 4 different bacteria, each was grown with 4 different energy substrates: olive oil, corn oil, flax seed oil, and glycerol. The bacteria were cultured in triplicate in tubes containing glass beads (which served as a solid support matrix), 6 mL of anaerobic medium containing minerals, vitamins, yeast extract, trypticase, with or without added glucose and with 0.2 mL of the respective triacylglyceride-derived energy substrates. Tubes were incubated horizontally and agitated at 39°C and growth and enzyme activity was stopped when cells reached early log and stationary phase (based from growth curves done before the study). Free fatty acid accumulation was measured colormetrically with the glycerol treatment acting as the negative control in this study. Results were analyzed using a general ANOVA with Tukey's separation of means. Because findings from studies conducted with or without added glucose supported the same conclusions, we present results from studies conducted with added glucose only. Olive oil and flax seed oil promoted the highest ($P < 0.05$) rates of free fatty acid accumulation for all bacteria, averaging 213.84 ± 37.94 and 245.76 ± 34.82 nmol/ml per h, respectively, when compared with corn oil (76.72 ± 36.93 nmol/ml per h). Compared with the other bacteria, *P. avidum* demonstrated the most rapid rates ($P < 0.05$) of lipolysis, which were 649.99 ± 77.86 and 700.02 ± 69.64 nmol/ml per h for cultures grown with olive oil and flaxseed oil, respectively. The results suggest that diets containing a high content of oleic acid and linolenic acid promote high rate of lipolysis in the rumen and *P. avidum* may contribute to a higher amount of lipolysis than previously considered.

Key words: rumen, lipolysis, energy substrates

W369 Exogenous fibrolytic enzymes: Unlocking nutrients from fiber for ruminant production. W. F. J. van de Vyver* and C. W.

Cruywagen, *Stellenbosch University, Stellenbosch, Western Cape, South Africa.*

Exogenous fibrolytic enzymes (EFE) as additives in ruminant feeds are being researched worldwide, but there is a need for a better understanding of the mode-of-action thereof. Four forages, treated with EFE, were evaluated in vitro and at microscopic level, in an attempt to determine the effect of EFE on tissue degradation. For the histological evaluation, weeping love grass and kikuyu leaf material and alfalfa and wheat straw stem material were used. Simultaneously, the forages were incubated in rumen fluid inoculated media for the determination of the in vitro digestibility. The main focus, however, was a quantitative assessment of the degradation of the plant tissue at histological level. The section to slide technique was used to mount plant tissues on microscope slides for incubation in buffered rumen fluid media. Degradation of cell wall components were quantified using image analysis software. The in vitro digestibility data were subjected to a Factorial ANOVA whereas histology data were analyzed with either a Bonferroni or Newman-Keuls multifactorial test, using Statistica 8.1 (2008). In vitro digestibility was significantly higher for EFE treated alfalfa and kikuyu at 24h of incubation ($P < 0.05$). Clear histological differences were observed for all tissue types over the incubation period. Cell wall of the metaxylem of leaf material were thinner for the EFE treated samples at 12h of incubation ($P < 0.05$). There was also a significant thinning effect of EFE on the cell wall of phloem at 12h of incubation for kikuyu as well as the adaxial epidermis at 24h. The abaxial epidermis at 12h was thinner for weeping love grass due to EFE treatment. Excluding the thinner epidermis of EFE treated alfalfa (at 12h incubation, $P < 0.05$), no significant effects of EFE on stem material was observed. It was concluded that image analysis can be useful to quantify changes in cell wall over an incubation period and that the addition of exogenous enzymes could be quantified by this system. There was a definite, subtle thinning effect of EFE on cell wall thickness of plant material which could be indicative of the mode-of-action of EFE.

Key words: fibrolytic enzymes, plant histology, digestibility

W370 Comparison rumen degradability of *Sedilitzia rosmarinus*, *Halocnemum strobilaceum* and *Kochia scoparia* with wheat straw and alfalfa hay. M. Mahmoodi-Abyane*, R. Valizadeh, A. A. Naserian, and A. Koocheki, *Ferdowsi University of Mashhad.*

Rumen degradability of 3 halophyte species including *Sedilitzia rosmarinus*, *Halocnemum strobilaceum* and *Kochia scoparia* were determined and compared with the measure parameters for alfalfa hay and wheat straw samples. In situ rumen degradability was determined at 0, 2, 4, 8, 12, 24, 36, 48, 72, 96 and 120 h after ruminal incubation. The results of ruminal degradability demonstrated that the "a" fraction (rapidly degradable) of *Halocnemum strobilaceum* was significantly highest ($P < 0.05$) among the halophytes and alfalfa hay or wheat straw, whereas the value "b" fraction (slowly degradable) for wheat straw was higher ($P < 0.05$) than other treatments. The "c" fraction (rate of degradation) of *Sedilitzia rosmarinus* and *Halocnemum strobilaceum* was significantly ($P < 0.05$) higher than that for other treatments whereas lowest level of "c" fraction was absorbed in wheat straw sample. Potential degradability (PD) level of *Sedilitzia rosmarinus* (76%) was significantly ($P < 0.05$) higher than other forage whereas lowest of this factor was observed in wheat straw (60%). Also effective degradability (ED) level in *Sedilitzia rosmarinus* (70%) was significantly ($P < 0.05$) highest among the other treatments whereas lowest level of ED was observed in wheat straw (60%). It was concluded that *Sedilitzia rosmarinus* and *Halocnemum strobilaceum* could be relatively a suitable forage for the dry area of many part of the Iranian wilderness.

Key words: rumen degradability, *Sedilitzia rosmarinus*, *Halocnemum strobilaceum*

W371 Comparison rumen degradability of *Phragmites australis*, *Nitraria schoberi* and *Atriplex canescens* species with wheat straw and alfalfa hay. M. Mahmoodi-Abyane*, R. Valizadeh, A. A. Naserian, and A. Koocheki, *Ferdowsi University of Mashhad, Mashhad, Khorasan Razavi, Iran.*

Ruminal degradability of 3 halophyte species including *Phragmites australis*, *Nitraria schoberi* and *Atriplex canescens* were determined and compared with the measure parameters for alfalfa hay and wheat straw samples. In situ ruminal degradability was determined at 0, 2, 4, 8, 12, 24, 36, 48, 72, 96 and 120 h after ruminal incubation. The results of ruminal degradability indicated that the a fraction (rapidly degradable) of *Atriplex canescens* was significantly ($P < 0.05$) highest among the halophytes and alfalfa hay or wheat straw whereas lowest of this fraction was observed in *Phragmites australis*. The value b fraction (slowly degradable) for wheat straw and *Phragmites australis* was significantly ($P < 0.05$) higher than other treatments, respectively. The c fraction (rate of degradation) of *Nitraria schoberi* was significantly ($P < 0.05$) higher than that for other treatments whereas lowest level of c was absorbed in *Phragmites australis* and wheat straw samples. Potential degradability (PD) level of alfalfa (0.6357) and *Atriplex canescens* (0.6065) were significantly ($P < 0.05$) higher than other forage whereas lowest of this factor was observed in *Phragmites australis* (0.4639). Also effective degradability (ED) level in alfalfa (0.5621) and *Atriplex canescens* (0.5366) were significantly ($P < 0.05$) highest among the other treatments whereas lowest level of ED was observed in *Phragmites australis* (0.2663) and wheat straw (0.5995). It was concluded that ruminal degradability of *Atriplex canescens* similar to alfalfa hay and *Phragmites australis* had similar value with wheat straw.

Key words: alfalfa, ruminal degradability, wheat straw

W372 The comparison of chemical composition of *Pragmates australis* ensiled forage by various feed additives. R. Valizadeh, M. Mahmoodi-Abyane*, and A. Salahi, *Ferdowsi University of Mashhad, Mashhad, Khorasan Razavi, Iran.*

The chemical composition of whole plant of *Pragmates australis* silage treated with different feed additives were investigated. The applied treatments were: 1) *Pragmates australis* (Pa) ensiled without additive, 2) Pa + 4% NaOH, 3) Pa + 4% urea, 4) Pa + 10% molasses, 5) Pa + 4% urea + 10% molasses and 6) Pa + 4% urea + 10% molasses + 4% NaOH (on DM basis). The NDF, ADF, CP, and ash content of initial sample and not ensiled forage were 78, 47, 14, and 12.7%, respectively, that significantly ($P < 0.05$) changed while ensiling by the various feed additives. The NDF content of ensiled sample with urea was highest (72.5%) whereas it was lowest in the NaOH treated forage(62.0%). ADF percent of urea treated forage (44.4%) and as well as ensiled sample without additive (44.8%) were higher than other treatment with various feed additives while NaOH treated forage and molasses ensiled forage decreased to 40.1 and 41.6%, respectively. CP content of the urea treated forage (14.1%) was also higher than that for other samples and lowest was observed in NaOH treated forage (9.7%). Ash content of the NaOH treated forage (19.0%) was significantly ($P < 0.05$) higher in caparison with other treatments

whereas lowest one was seen in ensiled sample with urea (12.3%). It concluded that molasses additive had good efficacy on chemical composition of this forage and higher level of this additive supplemented must be beneficial.

Key words: chemical composition, silage, *Pragmates australis*

W373 The comparison of qualitative characteristics of *Pragmates australis* ensiled forage by various feed additives. R. Valizadeh, M. Mahmoodi-Abyane*, and A. Salahi, *Ferdowsi University of Mashhad, Mashhad, Khorasan Razavi, Iran.*

The qualitative characteristics of whole plant of *Pragmates australis* silage treated with different feed additives were investigated. The applied treatments were: 1) *Pragmates australis* (Pa) ensiled without additive, 2) Pa + 4% NaOH, 3) Pa + 4% urea, 4) Pa + 10% molasses, 5) Pa + 4% urea + 10% molasses, and 6) Pa + 4% urea + 10% molasses + 4% NaOH (DM basis). Initial sample of forage with 25% DM ensiled and silages opened after 60 d. Comparison of DM content silages after ensiling indicated that treatment without additive had lowest level of DM (26.7%) while forage supplemented with tree additives had highest one (32.3%). pH level was significantly ($P < 0.05$) different among the treatment. Lowest level of pH observed in ensiled sample was with molasses (4.2) whereas urea treated forage (8.3) had highest of pH. Highest level of acidity also observed in sample with molasses (12.6%) whereas the NaOH treated forage (4.1%) had lowest of acidity. Ammonia-N (mg/dl) content of the urea treated forage (63.8) was also higher than that for other samples and lowest was observed in molasses treated forage (4,0). It concluded that fresh *Pragmates australis* could be harvested and treated with the appropriate supplement (molasses) and ensiled for subsequent utilization when the availability of forages is limited.

Key words: qualitative characteristics, *Pragmates australis*, silage

W374 A comparison of methods to analyze physical effectiveness fiber. R. S. Goulart*, L. G. Nussio, A. V. Pirez, J. L. P. Daniel, R. C. do Amaral, and V. P. Santos, *University of Sao Paulo/ESALQ, Piracicaba, Sao Paulo, Brazil.*

The physical effectiveness factor (pef) or effectiveness factor (ef) from fiber sources were evaluated in a 6 × 6 Latin square trial using 6 Nellore steers in a bioassay methods (BM) as recommended by Armentano and Pereira (1997). Laboratory methods (LM) were also performed according to Mertens (1997) and Lammers et al. (1996) to estimate the pef of the fiber sources (pef ≥ 1.18 or pef ≥ 8.0mm, respectively). Six diets were formulated with different fiber contents and sources: negative control (NC) (10% of the NDF from corn silage – CS – in TMR), positive control (PC) (CS with 20% of the NDF in TMR) and 4 diets containing 10% of NDF from CS added with 10% of the NDF from each the following sources: sugarcane (SC), sugarcane bagasse (SCB), soybean hulls (SH) and low oil–cottonseed meal (LOCM). By using the BM, differences in pef were observed ($P \geq 0.05$) between the standard fiber source, CS (pef = 100%) and the following fiber sources: SCB, SC, SH and LOCM (116, 106, zero and 68%, respectively) considering chewing time in min/day. When chewing time in min/kg of DMI was considered as target trait higher values of pef were observed for the SCB (250%), following SC (120%), SH (zero) and LOCM (68%). Ruminal mat consistency calculated by method of Welch (1982) showed the following values of pef: 100, 135, 150, 0, and 61% (CS, SCB, SC, SH and LOCM, respectively). The mean ruminal pH values were utilized to estimate the pe values: 100, 162, 145, 66 and 166% (CS, SCB, SC, SH and LOCM, respectively). Estimated values from the LM showed a larger range when compared with the BM. The pef ≥ 1.18 values were: 95, 60, 88, 71, 87% and the pef ≥ 8.0mm values were: 87, 63, 77, 20, 72% for CS, SCB, SC, SH and LOCM, respectively. The LM showed low or no correlation ($P \geq 0.05$) with any animal response parameter utilized in this study. Values of effectiveness can vary significantly within the same method and across methods (bioassay and laboratory). This study demonstrated that particle size analyses were affected by LM. There is a need to achieve standardization and validation of the method for measuring pef and consequently establish its requirements for beef cattle.

Key words: roughage, byproducts, Nellore

W375 Rumen degradability of sugarcane (*Saccharum* spp.) treated with different hydrolysis agents used in Brazilian farms. S. L. S. Cabral Filho*[1,2], D. C. Pinto[1], and R. A. Mandarino[1], *[1]Universidade de Brasília, Brasília, Distrito Federal, Brasil, [2]Fazenda Experimental Agua Limpa, Brasilis, Distrito Federal, Brasil.*

The feeding sugarcane to cattle has been an alternative for Brazilian farmers in Brazil lowering the costs of production. The processing of sugarcane with hydrolysis agents has been promoted as a way to improve the fiber degradability of sugarcane. The aim of this study was to evaluated changes in effective ruminal degradability of the fiber fraction (ENDFD and EDADF) of non-treated sugar cane (SCNT) and sugar cane submitted to treatments of 5% of NaOH (SCT1), 1.5% of CaO (SCT2) and 5% of urea (SCT3). A dose of treatment for SCT1 was based in the recommendations of commercial products used in Brazil, for SCT2 and SCT3 were based in research results. The ruminal degradability was evaluated by in situ using nylon bags incubated in 2 fistulated cattle. The means were compared with Tukey test ($P < 0.05$) in a randomized design scheme with 3 replicates per treatment. The treatments SCT1 and SCT2, promoted a significant improvement in degradability of the fiber of sugarcane, compared with SCNT ($P < 0.05$). The means were 37, 42, 63 and 37% of ENDFD and 35, 39, 61 and 35% of EADFD, for SCNT, SCT1, SCT2 and SCT3, respectively. The treatment SCT3 resulted in no improvements in degradability ($P > 0.05$). The experiment suggests the adoption of treatment with 5% NaOH or 1.5% CaO, since they improved the degradability of the fiber. However, care should be used because they are, especially NaOH, corrosive compound. More experiments are necessary to evaluate the economic advantages of those treatments.

Key words: forage, fiber, in situ

W376 Effect of dietary fish oil level on selected strains of rumen bacteria in continuous culture fermenters. A. Ishlak*, A. A. AbuGhazaleh, P. Gudla, and D. Hastings, *Southern Illinois University, Carbondale.*

Previous studies have shown that adding fish oil (FO) to cows diet increased vaccenic acid (VA) accumulation in the rumen. Therefore, the objective of this study was to evaluate the effects of FO level on selected strains of rumen bacteria involved in trans fatty acids formation. A single-flow continuous culture system consisting of 4 fermenters was used in a 4 × 4 Latin square design with 4 9 d consecutive periods. Treatment diets were: 1) control diet (53:47 forage to concentrate; CON), 2) CON + FO at 0.50% (DM basis; FOL), 3) CON + FO at 2% (FOM), and 4) CON + FO at 3.5% (FOH). Alfalfa hay and grass hay (4:1 DM basis) were used as forage source. Fermenters were fed treatment diets 3 times daily at 120 g/d. Samples were collected

from each fermenter on d 9 of each period at 1.5, 3 and 6 h post morning feeding and then composited into one sample per fermenter. Data were analyzed as a Latin square using the PROC MIXED of SAS. Preplanned comparisons were linear, quadratic, and FO versus control. Increasing dietary FO level resulted in a linear decrease ($P < 0.01$) in acetate and isobutyrate concentrations. Propionate, butyrate, valerate and isovalerate concentrations were not affected ($P > 0.05$) by treatment diets. Concentrations of C18:0 in fermenters linearly decreased ($P < 0.01$) while concentrations of trans-10 C18:1 and VA linearly increased ($P < 0.01$) as dietary FO level increased. The DNA abundance for *Butyrivibrio fibrisolvens* (64.63, 32.20, 18.54, and 27.04 pg/36ng of total DNA for treatment diets 1 to 4, respectively), *Butyrivibrio* VA subgroup (1.54, 1.34, 0.50 and 0.70 pg/24 ng of total DNA), *Butyrivibrio* SA subgroup (39.79, 38.97, 19.16, and 18.89 pg/18 ng of total DNA) and *Butyrivibrio proteoclasticum* (1.46, 1.25, 0.40 and 0.60 pg/18ng of total DNA) linearly decreased ($P < 0.01$) as dietary FO level increased. Fish oil had no effect ($P > 0.05$) on the DNA abundance for *Anaerovibrio lipolytica* and *Ruminococcus flavefaciens*. In conclusion, FO effects on VA accumulation in the rumen may be explained in part by FO influence on *Butyrivibrio* species.

Key words: fish oil, fatty acids, bacteria

W377 Effects of rumen-protected niacin on lipid metabolism, oxidative stress and production of transition dairy cows during summer in Wisconsin. K. Yuan*[1], R. Shaver[1], S. Bertics[1], M. Espineira[1], and R. Grummer[2], *[1]Department of Dairy Science, University of Wisconsin-Madison, Madison, [2]Balchem Corporation, New Hampton, NY.*

The objective of this study was to evaluate the effects of a rumen-protected niacin product (RPN; NiaShure, Balchem Corp., New Hampton, NY) on lipid metabolism, oxidative stress and performance of transition dairy cows during the summer in Wisconsin. Thirty multiparous Holstein cows were paired according to expected calving date and randomly assigned to either RPN at 12/g/cow/d or control (C) un-supplemented diets. Treatment diets were fed from 21 d before expected calving through 21 DIM. Ambient temperature and humidity were monitored weekly to calculate temperature-humidity index, and individual cow rectal temperatures were measured weekly to characterize heat stress conditions during the experiment. Blood samples were taken on d −21, 1, 7, 14, and 21 relative to calving for analyses. Data were analyzed for a randomized complete block design using Proc Mixed of SAS with repeated measures. Pre- (10.2 vs. 11.7 kg/d) and postpartum (15.5 vs. 15.9 kg/d) DMI, milk yield (33.4 vs. 33.3 kg/d), milk fat percent (4.87 vs. 4.54%), milk protein percent (3.19 vs. 3.08%), linear somatic cell score (3.40 vs. 2.34) and rectal temperature (38.7 vs. 38.8°C) were unaffected ($P > 0.05$) by treatment. While body weight and body condition score decreased ($P < 0.01$) during the experimental period, no treatment effects ($P > 0.05$) were observed. Time ($P < 0.01$) and time × treatment ($P < 0.05$) effects were observed for plasma NEFA. On d 1 postpartum, NEFA reached 1138 ± 80 μEq/L for control cows compared with 698 ± 80 μEq/L for RPN cows. Cows in RPN group tended to ($P < 0.10$) have lower plasma NEFA concentrations than control cows on d 7 and 14 postpartum. Plasma glucose concentrations were similar ($P > 0.05$) for RPN and C. Plasma SOD was unaffected ($P > 0.05$) by treatment; a trend for a time effect ($P < 0.10$) on SOD was observed. In conclusion, under summer conditions in Wisconsin, dietary supplementation with 12g/d per cow RPN decreased plasma NEFA concentrations, but did not affect the anti-oxidant enzyme SOD, lactation performance or body temperature of transition dairy cows.

Key words: transition cows, rumen-protected niacin, oxidative stress

W378 Using rumen microbes for consolidated bioprocessing to convert plant fiber to ethanol or other biofuels. R. A. Kohn* and S.-W. Kim, *University of Maryland, College Park.*

Microorganisms that live in the cow's rumen orchestrate the fastest biological degradation of biomass on earth. For example, a strain of *Ruminococcus albus* readily degrades ligno-cellulose without pretreatment to produce acetate and ethanol. The objective of this study was to isolate fiber-digesting microorganisms from the rumen that produce ethanol to a high concentration. Rumen fluid was collected from a fistulated cow and enriched for fiber digesting microbes by incubating in media with timothy grass hay as the main substrate. Every 3 to 5 d a portion of the culture was transferred to new media. For some enrichments, the media contained 6% or 10% ethanol by volume. Individual strains that grew on Avicel, filter paper or cellobiose were isolated on agar from diluted enrichments. Several isolates could digest various types of biomass (e.g., cellulose, hemicellulose, grass) and convert it directly to ethanol. Microbial cultures from the rumen converted 1% cellobiose to 0.5% ethanol increasing ethanol concentration from initial 6.0% to more than 6.5%. A second addition of cellobiose further increased ethanol to more than 7.0%. The 16s rDNA sequences of 20 strains that converted cellobiose to ethanol were >97% homologous with at least one of *Clostridium bifermentans*, *C. sordelli*, *C. sporogenes*, *Enterococcus casselflavus*, *E. muntii*, *E. sangunicola*, *E. faecium*, *E. lactis*, *Pediococcus acidilactici*, *Lactobacillus mucosae*, or *Staphylococcus epidermidis*. Some of these bacteria also produced 1-butanol or 1-propanol from plant fiber. Additional bacteria (*Enterococcus avis*) produced high concentrations of alcohols from H_2 and CO_2 or CO. Microorganisms like these can produce ethanol directly or indirectly from waste biomass or grass (patent pending). The biomass is sterilized with heat and pressure and then simultaneously digested and fermented to ethanol.

Key words: biofuel, fiber digestion, cellulosic ethanol

W379 Fiber-digesting rumen bacteria that predominantly produce propionate or butyrate. S.-W. Kim* and R. A. Kohn, *University of Maryland, College Park.*

Most known fiber-digesting bacteria from the rumen of cattle produce acetic acid as a major end product. The present investigators isolated 2 new species of rumen bacteria that primarily produce propionate or butyrate directly from cellulose. When one strain was incubated with Avicel, 45% of the NDF disappeared within 4 d incubation (n = 2). A control culture of *Ruminococcus albus* (strain 7) resulted in 66% NDF disappearance in the same time frame (n = 2). The molar percentages of VFA produced by the new strain were 45% acetate, 55% propionate and 0% butyrate. A second bacterial strain digested 65% of Avicel NDF in 4 d (n = 2), and produced the molar percentages of VFA of 1.3% acetate, 3.5% propionate, and 86.2% butyrate. Both strains were gram-positive rods and no spores were observed. The propionate-producing strain was 96.08% homologous with *Selenomonas ruminantium*, and the butyrate-producing strain was 94.31% homologous with *Clostridium bifermentans* on the basis of 16S rDNA sequence. Neither closest-related species is known to digest cellulose and homology of 16S rDNA less than 97% suggests the isolates are members of unique species. Further characterization is needed. We propose that such microbes may be useful as probiotics or for conversion of plant fiber to VFA to be used as feeds or to produce other bioproducts.

Key words: fiber digestion, butyrate, propionate

W380 The combination of garlic oil and cinnamaldehyde modify rumen fermentation profile reducing methane production. P. W. Cardozo*[1], M. Blanch[1], M. D. Carro[2], and M. J. Ranilla[2], *[1]Novus International Inc., St. Charles, MO, [2]Deptartamento de Producción Animal, Universidad de León, León, Spain.*

The objective of this study was to analyze the effects of 3 doses (200, 300 and 400 mg/L of product) of NEXT Enhance 300 (NE300; containing cinnamaldehyde and diallyl disulfide) on in vitro ruminal fermentation. Batch cultures (120 mL serum bottles) of mixed ruminal microorganisms (BCRM) were used to test the effects of the additive. Three hundred mg of 60:40 alfalfa hay:concentrate diet was used as a basal substrate. The rumen fluid inoculum was obtained from 4 rumen-cannulated Merino sheep fed the same diet incubated in BCRM, mixed and strained through 4 layers of cheesecloth into an Erlenmeyer flask with an O_2-free headspace. Particle-free fluid was mixed with the buffer solution (no trypticase added) in a proportion 1:4 (vol/vol) at 39°C under continuous flushing with CO_2. Thirty mL of buffered rumen fluid were added into each bottle under CO_2 flushing and were sealed with rubber stoppers and aluminum caps, and incubated at 39°C for 24 h. After incubation total gas production was measured, and a gas sample was removed for methane production. Bottles were then uncapped, the pH was measured immediately, and samples for volatile fatty acid (VFA) and ammonia-N analyses were taken. Incubations were repeated on 4 different days to allow statistical analysis of results. Differences were declared at $P < 0.05$. Doses of 400 mg/L of NE300 decreased total VFA production and apparently fermented organic matter compared with control (CTR, no additive), thus indicating some inhibition of ruminal fermentation. NE300 at 200 mg/L reduced acetate:propionate ratio, methane production and methane/VFA ratio compared with CTR. NE300 at 300 mg/L reduced ammonia-N concentrations, methane production, acetate proportion, and acetate:propionate ratio, and increased propionate proportion compared with CTR. In conclusion, NE300 at 300 mg/L decreased methane production and increased propionate proportion without affecting total VFA production, and this would indicate a higher supply of energy for the host animal.

Key words: cinnamaldehyde, garlic oil, methane

W381 Ruminal kinetics of the diets with increasing levels of crude propane-1,2,3-triol. R. Mello*[1], C. M. M. Bittar[2], L. A. M. A. da Costa[3], R. C. de Araújo[2], and A. L. Abdalla[2], *[1]Universidade Federal de Santa Maria, Santa Maria, Rio Grande do Sul, Brazil, [2]Universidade de São Paulo - Escola Superior de Agricultura 'Luiz de Queiroz', Piracicaba, São Paulo, Brazil, [3]Universidade Federal de Roraima, Boa Vista, Roraima, Brazil.*

The objective was to assess the effect of different levels of propane-1,2,3-triol in the diets on rumen fermentation kinetics. Treatments were 0, 3, 6, 9, 12, 15, 18, 21 and 24% addition levels of crude propane-1,2,3-triol, co-product derived from the production of biodiesel fuels with palm oil (*Attalea maripa*), replacing corn on dry matter of the diets. A randomized block experimental design with 9 treatments and 3 replications was used, considering the incubation as blocking criterion. The ruminal kinetics was analyzed by in vitro gas production technique. Substrates were incubated with ruminal fluid buffered in triplicate. Gas production was followed over time (72h) in an automated system by radiofrequency (Ankom). Data were fitted by dual-pool logistic model and parameters estimated through the Gauss-Newton algorithm implemented in the NLIN procedure of SAS® software. The increase of propane-1,2,3-triol resulted in longest lag time: Lag (h) = 0.220+0.203x; $r^2 = 0.91$; i.e., a delay of 12 min in the latency period to each 1% of propane-1,2,3-triol. The maximum volume of gas produced (mL per gram of incubated organic matter) by degradation of soluble fraction ($V_1 = 84.71–2.415x$; $r^2 = 0.88$) and insoluble potentially degradable fraction ($V_2 = 78.62–2.264x$; $r^2 = 0.87$) reduced, while the specific rates of gas production by degradation of soluble fraction ($k_1 = 0.106$) and insoluble potentially degradable fraction ($k_2 = 0.031$) were constant as the propane-1,2,3-triol level raised in the diets. Total volume of gas produced also reduced, can be represented by equation: VT (V_1+V_2) = 163.34–4.680x ($r^2 = 0.99$). This suggests that propane-1,2,3-triol has an effect in vivo glycogen to be absorbed directly (intact) or indirectly (as propionate) by the ruminal epithelium. Volume of methane produced (mL/g OM) also decreased with increase of propane-1,2,3-triol in the diets ($CH_4 = 43.8633–0.3514x$; $r^2 = 0.56$). Thereby, addition of propane-1,2,3-triol can help in mitigation enteric methane and improve energy supply. Thus, the inclusion of propane-1,2,3-triol in ruminant diets may be an important alternative to mitigate greenhouse gas emissions.

Key words: 1,2,3-propanetriol, glycerol, glycerin

W382 Effect of various semi-arid medicinal plant essential oils on in vitro ruminal methane emission and feed fermentation efficiency. H. Jahani-Azizabadi*[1], M. Danesh Mesgaran[1], A. R. Vakili[1], and K. Rezayazdi[2], *[1]Dept. of Animal Science, Excellence Center for Animal Science, Faculty of Agriculture, Ferdowsi University of Mashhad, Mashhad, Khorasan Razavi, Iran, [2]Dept. of Animal Science, Faculty of Agriculture, University of Tehran, Karaj, Tehran, Iran.*

The objective of the present study was to investigate the in vitro effect of some semi-arid medicinal plant essential oils on ruminal methane emission and feed fermentation efficiency (FFE). A mixed diet of alfalfa hay: concentrate (50:50, based on DM) was provided. It was then ground to pass through a 1- mm screen. Approximately, 500 mg of the diet alone (as control) or plus essential oil of cinnamon, dill, oregano or peppermint (100 µL/ g DM) were placed into a 125 mL serum bottle (n = 6) containing 50 mL of buffered-rumen fluid (2:1). Rumen fluid was obtained from 3 ruminally fistulated sheep (49.5 ± 2.5 kg, body weight), before the morning feeding. Bottles were placed in shaking water bath for 24 h at 38.5°C. Gas produced of each bottle was recorded using a pressure transducer and then sampled. Gas pressure was converted into volume using an experimentally calibrated curve. Then, bottle content was filtered (42 µm) and residual was dried (60°C, 48 h) to determine dry matter disappearance (DMD). Data were statistically analyzed using SAS (V. 9/1) and Dunnett's test was used to compare the means ($P < 0.05$). Feed fermentation efficiency was estimated as FFE = DMD (g/kg)/cumulative gas (ml) produced at 24 h. Methane content of the produced gas was determined using gas chromatography procedure. Results indicated that these essential oils caused a significant ($P < 0.05$) decrease in methane and total gas produced over 24 incubation compared with those of the control (Table 1). The essential oil of Dill enhanced FFE ($P < 0.05$) compared with that of the control. Present results demonstrated a positive effect of the essential oils on ruminal fermentation pattern.

Table 1. In vitro effect of medicinal plant essential oils on total gas produced, methane emission and feed fermentation efficiency

Item	Control	Cinnamon	Dill	Oregano	Peppermint	SEM
Total gas (ml/ g DMD)	276.1	115.4 *	253.1 *	186.5 *	187.8 *	0.61
Methane (ml/ g DMD)	41.28	13.97 *	36.89 *	24.28 *	23.61 *	4.8
FFE	6.1	10.6 *	5.9	6.0	6.5	0.5

*Within a row, means with an asterisk differ significantly from the control (P< 0.05).

Key words: methane, essential oil, fermentation efficiency

W383 Rumen parameters and digestibility of diets with different levels of crude propane-1,2,3-triol. R. Mello*[1], C. M. M. Bittar[2], L. A. M. A. da Costa[3], P. B. Costa[4], J. K. Kirinus[1], and J. L. Nörnberg[1], *[1]Universidade Federal de Santa Maria, Santa Maria, Rio Grande do Sul, Brazil, [2]Universidade de São Paulo - Escola Superior de Agricultura 'Luiz de Queiroz', Piracicaba, São Paulo, Brazil, [3]Universidade Federal de Roraima, Boa Vista, Roraima, Brazil, [4]Universidade Estadual do Oeste do Paraná, Marechal Cândido Rondon, Paraná, Brazil.*

The objective was to assess the effect of increasing levels of propane-1,2,3-triol in the diets on rumen fermentation parameters and digestibility. Treatments were 0, 3, 6, 9, 12, 15, 18, 21 and 24% addition levels of crude propane-1,2,3-triol, co-product derived from biodiesel production with palm oil (*Attalea maripa*), replacing corn on DM of the diets. A randomized block experimental design with 9 treatments and 3 replications was used, considering the incubation as blocking criterion. Substrates were incubated with ruminal fluid buffered in triplicate. The digestibility was evaluated after 48 h and ruminal parameters were measured after 72 h of in vitro incubation. Data were analyzed in the SAS software. The table below shows the least squares means of dependent variables. The acetate and butyrate concentrations, acetate: propionate ratio, in vitro true digestibility (IVTD) of DM, organic matter (OM) and NDF coefficients decreased ($P < 0.05$); and the pH values increased ($P < 0.05$) as the propane-1,2,3-triol level raised in the diets. Thus, the inclusion of propane-1,2,3-triol with 35.6% purity in substitution of non-fibrous carbohydrates on DM of ruminant diets negatively affect the ruminal fermentation parameters and digestibility, but can be an important alternative of destination to the surplus generated from biodiesel chain.

Table 1. Least squares means

Variables	*P*-value	Equation	r^2
pH	0.0016	5.7953+0.0144x	0.92
NH3-N, mg/dL	0.7898	17.7	-
Microbial protein, mg/L	0.0859	273.0	-
C2, mM/mL	0.0106	37.6280-0.5702x	0.51
C3, mM/mL	0.9017	24.0	-
C4, mM/mL	0.0288	7.9102-0.0893x	0.93
VFA, mM/mL	0.0699	64.8	-
C2:C3	0.0003	1.6237-0.0272x	0.66
IVTD-DM, %	0.0001	77.7867-0.2322x	0.91
IVTD-OM, %	0.0001	75.3363-0.3033x	0.93
IVTD-NDF, %	0.0001	22.0815-0.6083x	0.80

Key words: 1,2,3-propanetriol, glycerol, glycerin

W384 Dose response effects of a garlic oil chemical compound propyl-propyl thiosulfate (PTSO) on rumen microbial fermentation in a dual flow continuous culture system. A. Foskolos*[1], A. F. De Souza[1], M. Rodriguez-Prado[1], A. Ferret[1], D. Bravo[2], and S. Calsamiglia[1], *[1]Animal Nutrition, Management and Welfare Research Group, Universitat Autònoma de Barcelona, Bellaterra, Spain, [2]Pancosma, Geneva, Switzerland.*

Oxy-propyl-thiosulphate (PTSO) is an active molecule purified from garlic bulb. The objective of this experiment was to investigate the effects of increasing doses of PTSO on ruminal fermentation in vitro. Eight dual flow continuous culture fermentors inoculated with rumen liquid from a dairy cow were used in 2 replicated periods (blocks). Temperature (39 ◦C), pH (6.4), and liquid (0.10/h) and solid (0.05/h) dilution rates were maintained constant. Fermenters were fed 95 g DM of a diet (21.6% corn silage, 43.6% dehydrated alfalfa, 11.4% soybean meal, 31.6% corn grain and 0.83% vitamin-mineral mix, DM basis) in 3 equal portions daily and treatments were no additive (CTR) and 50, 100 and 150 mg/L of PTSO. Each experimental period consisted of 5 d for adaptation and 3 d for sampling. Samples were collected 2 h after the morning feeding and from the 24-h effluent of the 3 sampling days. Results were analyzed with PROC MIXED and significance was declared at $P < 0.05$. Contrasts were used to analyze for linear, quadratic and cubic responses. Total VFA and molar proportions of acetic and propionic acids concentrations and the acetate to propionic acid ratio responded quadratically with higher total VFA and propionic acid and lower acetic acid concentrations and acetic to propionic ratio in the intermediate doses. Branch-chained VFA decreased linearly by increasing doses of PTSO and ammonia-N concentration was not affected by treatments. In the samples from the 24-h incubations, only the total VFA and BCVFA concentrations responded quadratically and linearly by increasing dose of PTSO, respectively. Results suggest the potential of PTSO to modify rumen fermentation in a direction consistent with better energy utilization.

Key words: essential oils, garlic, fermenters

W385 Estimation of protein fractions of tropical grasses by near infrared reflectance spectroscopy. R. G. Basurto[1], G. Buendia-Rodriguez[1], E. R. Ramírez[1], M. A. Barron[2], J. J. G. Bustamante[3], R. E. Santos[4], J. J. M. Maldonado[5], and S. S. Gonzalez-Muñoz*[6], *[1]CENID Fisiologia Animal-INIFAP, Queretaro, Mexico, [2]CE Huimanguillo-INIFAP, Tabasco, Mexico, [3]CE Santiago Ixcuintla-INIFAP, Nayarit, Mexico, [4]CE Iguala-INIFAP, Guerrero, Mexico, [5]CE Rosario Izapa-INIFAP, Chiapas, Mexico, [6]Colegio de Postgraduados, Montecillo, Estado de Mexico, Mexico.*

The aim of the study was to investigate the use of near infrared reflectance spectroscopy (NIRS) as an alternative method to estimate crude protein (CP), degradable (DIP) and undegradable (UIP) intake protein of tropical grasses. A total of 945 samples of 13 species were collected by clipping at different ages of re-growth (28, 42, 56, 70 and 84 d) in plots in 4 states (Chiapas, Guerrero, Nayarit and Tabasco) in Mexico. The grass species included were *D. aristatum*, *C. dactylon*, *H. altissima*, *U. brizantha*, *D swazilandensis*, *C. plectostachyus*, *U. maximum*, *B. humidicola*, *C. echinatus*, *A. gayanus*, *B. brizantha* x *ruziziensens*, *D. eriantha* and. DIP was estimated as the protein fraction that disappeared after incubation with a protease ofand UIP was the remaining protein in the sample. Samples were scanned using a spectrophotometer Nicolet FT-IR 6700 (Thermo Fisher Scientific, Inc.) over a wavelength range of 1000 to 2500 nm in reflectance. Data were stored as log (1/R) at intervals of 4 nm. Calibration equations were developed using modified partial least squares with the TQ Analyst

program (v8.0). The selection of the equations was based on: the coefficient of determination of calibration (R^2cal), the minimization of the standard error of calibration (SEC), the standard error of cross validation (SECV), and the ratio SECV/SD. If the ratio was >0.33, then calibration had a low predictive power. The best NIRS models obtained are shown in Table 1. It is concluded that NIRS calibration for PC has good precision, but DIP and UIP calibrations are less precise.

Table 1. Laboratory data and calibration and validation statistics of NIRS models

ITEM (% of DM)	N	Mean	Range	SD[1]	R^2cal	SEC	SEP	SECV	Ratio
CP cal[2]	675	7.98	2.7 - 20.7	3.01	0.94	0.79			
CP val[3]	244	7.91	3.6 - 18.7	2.85			0.90	0.94	0.31
DIP cal	688	4.49	1.1 - 11.2	1.93	0.86	0.71			
DIP val	216	4.63	1.1 - 11.5	1.92			0.83	0.84	0.43
UIP cal	680	3.44	1.0 - 8.6	1.32	0.90	0.42			
UIP val	241	3.39	1.2 - 7.5	1.20			0.48	0.45	0.35

[1]SD = standard deviation.

[2]CPcal=Calibration set.

[3]CPval=Validation set.

Key words: NIRS, protein degradation, tropical grasses

W386 Commodity blood meal variation: digestible RUP and amino acids. R. Brown*[1], D. Stucker[1], J. R. Knapp[2], and N. R. St-Pierre[3], *[1]Venture Milling, Salisbury, MD, [2]Fox Hollow Consulting, LLC, Columbus, OH, [3]The Ohio State University, Columbus.*

The objective was to determine the variation in nutrient availability of commodity blood meal as a source of rumen undegradable protein (RUP). The nutritional value of RUP sources is based on their ability to deliver amino acids for absorption in the small intestine and is affected by the protein content, the rumen degradability of the protein, and the post-ruminal digestibility of the RUP. To date, a modification of the procedure of Calsamiglia and Stern (1995) appears to be the best in predicting the nutritional value of ingredients rich in RUP. This 3-step procedure consists of an in sacco incubation in rumen-fistulated cows followed by sequential in vitro protease digestions with pepsin and pancreatin. The residues from the incubation and digestions can be analyzed for amino acids, and amino acid digestibilities determined. The procedure has been modified in our laboratory by partial standardization of enzymes, use of fuzzy standards, and Bayesian statistics to adjust for inter-assay variation. Amino acid analyses were performed by the University of Missouri Agricultural Experiment Station Chemical Laboratories. Commodity blood meal samples (n = 265, porcine and bovine) were obtained over the past 5 years from commercial sources across the US The results using this procedure showed reasonably consistent crude protein contents (90.1 ± 3.7%, mean ± S.D) on an as fed basis. However, RUP (% of CP) was more variable (76.8 ± 14.8%CP) and RUP digestibility was highly variable (64.6 ± 23.1%RUP). No relationship between RUP and RUP digestibilities was observed. Also, average RUP digestibility was lower than the 80% reported for ring-dried blood meal in the 2001 NRC Requirements for Dairy Cattle. Amino acid digestibilities were generally similar to RUP digestibility (65 ± 24%), with the exception of lysine digestibility, which was consistently lower (56 ± 27%). Lysine digestibility approached 0% at RUP digestibility of 20%. These data provide a significant improvement in our knowledge regarding the digestibility and nutritional value of commodity blood meal and should improve feed library values found in ration formulation software currently used throughout the dairy industry.

Key words: blood meal, lysine, RUP

W387 Tannin content and rate of ruminal protein degradation of legume hays. S. Colombini*[1], G. A. Broderick[2], J. H. Grabber[2], and W. K. Coblentz[3], *[1]University of Milan, Milan, Italy, [2]U.S. Dairy Forage Research Center, Madison, WI, [3]U.S. Dairy Forage Research Center, Marshfield, WI.*

This study evaluated ruminal protein degradation rates of legume hays that varied in tannin content. Two cuttings of 5 varieties of birdsfoot trefoil (*Lotus corniculatus*) that were selected for different tannin contents, but similar NDF and CP, and Spredor-4 alfalfa (control) were conserved as hay. Samples were ground (1 mm) and analyzed for chemical composition and tannin content. Protein degradation rate was determined using ruminal inocula in the Michaelis-Menten inhibitor in vitro method; 3 incubations were performed. Extent of degradation was estimated from net release of N in ammonia (phenol-hypochlorite colorimetry) plus amino acids and small peptides (o-phtaldialdehyde colorimetry). Samples also were incubated in situ to estimate RDP. Data were analyzed using mixed procedure of SAS and are in the table. There were differences among trefoils in tannin content with the greatest values for Dewey and Goldie and lowest for Exact. Within cut, alfalfa had the most rapid degradation rate and Exact had the numerically greatest rate among trefoils. Rate was significantly affected ($P < 0.001$) by variety and cutting; there also was a variety*cutting interaction ($P = 0.017$). Regression between degradation rate and tannin content was: $y = -0.0027 (\pm 0.0007) x + 0.231 (\pm 0.019)$ ($r^2 = 0.61$). Regression between in situ RDP and tannin content was: $y = -0.194 (\pm 0.024) x + 84.0 (\pm 0.68)$ ($r^2 = 0.87$). Soluble N content must be determined to compute RDP within the in vitro method. Degradation rates were more rapid for second cutting hays; this may be explained partly by greater NDIN content in hays from first vs. second cutting (21 vs. 18% of total N).

Table 1. Results

Variety	Cut	Tannin (g/kg DM)	NDF (% DM)	Total N (% DM)	NDIN (% total N)	In vitro rate(/h)
Dewey	1	36.8	36.7	3.05	26.9	0.126
Georgia	1	23.0	37.1	3.07	20.8	0.140
Exact	1	15.6	38.2	3.13	18.2	0.150
Lotanova	1	27.8	38.2	3.00	20.7	0.134
Goldie	1	36.7	38.1	2.91	23.2	0.137
Alfalfa	1	0	42.0	3.11	16.6	0.207
Dewey	2	40.2	39.6	2.88	21.5	0.141
Georgia	2	27.0	38.8	3.23	15.2	0.149
Exact	2	20.1	38.3	3.30	18.8	0.173
Lotanova	2	31.6	36.8	3.30	16.3	0.172
Goldie	2	38.8	37.9	3.20	20.5	0.150
Alfalfa	2	0	38.7	3.16	15.4	0.290

Key words: protein degradation, birdsfoot trefoil, tannins

W388 Evaluation of acid-insoluble ash and indigestible neutral-detergent fiber as total tract digestibility markers. C. Lee*, A. N. Hristov, T. Cassidy, and K. Heyler, *Pennsylvania State University, University Park.*

The objective of this experiment was to evaluate acid insoluble ash (AIA) and indigestible NDF (INDF) as intrinsic digestibility markers in comparison with total fecal collection (TC). The experiment was part of a larger experiment, which involved 8 Holstein cows (102 ± 28 DIM; 26.0 ± 0.79 kg/d DMI; 40.9 ± 1.46 kg/d milk yield). The experimental design was a replicated 4 × 4 Latin square with the following treatments: 15.6% crude protein (CP) diet (HighCP), 14.0% CP diet (LowCP), 14.0% CP diet supplemented with a ruminally protected Lys (AminoShure-L, 100 g/cow/d; LowCPLys), and 14.0% CP diet supplemented with ruminally–protected Lys plus a ruminally–protected Met (Mepron, 24 g/cow/d; LowCPLysMet). Each period consisted of 14 d of adaptation and 7 d of sample collections. Total feces were collected for 5 consecutive days during each period. Composite TMR and fecal samples were analyzed for nutrients, AIA (digestion with 2 N HCl) and INDF (12 d ruminal incubation in 25μm pore size bags). Apparent total tract digestibilities of all nutrients were greater for AIA compared with INDF and TC (Table 1). Digestibility estimated using INDF or TC were not different. There was method × treatment interaction (TC and INDF) for all nutrients (P = 0.02 to 0.07), except CP. Examination of the method × treatment mean comparisons revealed no significant differences between TC and INDF. In conclusion, using AIA as a digestibility marker yielded lower fecal output estimates and consequently greater apparent digestibility values for all dietary nutrients compared with TC or INDF. Apparent total tract digestibility of nutrients did not differ between TC and INDF. In the conditions of this experiment, INDF was a more appropriate intrinsic digestibility marker than AIA.

Table 1. Comparisons of methods for determining total tract apparent digestibility

	Method				
Item	TC	INDF	AIA	SEM	*P*-value
DM	61.0[b]	59.4[b]	67.9[a]	1.10	<0.001
OM	62.2[b]	60.8[b]	69.0[a]	1.13	<0.001
NDF	40.4[b]	38.2[b]	51.1[a]	1.21	<0.001
ADF	35.5[b]	33.0[b]	47.0[a]	1.35	<0.001
CP	52.4[b]	50.4[b]	60.8[a]	1.66	0.002

Key words: dairy cow, digestibility, intrinsic marker

W389 Nutritional value of *Smallanthus sonchifolius* and *Moringa oleifera* tropic forage as alternative in ruminant feeding. L. C. Bernal Bechara*, *Universidad de La Salle, Bogotá, Colombia.*

The aim objective was to evaluate the nutritional quality of *Smallanthus sonchifolius* and *Moringa oleifera* to determinate their physical and chemical properties as a tool to predict its nutritive value. Two treatments were evaluated: a. *Smallanthus sonchifolius* leaves and b. *Moringa oleifera* leaves; with 4 replications per forage type. Physical properties evaluated were density (g/ml), solubility (%), the water holding capacity (g/g) and buffering capacity (meq). The samples were reduced to a particle size of 1 mm. Chemical fractions were analyzed for dry matter (DM, %), crude protein (CP, %), neutral detergent fiber (NDF, %), acid detergent fiber (ADF, %), ether extract (EE; %), total digestible nutrients (TDN,%), net energy NE of lactation, maintenance and gain (NEl, NEm, NEg; Mcal/kg) and in vitro digestibility of dry matter IVDDM (%). A completely randomized was evaluated experimental design. The data of the selected variables was analyzed using by procedure a GLM model and differences between means treatments were analyzed using Tukey in the SAS Statistical package. Density, water absorption capacity and buffering capacity did not difference (P > 0.05) between forages types, but solubility was greater (P < 0.001) in *Smallanthus sonchifolius* (14%) than *Moringa oleifera* (7%). There was no difference in DM, CP and EE between forages, but NDF and ADF were greater in *Moringa oleifera* than *Smallanthus sonchifolius* (61.24% vs. 42.77% FDN; 38.96 vs. 26.33% FDA, respectively). TDN, net energy and IVDDM was in *Smallanthus sonchifolius* than *Moringa oleifera* (69.47 vs. 60.56% TDN; 57.6 vs. 48% IVDDM; 1.5 vs. 1.3 Mcal/kg NEl; 1.7 vs. 1.4 Mcal/kg NEm; 1.0 vs. 0.7 Mcal/kg NEg). These physical and chemical characterization results suggest that leaves of *Smallanthus sonchifolius* are potential forage to be used in cattle feeding, because of its low fiber content and greater IVDDM than *Moringa oleifera*.

Key words: *Moringa oleifera*, nutritional quality, *Smallanthus sonchifolius*

W390 Postprandial hypoglycemia after feeding of alcohol-fermented apple pomace silage. M. Kondo, H. Moriuchi, J. Fang, H. Suzuki, and M. Matsuzaki*, *Hirosaki University, Hirosaki, Aomori, Japan.*

Four Suffolk ewes were used to study the effect of feeding apple pomace silage (APS) with different ethanol content on postprandial glucose homeostasis in a 4 × 4 Latin square design trial. Ewes were fed alfalfa hay cube and either a concentrate (Ctrl), low-ethanol APS (L-APS), high-ethanol APS (H-APS) or the concentrate supplemented with equal amount of ethanol in H-APS (+EtOH). Alfalfa hay cube and the concentrate or APS provided half of TDN requirement for maintenance. The 70% apple pomace, 6% soybean meal, 12% wheat bran and 12% beet pulp (as FM basis) were mixed for APS preparation to contain equal amount of TDN and CP as the concentrate. Ethanol content of APS was manipulated by ensiling with either fresh apple pomace, which has slight amount of ethanol, or alcohol-fermented apple pomace, which left on 2-mo after production. The resultant L-APS and H-APS contained 1.4 and 3.3% of ethanol, respectively. At the end of each 14-d period, blood samples were collected via catheters before and after the morning feed for 120 min and then another 120 min after intravenous insulin challenge (0.1Î1/4U/kg BW). Plasma glucose was assayed for all samples and the concentrations of Insulin, glucagon, ethanol and D-3-Hydroxybutyric acid (DHBA) were assayed for samples for the first 120 min. The area under or upper the curve (AUC) of each plasma measurement was calculated. Plasma glucose was decreased and ethanol level increased after ingesting ethanol in the L-APS, H-APS and +EtOH treatments (P < 0.05). The AUCs of plasma glucose and ethanol in H-APS treatment were greater (P < 0.05) than the Ctrl, with the L-APS and +EtOH intermediate. Plasma insulin level was elevated only in the L-APS after feeding (P < 0.05) while glucagon level was unchanged by feeding in all treatments. Plasma DHBA was gradually increased after feeding and that in the L-APS was higher than other treatments (P < 0.05). The glucose AUC after insulin challenge was greater (P < 0.05) in the Ctrl than other treatments. A significant correlation between the AUCs of plasma glucose and ethanol (P < 0.05) suggest that postprandial hypoglycemia after APS feeding is due primarily to ingestion of ethanol.

Key words: apple pomace, glucose, ethanol

W391 Inclusion of substrate of *Pleurotus ostreatus* on kinetics of in vitro fermentation of *Brachiaria* hay. S. L. S. Cabral Filho*[1,2], R. S. Oliveira[1], R. A. Mandarino[1], and C. A. Lobo[1], *[1]Universidade de Brasília, Brasilia, Distrito Federal, Brasil, [2]Fazenda Experimental Agua Limpa, Brasilia, Distrito Federal, Brasil.*

The demand for increased and faster production of food in the world makes the production of mushrooms an important alternative. However, each 80g of mushrooms produced resulted in 100g of substrate residue. The aim of this study was to assess the inclusion of the substrate production of *Pleurotus ostreatus* on in vitro fermentation of hay-based diet of *Brachiaria brizantha* for ruminants, as well as measuring gas production and rumen kinetics for different levels of inclusion of substrate. The experiment was conducted using a semi-automatic gas production technique, the rumen inocula were collected from 3 fistulated bovines, grazing *Brachiaria* pasture. We used a *Brachiaria brizantha* hay and exhausted substrate for *Pleurotus* production, for the composition of the treatments, which were defined as: ES (100% of exhausted substrate), BH (100% *Brachiaria* hay), ES5 (5%ES +95% BH), ES20 (20%ES +80%BH) and SE30 (30%ES +70%BH). The experiment was conducted in a 5 × 3 factorial with 5 treatments and 3 inocula (3 donor animals). The dry matter degradability (DMD) was determined after 96h of fermentation. No significant differences among treatments were observed on the potential gas productions (A) BH, ES5, ES20 and ES30. The averages were 262.6, 284.3, 256.6 and 261.7 mL, respectively ($P > 0.05$), showing that the inclusion of the substrate did not affect the fermentation of *Brachiaria* hay. The ES treatment presented a lower potential gas production and DMD (165.9 mL and 52%, $P < 0.05$) demonstrated the lower quality of the exhausted substrate compared with hay, despite the presence of enzymes that degrade the cellulose in the mycelium of *Pleurotus*. The ES treatment had a shorter lag phase (L = 2.6 h, $P < 0.05$), which can be attributed to higher concentration of soluble carbohydrates due to higher proportion of wheat meal and mycelium in this treatment. The inclusion of the exhausted substrate did not impair microbial degradation of hay and it by-product can be used in ruminant feed.

Key words: gas production, roughages, mushrooms

W392 Evaluation of protein fractions of tropical grasses by near infrared reflectance spectroscopy. R. G. Basurto[1], G. Buendía-Rodríguez[1], S. S. González-Muñoz*[6], R. E. Ramirez[1], M. A. Barrón[2], G. J. J. Bustamante[3], R. E. Santos[4], M. J. J. Maldonado[5], and C. J. A. Bonilla[3], *[1]CENID Fisiología y Mejoramiento Animal, Ajuchitlán, Querétaro, [2]CE Huimanguillo–CIRG, Huimanguillo, Tabasco, [3]CE Santiago Ixcuintla–CIRPAS, Nayarit, [4]CE Iguala–CIRPAS, Iguala, Guerrero, [5]CE Rosario Izapa–CIRPAS, Tapachula. INIFAP–México, [6]Colegio de Postgraduados, Montecillo, Estado de México, México.*

The aim of study was to evaluate the use of near infrared reflectance spectroscopy as alternative method to determine CP, and degradable (DIP) and undegradable (UIP) intake protein of tropical grasses. Nine hundred and 23 samples of 13 species were collected by clipping sampling at different ages of re-growth (28, 42, 56, 70 and 84 d) in plots in the states of Chiapas, Guerrero, Nayarit and Tabasco, México. The species were *D. aristatum*, *C. dactylon*, *H. altissima*, *U. brizantha*, *D swazilandensis*, *C. plectostachyus*, *U. maximum*, *B. humidicola*, *C. echinatus*, *A. gayanus*, *B. brizantha* × *ruziziensens*, *D. eriantha*, and *U. mutica*. DIP was estimated as the protein fraction that disappeared after incubation with a protease, and UIP was equal to the remaining protein in the samples. The samples were scanned at a spectrophotometer Nicolet FT-IR 6700 (Thermo Fisher Scientific, Inc.) over a wavelength range from 1,000 to 2,500 nm in reflectance; data were stored as log (1/R) at intervals of 4 nm. Calibrations equations were developed using modified partial least squares with TQ Analyst program (v8.0). The selection of the equations was based on: coefficient of determination of calibration (R^2 cal), the minimization of standard error of calibration (SEC) and standard error of cross validation (SECV) and ratio SECV/SD; if the ratio is >0.33, then calibration had a low predictive power. It is concluded that NIRS calibration for PC showed good accuracy, but calibrations were less accurate for DIP and UIP.

Table 1.

		Chemical analysis			Statistics				
Item	N	Mean	Range	SD	R^2 cal	SEC	SEP	SECV	Ratio
Crude protein (DM)									
Calibration	677	7.98	1.0–8.6	3.01	0.94	0.79			
Validation	244	3.01	1.2–7.5	2.05			0.90	0.94	0.31
DIP (% DM)									
Calibration	681	3.44	1.0–8.6	1.32	0.91	0.39			
Validation	242	3.39	1.2–7.5	1.20			0.46	0.44	0.34
UIP (% DM)									
Calibration	689	4.57	1.1–13.0	2.06	0.86	0.76			
Validation	212	4.61	1.1–11.5	1.93			0.87	0.82	0.41

SD = Standard deviation.

Key words: NIR, protein fractions, tropical grasses

W393 The effect of storage structure on haylage and corn silage fermentation. C. Rasmussen*, D. Petri, S. Jens, and A. H. Smith, *Danisco USA, Waukesha, WI.*

Decreasing nutritional and dry matter losses of ensiled forages has always been an important topic of research and debate. Many factors contribute to silage quality (time of harvest, packing density, aerobic exposure, etc.), but one factor often overlooked is storage structure. The objective of this study was to determine if certain storage structures produce better quality silage and if certain storage structures are better suited for specific crops. Samples used in this study included 170 haylage and 242 corn silage stored in bunkers, bags, upright silos, or piles received from 2009 and 2010 and originating from commercial farms within the United States, primarily the upper Midwest. Samples were analyzed for pH, dry matter, lactate, acetate, ethanol, yeast, and mold. Data was analyzed as a 2 × 4 factorial Anova using Proc Mixed procedure as well as Proc corr procedure for correlation analysis (SAS 9.1.3). The mean pH for corn silage and haylage at 3.96 ± 0.031 and 4.76 ± 0.036 respectively would be considered high for well-ensiled crops reflecting the fact that samples received for analysis were generally those of questionable quality. All other measured parameters were within normal ranges. The pH was significantly higher for silos ($P \leq 0.05$), which was correlated with significantly higher levels of spoilage organisms, both yeast and mold ($P \leq 0.05$). Further investigation is needed to determine whether fermentation is more effective in bunkers, piles and bags and if the samples obtained for analysis from these structures are from deeper regions with less oxygen exposure than silo samples.

Key words: silage, corn, haylage

W394 The effect of direct fed lactic acid bacteria combined with monensin. R. C. de Souza*[1], R. B. Reis[1], J. Holliday[2], E. Rabelo[4], and R. A. Filho[3], *[1]Federal University of Minas Gerais, Belo Horizonte, Minas Gerais, Brasil, [2]Chr. Hansen - Animal Health and Nutrition, Hørsholm, Denmark, [3]Chr. Hansen - Animal, Valinhos, São Paulo, Brasil, [4]Rehagro Team Consultation, Belo Horizonte, Minas Gerais, Brasil.*

Monensin is widely accepted in the American cattle industry, but alternatives to ionophores such as direct fed microbials (DFM) are receiving increased awareness. The question is, if the 2 combined can have a synergistic effect. To address this issue, both a continuous culture experiment and an in vivo study were conducted. The in vivo study included 40 multiparous Holstein cows (milk yield between 8.000 and 10.000 kg) which were supplemented with monensin and a DFM (contaning *E. faecium* and *S. cerevisiae*, Probios TC, Chr. Hansen). The continuous culture trial included a diet with a forage:concentrate ratio of 50:50 combined with four treatments (No additive, DFM, Monensin, and DFM+Monensin). The in vivo trial tested the effect of the DFM on milk yield and milk composition following three alternative applications: included solely pre-partum, solely post-partum or both pre and post-partum. Post-partum, the cows were fed a diet containing corn silage (forage:concentrate ratio of 50:50) and sufficient monensin to supply 16 ppm in the diet DM. The results from the continuous culture showed that monensin significantly ($P < 0.05$) reduced NDF digestibility compared to control, while adding the DFM diminished this effect. There were no treatment effects on the molar proportion of the VFA of any of the treatments. In the in vivo study, supplementing the DFM on diets with monensin, resulted in an additional increase ($P < 0.01$) in milk yield (32.27, 28.37, 35.65 and 36.20, respectively for treatments no additive, DFM pre-partum, DFM solely postpartum and DFM pre and post-partum), milk fat and protein production in both the post-partum and the post and pre-partum period. A negative effect on milk yield ($P < 0.01$) was observed when feeding DFM solely pre-partum. The DFM supplementation only after parturition was better for the increasing milk production and its quality according to composition compared to treatments with no additive and DFM pre-partum.

Key words: transition, DFM, monensin

W395 Morphological response of the ruminal and omasal mucosae to the variation in the energy of the diet. R. F. de Lima, J. C. de Resende Júnior*, J. L. P. Daniel, S. de F. Costa, M. B. Moreira, and M. G. Cardoso, *Universidade Federal de Lavras.*

The rumen capacity to absorb volatile fatty acids (VFA) is proportional to the extent of their absorptive surface which responds positively to the direct and indirect stimulation of VFA. There are indications that the wall of the omasum, which in dairy cows is responsible for about 40% of absorption of VFA, also could respond to the same stimuli of proliferation of the rumen wall. Aiming to test this hypothesis we compared the morphology of fragments of rumen and omasum obtained by biopsy. Four nonlactating cows and not pregnant, not defined breeds and unknown ages were sequentially fed 2 diets. One diet only of chopped grass (CG) and other with concentrate plus chopped grass (CCG). In the first 18 d of the experiment the animals were fed CG diet. In subsequent 18 d the cows received the CCG diet. Then were fasted for 72 h. Biopsies of the ventral sac of the rumen were made at the end of the period of the CG diet, at 4 and 18 d of the CCG diet and at end of fasting period. After fasting the cows were fed with the CCG diet again by 18 d with biopsies on d 4, 12 and 18. Data were analyzed as repeated measures considering the effect of cow, compartment, diet, possible interactions and error. The DMI and the TDN intake were higher ($P < 0.001$) in periods in which the animals were fed with the CCG diet. The mitotic index (MI) of the basal layer in the epithelium of the rumen and of the omasum were higher ($P = 0.01$ for interaction between compartment and diet) in the fourth days of CCG diet and the same occurred with the VFA concentration in the rumen ($P <$ 0,001). There was positive correlation between MI of the rumen and the omasum ($R^2 = 0.66$; $P < 0,01$) . The width of the rumen papillae varied among treatments and was greater at 18 d of CCG diet ($P < 0.001$), which revealed proliferative stimulus of the rumen wall. The similarity ($P = 0.67$) in thickness of the not keratinized layers of the epithelium and the positive correlation between the MI of the rumen and of the omasum, indicate that the stimulation of cell division caused by the energy content of the diet has simultaneous effect in both compartments. However the omasum seems respond more quickly to the stimulus.

Key words: acidosis, ruminant stomach morphology, transition diet

W396 Determination of solubility of alternate magnesium sources and their impact on pH with an optimized in vitro rumen fermentation protocol. S. J. Taylor*[1], J. Apajalahti[2], E. Pennala[2], C. Murphy[1], and T. Rinttilä[2], *[1]Celtic Sea Minerals Ltd., Cork, Ireland, [2]Alimetrics Ltd., Espoo, Finland.*

Absorption of Mg from the rumen of mature ruminants is dependent on its concentration in the liquid phase. An in vitro model of rumen function modified to investigate the mode of action of materials known to affect pH (Taylor et al. 2011) was used to investigate the solubility of different sources of Mg. Simulation protocol. The simulation used 1 g (DM) feed (50% grass silage, 40% barley meal, 10% soy). The bicarbonate and phosphate buffer (Agriculture Handbook, Vol 379, USDA 1970) was diluted 1:4 with 0.9% NaCl. The simulation was inoculated with 5% of fresh, strained rumen fluid from a fistulated cow on a high energy diet and continued for 9 h in triplicate. Anaerobic techniques were applied throughout. Ten treatments included negative control, Acid Buf alone (50 mg/40mL) and Acid Buf plus 8 different sources of Mg oxide (15mg/40mL). Products referred to as country codes in the table were obtained from international feed industry. Analyses. Mg and pH were determined at indicated time points from inoculation. Soluble Mg was analyzed by ICP. Results were compared with the volume of 0.1N HCl consumed by 0.25 g of product in 2 h at pH 5.5 using Titrino Automated pH meter. Inclusion of Acid Buf reduced the drop of pH. Mg was released into solution at a rate dependent on the source and correlated with the titration. Release of Mg significantly suppressed the decline of pH.

Table 1. Results

	2 h	9 h	9 h		Titration with 0.1 *N* HCl
Treatment	Mg (mg/L)	Mg (mg/L)	% Mg solubility	pH	ml*
Control	29^{d}	44^{c}		5.18^{d}	
Acid Buf (AB)	70^{c}	123^{b}	99	5.44^{c}	
AB & Norway	173^{b}	313^{a}	101	5.85^{a}	110.7
AB &S Africa	90^{c}	150^{b}	14	5.62^{b}	16.5
AB & Aus	81^{c}	130^{b}	4	5.61^{bc}	3.7
AB & CNA	81^{c}	177^{b}	28	5.68^{ab}	8.8
AB & UK	84^{c}	160^{b}	20	5.61^{bc}	9.04
AB & Spain	73^{c}	140^{b}	9	5.59^{bc}	16.74
AB & US	92^{c}	173^{b}	27	5.69^{ab}	86.8
AB & Ire	197^{a}	297^{a}	92	5.82^{a}	110.8

*HCl consumed by products (excluding Acid Buf) Numbers with the same suffix are not significantly different ($P = 0.05$).

Key words: magnesium, rumen, solubility

W397 Influence of *Salix babylonica* and *Leucaena leucocephala* extracts on ruminal fermentation activities in growing lambs. R. P. Hernández[1], A. Z. M. Salem*[1], R. R. Rojo[1], and D. L. Camacho[2], *[1]Universidad Autónoma del Estado de México, Centro universitario UAEM – Temascaltepec, Km 67.5 Carr. Toluca – Tejupilco Estado de México CP 51300, México, [2]Universidad Autónoma de Guerrero, Facultad de Medicina Veterinaria y Zootecnia, Carretera Altamirano – Iguala Km 3 CP 40660 Cd. Altamirano Guerrero, México.*

Sixteen Katahdin × Pelibuey crossbreed male lambs 3 to 4 mo of age and 24 ± 0.3 kg BW were used to study effects of administration of extracts rich in secondary compounds from *Salix babylonica* (SB) and *Leucaena leucocephala* (LL) on ruminal pH and protozoal account as well as total and individual VFA and ammonia N concentrations. After 2 wk of adaptation consuming a total mixed ration (TMR; 219 and 141 g/kg of crude protein and NDF, respectively), lambs were weighed and distributed by BW into 4 groups of 4 lambs/group in a completely randomized design with: Control group TMR; SB group TMR (as Control plus *S. babylonica* extract at 30 mL/ lamb /d); LL group TMR (as Control plus *L. leucocephala* extract at 30 mL/ lamb/d); SBLL group TMR (as Control plus 30 mL/lamb/d of *S. babylonica* and *L. leucocephala* extracts in a (1:1, v:v) mixture) for a 63-d experiment. Data were analyzed using the MIXED procedure for repeated measures. A weekly stock volume of the individual extracts as well as their 1.1 mixture were prepared for daily administration. Extracts were orally administered before the 08:00 h feeding to each lamb. pH values were increased ($P = 0.004$) with SBLL (1:1, v:v) compared with other groups. Protozoal amounts were no affected ($P = 0.531$) by the administration of extracts to lambs. Individual extracts (SB or LL) increased ($P = 0.0435$) the propionic acid concentration versus control or SBLL groups. Ruminal acetic acid ($P = 0.5053$) and total VFA ($P = 0.2709$) were not affected by extracts administration, while butyric acid ($P = 0.0435$) and ammonia N concentrations ($P = 0.032$) were increased with the SB or LL extracts vs. SBLL or control. In conclusion, individual extracts of SB or LL had effective impacts on ruminal fermentation activities and increased the propionic acid concentrations that suggested an improvement in animal daily gain.

Key words: extracts, lambs, ruminal fermentation

W398 Effect of live yeast *Saccharomyces cerevisiae* (strain Sc 47) on ruminal parameters of growing Mehraban lambs. N. Baleghi[1], A. Taghizadeh[2], A. FarahAvar[3], and H. Khalilvandi-Behroozyar*[3,4], *[1]Islamic Azad University, Maragheh Branch, [2]University of Tabriz, [3]University of Tehran, [4]Urmia University.*

Yeast (*Saccharomyces cerevisiae*) products may exert beneficial effects on ruminant productivity by either increasing fermentability of fiber and/or allowing rumen microbes to more effectively metabolize end products of ruminal starch fermentation. The objective was to evaluate the possible effects of live yeast on different ruminal parameters in fattening Mehraban lambs. Twelve male lambs (average BW 34 ± 4.2 kg) randomly assigned to 3 groups: a) control, without additive b) 1 g/ day/head and c) 1.5 g/day/ head S. cerevisiae (strain Sc 47) with 8 × 10^9cfu per gram. Additives supplemented via gelatin capsules to TMR ration (alfalfa hay, wheat straw, barley grain, canola meal, wheat bran, Mineral-vitamin mix, calcium carbonate and salt) formulated for 200 g/d weight gain using CNCPS-S. Animals fed experimental rations for a period of 70 d in 2 equal meals. Ruminal fluid samples were taken from rumen at 4 h after morning meal in the last day of experiment to determine rumen pH and concentration of NH3-N and VFA. Gas chromatography was used to determine VFA profiles equipped with a packed column. Protozoal counts were determined using light microscopic numeration with hematocytometer. Data were analyzed by GLM procedure of SAS 9.1 with CRD design and Duncan test ($P \leq 0.05$). Treatments were failed to have statistically significant effects on measured variables, but there was a tendency ($P \leq 0.1$) for higher total VFA, acetate and ammonia nitrogen concentrations and protozoa counts in lambs receiving 1.5 g/head/ day compared with control.

Table 1. Characteristics of ruminal fermentation in sheep fed Saccharomyces cerevisiae

	1	2	3	SEM
Mean pH	6.32	6.38	6.61	0.081
Total VFA mM	66.91	76.00	84.1	4.85
Acetate (%)	39.77	51.71	52.85	9.34
Propionate+Isobutyrate	19.72	12.11	20.16	5.09
Butyrate (%)	6.15	10.81	9.52	1.86
Valerate (%)	0.75	0.82	1.02	0.01
Isovalerate (%)	0.52	0.55	0.55	0.01
NH3-N (mg/dl)	7.21	7.95	8.22	0.65
Protzoal count ($\times 10^4$ /mg ruminal fluid)	54.21	74.86	85.71	15.61

1: control, 2: 1 g/day/head of yeast, 3: 1.5 g/day/head of yeast.

Key words: *Saccharomyces cerevisiae*, ruminal parameters, Mehraban lambs

W399 Intake and digestibility by wethers fed a fresh ryegrass-based diet intraruminally infused with *Acacia mearnsii* tannins. F. Hentz*[1], C. J. Härter[2], G. V. Kozloski[1], S. C. Àvila[1], and D. S. Castagnino[2], *[1]Universidade Federal de Santa Maria, Santa Maria, RS, Brazil, [2]Universidade Estadual Paulista, Jaboticabal, SP, Brazil.*

Eight Polwarth × Texel wethers (30 ± 4.8 kg BW), housed in metabolic cages and offered fresh ryegrass (*Lolium multiflorum*) ad libitum (10% refusals) were used in a 4 × 4 Latin Square-designed experiment to evaluate the effects of infusing *Acacia mearnsii* tannin extract (containing 0.625 g/g of condensed tannins) on intake and whole tract apparent digestibility. Treatments consisted of no tannin (0) or intraruminal infusion of 20, 40 or 60 g tannin/kg of ingested DM, according to the DMI of the previous day. Experimental periods lasted for 15 d (10 d adaptation, 5 d collection periods). Feed, orts and fecal output were recorded daily on d 10 to 15 and samples collected and composited within animal and period. Data was analyzed using the MIXED procedures of SAS. When the treatment effect was significant ($P < 0.05$) or tended to be significant ($0.05 < P \leq 0.10$), the means of different treatments were compared by orthogonal contrast (0 vs. tannins), and the effect of levels of tannin infusion was analyzed by regression for linear and quadratic effects. There were no quadratic effects for any variable. Total DM, OM and digestible OM intake and digestibility were greatly reduced ($P < 0.05$) with tannin infusion (Table 1). Moreover, this negative effect increased linearly at increased levels of tannin infusion for OM digestibility and digestible OM intake ($P < 0.05$). Although N intake tended to decrease ($P = 0.077$) and N digestibility decreased ($P < 0.01$) with tannin infusion, they did not vary ($P > 0.05$) within the levels of tannins. In conclusion, dietary inclusion

of Acacia meanrsii extract in concentrations above 20 g/kg of DMI negatively affect nutrients supply to wethers fed a temperate grass-based diet.

Table 1. Intake and total tract digestibility by wethers fed a fresh ryegrass-based diet intraruminally infused with Acacia mearnsii tannins (n=8 per treatment)

Item	0	20	40	60	SEM	(P > F) 0 vs. tannins	Linear regression (tannins)
Total intake, g/d							
DM	639	556	423	389	36.4	0.021	0.101
OM	573	492	374	344	33.0	0.019	0.106
N	21.1	19.9	16.1	13.7	1.29	0.077	0.133
Digestible OM	450	357	235	213	29.6	0.009	0.047
Apparent digestibility							
DM	0.74	0.69	0.60	0.58	0.01	0.003	0.034
OM	0.78	0.72	0.63	0.61	0.01	0.001	0.048
N	0.78	0.72	0.68	0.63	0.01	<0.001	0.301

Key words: condensed tannins, digestion, nutrients supply

W400 Effect of sorghum grain supplementation on glucose metabolism 2: Ovine. M. Aguerre*[1], C. Cajarville[2], A. L. Astessiano[3], M. Carriquiry[3], and J. L. Repetto[1], *[1]Departamento de Bovinos, Facultad de Veterinaria, Universidad de la República, Montevideo, Uruguay, [2]Departamento de Nutrición Animal, Facultad de Veterinaria, Universidad de la República, Montevideo, Uruguay, [3]Departamento de Producción Animal y Pasturas, Facultad de Agronomía, Universidad de la República, Montevideo, Uruguay.*

Corriedale × Milchschaf lambs (n = 12; 45.6 ± 6.2 kg), blocked by BW, were used to evaluate the effects of sorghum grain supplementation (0 vs. 1.5% BW, S0 vs. S1.5, respectively) on plasma glucose, insulin and glucagon concentrations, and on hepatic expression of genes related to glucose metabolism. Lambs were fed ad libitum fresh *Lotus corniculatus* (31.8% DM, 12.4% CP, 41.8% NDF). At the end of treatments (31 d) blood samples were taken every 2h from 0 to 6h post-supplementation, to determine glucose by colorimetry and insulin and glucagon by RIA. Liver biopsies were collected to quantify abundance of pyruvate carboxylase (PC), phosphoenolpyruvate carboxykinase (PCK–1) and insulin receptor (IR) mRNA by SYBR–Green real time PCR, using hypoxanthine-guanidine phosphoribosyltransferase as endogenous control. Data were analyzed with MIXED procedure (SAS). No differences on glucose levels were found between treatments (60.0 vs. 58.3 ± 5.61 mg/dL, P = 0.756; for S0 and S1.5 respectively) and the shape of the curves was similar over the 6h post-supplementation. Mean insulin concentrations were not different between treatments (10.1 vs. 8.80 ± 2.04 µUI/mL, P = 0.404; for S0 and S1.5 respectively), recording a 2-fold increase from 0 to 2h in S0 group (5.55 vs. 12.3 ± 2.51 µUI/mL, P = 0.028) and from 0 to 4h in S1.5 group (6.06 vs. 14.2 ± 2.88 µUI/mL, P = 0.026) returning to baseline at 6h in both groups. Glucagon concentrations were lower in S0 than S1.5 (50.1 vs. 63.7 ± 5.27, P = 0.053) but no interaction between hour and treatment was found (P = 0.415). Plasma glucagon tended to be negatively correlated with OM intake (r = –0.52, P = 0.101). The IR and PC mRNA did not differ between treatments (11.3 vs. 12.8 ± 2.23, P = 0.663 and 38.9 vs. 35.9 ± 7.82, P = 0.758 for S0 and S1.5 respectively), but PCK–1 mRNA was greater in S0 than S1.5 (11.2 vs. 8.60 ± 2.66, P = 0.048). In conclusion no major changes were observed in the glucose metabolism of lambs after sorghum grain supplementation. The results were consistent with a decrease in OM intake in supplemented lambs.

Key words: grazing sheep, hormones, liver mRNA

W401 Inter-individual variability in in vitro methane production by ruminal microorganisms from sheep fed different diets. 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, León, Spain, [2]IGM (CSIC-ULE), Finca Marzanas s/n, Grulleros, León, Spain.*

A large variability in methane emissions between individual sheep and cattle has been repeatedly reported. The aim of this study was to investigate the inter-individual variability in methane production in batch cultures of ruminal microorganisms (BCRM) inoculated with ruminal fluid from sheep fed different diets. Our hypothesis was that potential differences between inocula may be masked by the homogeneous conditions (pH, temperature, retention time) in the BCRM. Six rumen-fistulated sheep (S1 to S6) were fed 4 diets differing in their forage:concentrate ratio and type of forage in a partially replicated 4 × 4 Latin square design. In each period, ruminal fluid from each sheep was used to inoculate BCRM containing 500 mg of the same 4 diets as substrate. Cultures were incubated at 39°C, and methane production was measured after 8 and 24 h of incubation. Mean values of methane production for each sheep (pooled values for all diets and substrates) at 8 h of incubation ranged from 299 to 519 µmol, with a coefficient of variation of 0.241. Methane production at 24 h of incubation was rather consistent in BCRM inoculated with ruminal fluid from S1, S4, S5 and S6 (mean values of 650, 716, 669 and 671 µmol, respectively), with a mean value of 677 µmol and a coefficient of variation of 0.041. Values for S2 and S3 were 552 and 858 µmol, respectively. When data from all 6 sheep were pooled together, the mean value (686 µmol) was similar to the one obtained for S1, S4, S5 and S6, but the coefficient of variation increased to 0.155. Because the study was conducted in vitro, differences between BCRM inoculated with ruminal fluid from different sheep fed the same diet can only be attributed to differences in microbial populations in the inocula and the survival of microbes over the incubation. These results support previous observations on the considerable variation in the amount of methane produced by individual animals, despite of the homogeneous incubation conditions in the BCRM, and illustrate the importance of using mixed inocula from more than 1 single animal for in vitro studies.

Key words: methane, in vitro ruminal fermentation, inter-individual variability

W402 Influence of sugar cane molasses levels on apparent digestibility of diets for finishing lambs. L. R. Flores*[1], J. J. Lomeli[1], I. A. Vazquez[1], I. Quintero[1], J. E. Borbolla[1], J. E. Guerra[2], and R. Barajas[1], *[1]FMVZ-Universidad Autonóma de Sinaloa, Culiacán, Sinaloa, México, [2]FA-Universidad Autónoma de Sinaloa, Culiacán, Sinaloa, México.*

Four Katahdin lambs 24.8 ± 0.9 kg were used to determine the influence of sugar cane molasses levels on apparent digestibility of diets for finishing lambs. In agreement with a Latin Square Design lambs were assigned to the following dietary treatments: 1) Corn-soybean meal based-diet with 87% of concentrate and 13% of roughage (16% CP; 2.45 Mcal of DE/kg), and no cane molasses added (CTRL); 2) Diet similar to CTRL with 8% of sugar cane molasses substituting corn in dry matter basis (M8); 3) Diet similar to CTRL with 16% of sugar cane molasses substituting corn in dry matter basis (M16); and 4) Diet

similar to CTRL with 24% of sugar cane molasses substituting similar proportion of corn in the dry matter of the diet (M24). Data was analyzed by ANOVA; CTRL (0 molasses added) vs. all other treatments (8, 16, and 24% of molasses) were compared by orthogonal contrast; linearity of increasing molasses levels on dietary digestibility was tested using polynomial procedures. Molasses inclusion at any tested-level increased ($P < 0.05$) fecal excretion of DM and organic matter. CP excretion was increased linearly ($P < 0.05$) as cane molasses level was augmented in the diet. Cane molasses inclusion decreased ($P < 0.05$) apparent digestibility of dry matter (80.3 vs. 75.7%), organic matter (82.0 vs. 77.1%), and crude protein (78.0 vs. 70.6%). Observed/expected CP digestibility was 9% lower in molasses diets compared with CTRL ($P < 0.05$). By substitution method using corn as reference, energetic value of sugar cane molasses was estimated to be 2.92 Mcal/kg of DM that is 85% of its expected value, and complete digestive tract digestibility of crude protein of Molasses was calculated in 17%. It is concluded, that sugar cane molasses substitution for corn in finishing diets for lambs, decreases diet-digestibility, and the expected energy content of sugar cane molasses would be near of 2.9 Mcal of DE kg of DM^{-1}.

Key words: digestibility, lambs, sugar cane molasses

W403 Influence of additional tannins-extract level on feedlot-performance of finishing lambs. R. Barajas*[1], B. Ortiz[1], A. Camacho[1], N. E. Villalba[2], L. R. Flores[1], J. J. Lomeli[1], and J. A. Romo[1], *[1]FMVZ-Universidad Autonóma de Sinaloa, Culiacán, Sinaloa, México, [2]Agricola Ganadera Mojolo, Culiacán, Sinaloa, México.*

An experiment was conducted to determine the influence of additional tannins-extract level on feedlot-performance of finishing lambs. Thirty 6 weaned lambs 24.5 ± 0.36 kg, 18 lambs of 3/4 Katahdin x 1/4 Pelibuey breed ; and remainder 18 lambs of 3/4 Dorper x 1/4 Pelibuey Breed, were used. Animals were blocked by breed and weight and placed in groups of 3 in 12 elevated pens. Lambs were assigned in a complete randomized block design to be fed with a 5:95 roughage:concentrate corn-soybean meal based-diets (14% CP; 2.07 Mcal of NEm/kg) containing DM basis 0, 0.3 or 0.5% of a tannins-extract (TE). Tannins extract was supplied from a blend of condensed-tannins of quebracho trees, with soluble-tannins of cheese-nut trees (Silvafeed-Bypro; SilvaTeam-Inudor, S.A., Argentina). Lambs fed with 0.3% tannins diet had the highest final weight ($P = 0.02$), and a quadratic response ($P < 0.01$) of final weight to tannins-extract level was observed. Final weight values were 36.7, 38.8 and 37.7 kg, for tannins-extract levels of 0.0, 0.3, and 0.5%, respectively. Average daily gain was improved in 12% ($P = 0.02$) by 0.3% of tannins-extract level compared with no additional tannins treatment. ADG of lambs fed 0.3% of TE was 7% higher than observed in 0.5% of TE fed-lams ($P = 0.08$). Average daily gain shown a quadratic response ($P = 0.03$) to tannins-extract level in the diet, mean values were 0.32, 0.35, and 0.33 kg/day, for treatments with 0.0, 0.3, and 0.5% of TE, respectively. Dry matter intake and gain/intake ratio were not affected by tannins extract level ($P > 0.20$). It is concluded, that addition of an extract-blend of condensed and soluble tannins in concentrations close to 0.3% of dietary DM improves performance of finishing lambs

Key words: feedlot-performance, lambs, tannins

Small Ruminant: Carcass, Genetics, Management, and Reproduction

W404 Carcass evaluations of sheep supplemented with brewer waste (ensiled and dried) grazing under the rainy season in tropics. F. P. Portilho*[1,2], S. L. S. Cabral Filho[1], H. Louvandini[1], A. M. Menezes[1], and B. S. L. Dallago[1], *[1]University of Brasilia, Brasilia, DF, Brazil, [2]Agrodefesa, Rio Verde, GO, Brazil.*

At reduced costs, industrial wastes enable usage of protein and mineral mixtures as ingredients in the formulation to improve the productive capacity. The aims of this study were to evaluate the carcass parameters of finishing sheep in pasture during the rainy season and to evaluate the effect of replacement of traditional protein source (soybean meal) by sources of low degradability in the rumen like cotton meal and brewery waste (dried and ensiled). We used 40 male sheep of Santa Inês breed, with average weight of 22.0 ± 3.14 kg, grazing on Aruana grass (Panicum maximum), receiving supplementation of 100 g/animal/d for 4 treatments, plus a control without supplementation. Treatments were represented by supplementation offered for sheep grazing at the end of the rainy season during 30 d (between March and April). The treatments were composed as follows: T1– mostly of dried brewer grain (DBG), T2– silage of brewer grain (SBG), T3– cotton meal (CM), T4– soybean meal (SBM) and T5– without supplement (control–C). The experiment was designed with randomized blocks, with 2 blocks (n = 20), 4 repetitions by treatment. Differences were not observed for carcass among the treatments evaluated ($P > 0.1$) with respect to pH of the carcass (5.14 ± 0.77), weight of thoracic organs (1.44 ± 0.31 kg), carcass length (55.5 ± 2.96 cm), body condition (2.52 ± 1.03), skin thickness (0.40 ± 0.09 cm), length of ham (50.9 ± 2.21 cm), ham weight (1.72 ± 0.35 kg), leg circumference (33.1 ± 2.15 cm), loin weight (0.32 ± 0.091 kg), palette (0.90 ± 0.23 kg), rib (1.33 ± 0.39 kg), neck (0.49 ± 0.10 kg) and diaper (0.19 ± 0.54 kg), water loss (16.1 ± 2.61 mL), tenderness (2.79 ± 0.95 kgf). The hot and cold carcass weight varied among the treatments ($P < 0.05$) comparing the supplemented and control. They were 12.3 and 11.9 kg (DBG), 10.6 and 10.4 kg (SBG), 8.5 and 8.2 kg (CM), 9 and 8.7 kg (SBM), 11.5 and 11.2 kg (C), respectively. The carcass weight had better trend for DBG and the worst one for the CM treated animals. Therefore the usage of brewer waste showed that it can be employed to replace protein sources without disparity in the carcass parameters.

Key words: brewer grains, supplementation, sheep

W405 Feed efficiency and carcass traits in crossbred Katahdin lambs supplemented with hydroponic green wheat. M. Guerrero-Cervantes*[1,4], M. A. Cerrillo-Soto[1,4], F. G. Ríos-Rincón[2,4], A. Estrada-Angulo[2,4], A. S. Juárez-Reyes[1,4], and H. Bernal-Barragán[3,4], *[1]Universidad Juárez del Estado de Durango, Durango, Durango, México, [2]Universidad Autónoma de Sinaloa, Culiacán, Sinaloa, México, [3]Universidad Autónoma de Nuevo León, Monterrey, Nuevo León, México, [4]Red Internacional de Nutrición y Alimentación en Rumiantes, Durango, Durango, México.*

Hydroponic green fodder is considered an important alternative to conventional protein sources in semiarid regions. This study was carried out to determine the effect of supplementing hydroponic green wheat (HGW) on feed efficiency and carcass traits in crossbred Katahdin lambs fed an oat-straw based diet. Thirty lambs (120 ± 15 d of age; 17.7 ± 0.250 kg BW) were fed during 13 weeks, placed in individuals pens and separated in 3 groups of 10 lambs each. The animals received 1 of 3 oat straw-based diets supplemented with 3 levels of HGW (TI 23% HGW; TII 19% HGW and TIII 13% HGW), which substituted corn grain and soybean meal of the diet. Experimental diets were isonitrogenous (13% CP). Data of daily weight gain, dry matter intake, feed efficiency and carcass traits were analyzed by ANOVA according to a completely randomized block design, using the initial body weight as covariate. No differences in the studied variables ($P > 0.05$) were determined; however, numerical increments were registered in daily weight gain, carcass yield, muscle percentage and feed efficiency in animals fed TI. Animals fed TII had a higher fat percentage than their counterparts. Lambs receiving TIII had slightly larger ($P > 0.05$) rib eye area. It is concluded that the utilization of HGW might improve feed efficiency and be cost-effective in growing lamb nutrition practices.

Table 1. Daily weight gain, feed efficiency and carcass traits

Item	Treatments			Mean
	T I	T II	T III	
Daily weight gain (g)	150±12	136±12	124±12	138±38
Daily DM intake (g)	1076±10	1091±10	1021±10	1063±60
Feed efficiency*	7.4±0.7	8.5±0.7	8.6±0.7	8.9±2.2
Carcass yield (%)	64.8±2.2	64.2±2.2	63.5±2.2	64.2±4.9
Rib eye area (cm^2)	13.0±1.0	12.8±0.9	13.7±0.9	13.2±2.1
Fat (%)	11.9±1.8	12.8±1.7	12.1±1.7	12.3±3.8
Muscle (%)	64.5±1.2	64.3±1.26	63.7±1.2	64.2±2.5
Bone (%)	23.6±1.2	22.9±1.2	24.2±1.2	23.5±2.6
Total feed cost (Dls)	17.4	18.7	20.7	

*DM intake/weight gain.

Key words: lambs, hydroponic green wheat, carcass traits

W406 Effect of diet and finishing weight on performance and carcass traits of meat goat kids. A. Gaesser*[1], G. Rentfrow[2], T. K. Hutchens[2], J. Schoonmaker[1], K. Andries[3], J. E. Tower[1], M. E. Einstein[1], and M. K. Neary[1], *[1]Purdue University, West Lafayette IN, [2]University of Kentucky, Lexington, [3]Kentucky State University, Frankfort.*

The objective of this study was to evaluate 2 diets differing in starch and fiber content fed to 2 different target finishing weights (TW) on growth performance and carcass traits of meat goat kids. Diets were isocaloric (0.9 Mcal/kg NEg) and isonitrogenous (15% CP) and differed in the primary energy source (corn (C) vs. soybean hulls (SH)). The TW of kids were 27 kg and 34 kg. Intact male crossbred (n = 32) kids that had been weaned (initial weight of 22 ± 0.7 kg) for 30 d were individually fed and housed until reaching the TW. Kids were randomly assigned to one of 4 2 × 2 factorially arranged treatments of C, SH, and TW of 27 and 34 kg and data were analyzed by a linear ANOVA model that included diet (C vs SH), target weight (27 vs 34 kg) and the interaction. There was no ($P > 0.05$) interaction between diet and TW for any of the goat response variables. Goats fed SH based diets had higher ($P < 0.05$) ADG (0.162 vs 0.119 ± 0.01 kg), higher ($P < 0.01$) feed intake (1.26 vs 1.02 ± 0.05 kg/d), and tended ($P = 0.07$) to have higher Gain to feed (G:F) (0.14 vs 0.12 ± 0.01 kg) than goats fed C. Dressing percent did not ($P > 0.05$) differ between goats fed SH (51 ± 0.5%) or C (50.3 ± 0.5%), but HCW was higher ($P < 0.05$) for

SH (15.8 ± 0.34 kg) than C (14.7 ± 0.34 kg) fed goats. Goats fed to a TW of 27 kg had higher ($P < 0.05$) G:F (0.14 vs 0.11 ± 0.002 kg) and tended ($P = 0.09$) to have higher ADG (0.152 vs 0.129 ± 0.009 kg) than goats fed to 34 kg. Dressing percent was higher ($P < 0.05$) when goats were fed to 34 kg (51.5 ± 0.49%) as compared with 27 kg (49.8 ± 0.49%). The quality grade and fat score were not ($P > 0.05$) influenced by feeding C or SH or finished weights of 27 or 34 kg. These results show that feeding SH as the primary dietary energy source resulted in higher growth performance than C, with no affect on carcass traits. Feeding goats to 34 kg as compared with 27 kg resulted in higher dressing percentage, with lower G:F.

Key words: goat, finishing weight, carcass

W407 Feedlot productive performance and carcass traits by hybrid lambs. M. T. Espinoza[1], M. A. Cerrillo-Soto[2,3], A. Estrada-Angulo[1,3], J. F. Obregon[1,3], J. J. Portillo[1,3], and F. G. Rios*[1,3], *[1]FMVZ-UAS, Culiacan, Sinaloa, Mexico, [2]FMVZ-UJED, Durango, Durango, Mexico, [3]Red Internacional de Alimentacion y Nutricion de Rumiantes, Durango, Durango, México.*

Genetic diversity by lambs should be considered when looking for diet optimization. To determinate productive response and carcass traits in hybrid lambs,a 70 d feedlot trial was conducted using 54 lambs (27 males and 27 females) with 73 ± 7 d initial age; and 15.7 ± 3.0 kg initial BW, from each genotype Pelibuey (100PB), Dorper × Pelibuey (50DR x 50PB) and Dorper × F1 dams Katahdin × Pelibuey (50DR × 25KT × 25PB) fed a 17% CP, 3.4 Mcal/kg DE (growth) and 15% CP, 3.4 Mcal/kg DE (finishing), concentrate-based diet. At slaughter carcass traits only from males were recorded. Data of growth performance were analyzed using ANOVA with repeated measures and means comparisons were performed using orthogonal contrasts. Carcass traits were analyzed using slaughter weight as covariate, and adjusted averages compared with Tukey-Kramer test. Average daily gain (ADG) throughout the experiment was 18.4% higher ($P < 0.01$) in hybrid lambs at d 28. ADG was higher ($P < 0.01$) for hybrid 50DR x 25KT × 25PB (301 g), than for F1 50DR × 50PB (276 g) and 100PB (236 g). Weight gain was 31% higher in males ($P < 0.01$) at d 28, 56 and 70 than female lambs. No differences among racial groups ($P > 0.05$) were observed in feed intake throughout the feeding periods. However males ate more feed than their counterparts (1146 ± 38 vs. 1018 ± 31 g/d). There were no differences in carcass characteristics among the evaluated racial groups. According to our data, it is concluded that growth performance and carcass characteristics of hybrid lambs, 50DR × 25KT × 25PB are similar than F1 50DR × 50PB.

Key words: crossed hair sheep, feed conversion, carcass yield

W408 Evaluation of carcass characteristics of feedlot lambs receiving repeated doses of zeranol. L. Carlos-Valdez*, A. Grado-Ahüir, G. Corral-Flores, L. González-Aguilera, L. Barron-Limón, G. Villalobos-Villalobos, D. Dominguez-Diaz, and I. Anguiano-Cardona, *Universidad Autónoma de Chihuahua, Facultad de Zootecnia y Ecología, Chihuahua, Chih., México.*

The objective of this study was to evaluate the effect of repeated doses of zeranol implant in carcass characteristics and dressing percentage. We used (n = 20) crossbred finishing male lambs (average 54.5 ± 3.6 kg) from a 70 d performance trial. During the trial the lambs were randomly allocated into 3 treatments: no implant (0ze, n = 6), 12 mg of zeranol (Ralgro, Schering-Plough) on d 0 (12ze, n = 7), and 12 mg of zeranol on d 0 with a second implant at d 28 (24ze, n = 7). The lambs were harvested at the Universidad Autonoma de Chihuahua slaughterhouse following the slaughter Mexican Government regulation NOM-006–200–1996. The carcasses were cut in half and put in a cold room (4°C) for 24 h, then were transferred and stored in a freezing room (−24°C), until processed. Chilled right halves were cut into primary cuts and weighed. Rib eye area and fat depth were determined; all variables were analyzed adjusting a linear model with treatment as the fixed effect. Lambs 24ze had greater dressing percentage ($P < 0.05$; 53.6 ± 0.55%) compared with 0ze and 12ze (50.33 ± 0.60 and 51.91 ± 0.55%, respectively). The hot carcasses and cold carcasses were heavier for 24ze ($P < 0.05$; 29.22 ± 0.69 and 28.8 ± 0.67kg, respectively), compared with 0ze (27.17 ± 0.74 and 26.73 ± 0.72kg, respectively), but there was no difference ($P > 0.05$) between 24z and 12ze. Leg weight expressed as a percentage of carcass weight was also greatest for 24ze ($P < 0.01$; 7.4 ± 0.19%), compared with 0ze and 12ze (6.6 ± 0.20 and 6.3 ± 0.19%, respectively). The rib eye area was greater for 24ze ($P < 0.04$; 7.96 ± 0.35) compared with 12ze (6.86 ± 0.35cm2). Back fat deposition was greater for 24ze ($P < 0.02$; 4.17 ± 0.67mm) and 12ze ($P < 0.01$; 4.42 ± 0.62mm) compared with 0ze (1.83 ± 0.67mm). There were no differences ($P > 0.05$) among treatments for loin, rack, shoulder and ribs weights. We concluded that repeated doses of zeranol implants have an advantage over non implanted and single implant doses, increasing dressing percentage and economical carcass characteristics such as leg muscle accretion and rib eye area, while back fat deposition was significantly greater for both implant treatments.

Key words: lambs, zeranol, carcass characteristics

W409 Performance and carcass characteristics of lambs fed with diets including protected fat and vitamin E. A. P. P. Pinto[1], I. F. Furusho-Garcia*[2], I. Leopoldino Junior[2], J. R. O. Pérez[2], V. A. A. Reis[2], S. P. Greca[2], N. G. Alves[2], and I. G. Pereira[1], *[1]Universidade Federal dos Vales do Jequitinhonha e Mucuri, Diamantina, Minas Gerais, Brasil, [2]Universidade Federal de Lavras, Lavras, Minas Gerais, Brasil.*

The experiment was conducted at the Federal University of Lavras to evaluate the effect of the use of protected fat, with presence or absence of vitamin E on the performance and carcass characteristics of lambs in confinement with different weights. Thirty-two of Santa Ines lambs fed roughage: concentrate ratio of 40:60%, ad libitum, with the absence or presence of protected fat (calcium soaps) totaling 6% ether extract in the complete diet; and presence or absence of vitamin E (α-tocopherol acetate DL), resulting in 4 experimental diets. The 2 live weights at start confinement: lightweight (23.05 kg ± 1.62) and heavy (32.63 kg ± 1.72). All animals were slaughtered at 84 d of confinement. The experimental design was completely randomized in a 2 × 2 x 2 (2 levels of protected fat (0 and 4%), 2 levels of vitamin E (0 and 0.05%) and 2 live weight). Data were analyzed by General Linear Methods Procedure (Proc GLM) of SAS (Statistical Analysis System); and means compared by *t*-test at 5% probability. The daily weight gain was not influenced by the factors evaluated ($P > 0.05$). The feed conversion of lambs lighter was worse ($P < 0.05$) for lambs fed diet containing no fat protected as shown in the table. The inclusion of vitamin E improved ($P < 0.05$) carcass dressing percentage (52.29%) compared with animals that were fed vitamin E (49.00%). Lighter lambs had lower ($P < 0.05$) carcass dressing percentage (48.13%)

compared with the heaviest lambs (52.29%). The addition of fat in the diet reduced ($P < 0.05$) dry matter intake and increased ($P < 0.05$) ether extract intake. The average weights of intestinal contents were higher ($P < 0.05$) in the absence of dietary fat (7.87 kg) compared with lambs fed fat (6.93 kg), this may be due to increased consumption of diets that contained no protected fat. In conclusion, lambs that start in the feedlot heavier weights have better performance and carcass characteristics, the use of protected fat improves the performance of lambs, and vitamin E improves carcass yield.

Table 1. Mean feed conversion due to the interaction between experimental weight and the presence of protected fat in diet

	Protected fat in diet		
Experimental weight	0%	4%	Mean
30-35 kg	4.487^{A,b}	4,725^{A,a}	4.606^{a}
20-25 kg	5,918^{A,a}	4,163^{B,a}	5.041^{a}
Mean	5,203^{A}	4,444^{A}	

Means followed by different letters, uppercase letters in rows and lowercase in columns, differ statistically by t test ($P < 0.05$).

Key words: lipids, nutrition, sheep

W410 Feeding system and breed affect goat kid growth and carcass composition. M.-E. Brassard*[1], L. Tessier[1], R. Gervais[1], E. Pouliot[1], C. Gariepy[2], G. F. Tremblay[3], R. Berthiaume[4], P. Y. Chouinard[1], and D. Cinq-Mars[1], *[1]Département des sciences animales, Université Laval, Québec, QC, Canada, [2]AAFC, Food Research and Development Centre, Saint-Hyacinthe, QC, Canada, [3]AAFC, Soils and Crops Research and Development Centre, Québec, QC, Canada, [4]AAFC, Dairy and Swine Research and Development Centre, Sherbrooke, QC, Canada.*

Forty weaned male goat kids (25.9 ± 1.4 kg) from meat (Boer) and dairy (mostly Alpine and Saanen) breeds were used to evaluate the effects of 2 feeding systems on growth and carcass composition. Twenty kids from each breed were blocked according to body weight in 10 groups and kids were randomly allotted to an intensive pasture system or a concentrate-based diet. Grazing kids from each breed were raised in group and had access to a mineral supplement. Kids receiving concentrates (corn, soybean meal, and vitamin and mineral premix) and grass hay were reared indoor in individual pen. Kids were slaughtered when they reached 44.5 ± 0.6 kg live weight. Weight for carcasses and body components were recorded and the left side of each carcass was cut into 7 commercial joints (foreshank, neck, shoulder, flank, rib, loin, and leg). Each joint was weighed and dissected into fat, muscle and bone. No interaction was observed between feeding system and breed unless specified otherwise. Average daily gain was greater for meat than dairy kids (156 vs. 116 g/d; $P < 0.01$). Kids fed the concentrate-based diet attained slaughter weight in 131 d while those fed intensive pasture required 149 d ($P < 0.05$). Breed and feeding system did not affect dressing percentage (48 ± 3%). Meat kids ($P < 0.01$) and kids fed concentrate-based diet ($P < 0.05$) showed greater values for fat weight and percentage in neck, foreshank, rib and leg. Concentrate feeding also increased fat values for shoulder, loin and flank especially when fed to meat kids (Feeding × Breed: $P < 0.05$). Muscle weight for loin and leg were greater for meat than dairy kids whereas the opposite was observed for neck and shoulder joints ($P < 0.05$). Pasture-fed kids had greater muscle percentage in shoulder and neck ($P < 0.05$). Feeding pasture also increased muscle percentage in loin and rib specifically when fed to meat kids (Feeding × Breed: $P < 0.05$). Dairy breed kids had higher bone percentage and weight for foreshank, leg, loin, and rib than meat breed kids ($P < 0.01$). Results from this study showed that breed and feeding system influence carcass quality in growing kids.

Key words: goat kid, carcass composition, commercial cuts

W411 Molecular survey of *Trypanosoma vivax* infection in Nigerian goats. T. Sanni[1], A. Yakubu*[2], M. A. Adefenwa[3], B. O. Agaviezor[4], C. O. N. Ikeobi[1], M. Wheto[1], M. Okpeku[5], M. I. Takeet[6], M. De Donato[7], and I. G. Imumorin[7], *[1]Dept of Animal Breeding and Genetics, University of Agriculture, Abeokuta, Nigeria, [2]Dept of Animal Science, Nasarawa State University, Lafia, Nigeria, [3]Dept of Cell Biology and Genetics, University of Lagos, Lagos, Nigeria, [4]Dept of Animal Science and Fisheries, University of Port Harcourt, Port-Harcourt, Nigeria, [5]Dept of Livestock Production, Niger Delta University, Amassoma, Nigeria., [6]Dept of Veterinary Microbiology and Parasitology, University of Agriculture, Abeokuta, Nigeria, [7]Dept of Animal Science, Cornell University, Ithaca, NY.*

Trypanosomiasis is a major protozoan parasitic disease that is endemic in Nigeria and much of Sub-Saharan Africa. To gain better understanding of the distribution of this disease in goats, a cross-sectional study was conducted in 3 geopolitical zones of Nigeria to determine the prevalence of trypanosomiasis in the 3 indigenous breeds of goats. Blood samples and some physiological parameters (rectal temperature, body temperature, respiratory rate and pulse rate) were collected from a total of 205 randomly selected animals from across the country. *Trypanosoma vivax* detection was carried out using *T. vivax*-specific polymerase chain reaction (PCR) primers that amplifies 400 bp of the trypanosome genome. Results showed that 71.22% of the total goats were infected with *T. vivax*, comprising 19.51% males and 51.71% females, respectively. Among the breeds examined, 21.46%, 42.44% and 7.32% of West African Dwarf, Red Sokoto and Sahel goats respectively were found to be infected with this parasite species. The prevalence rate was 30.73%, 20.00% and 20.49% in the northeastern, northwestern and southwestern parts of the country respectively. Breed-sex-zone interaction effect was significant ($P < 0.05$) for *T. vivax* score; indicating the separate rankings of the 3 genotypes under the 2 sexes and 3 zones investigated. The logistic regression analysis revealed that among the physiological indices, respiratory rate was the trait of utmost importance in predicting the presence of *T. vivax* with Hosmer-Lemeshow goodness-of-fit. The present information could aid management and conservation strategies toward attenuating the rate of trypanosomiasis prevalence in Nigerian goats.

Key words: *Trypanosoma vivax*, Nigeria, goats

W412 Gene expression changes in goat testes during development and in sperm during the breeding and nonbreeding seasons. A. N. Faucette*[2], P. K. Riggs[2], D. W. Forrest[2], L. Nuti[1], G. R. Newton[1], and N. H. Ing[2], *[1]Prairie View A&M University, Cooperative Agriculture Research Center, Prairie View, TX, [2]Texas AgriLife Research, College Station.*

Current clinical tests to screen for fertility include analyses of sperm number, morphology, motility, chromatin quality, and acrosomal integrity in semen. These endpoints fluctuate due to many factors unrelated

to overall fertility. Our working hypothesis is that regulated genes involved in spermatogenesis may be useful predictors of male fertility. Our goals were to analyze alterations in gene expression in the goat testes during development and analyze alterations in gene products in sperm from mature bucks between breeding and non-breeding seasons. For the former, testes were harvested from 5 Alpine bucks at 0, 2, 4, 6, and 8 mo of age. Northern blotting and in situ hybridization indicated that the largest changes in gene expression during testes development happen in the first 4 mo in the goat. Sertoli cell marker Sex determining region Y-box 9 (SOX9) mRNA peaked at 2 mo of age then declined. At 4 mo, expression of Stimulated by Retinoic Acid gene 8 (STRA8) and Protamine 1 genes was strongly upregulated in early and maturing germ cells, respectively. RNA from ejaculated sperm collected from 3 mature Alpine bucks in October (peak breeding season) and April (not peak breeding) was interrogated for 44,000 gene products on Bovine Gene Expression Microarrays (Agilent). 43 gene products were expressed 3-fold or more highly in peak breeding season, while concentrations of 12 mRNAs decreased 3-fold or more ($P <$ 0.01). Discovery of 5-fold greater levels of glycerol kinase 2 (GK2) mRNA in sperm from the peak breeding season and 6-fold lower levels of Sperm Adhesion Molecule 1 (SPAM1) mRNA are being confirmed and extended to more Alpine and Boer goat sperm samples with real time PCR. Results of these experiments may be useful in developing novel fertility tests based on mRNA levels in testes and ejaculated sperm that will assist improving reproductive efficiencies in animal production systems. USDA 2009-34136-119794 to GRN.

Key words: goat, sperm mRNA, fertility

W413 Feeding management affect the occurrence of self-suckling in dairy goats. J. Martínez-de la Puente, I. Moreno-Indias*, A. Morales-delaNuez, L. E. Hernández-Castellano, M. D. Ruíz-Díaz, N. Castro, and A. Argüello, *Universidad de las Palmas de Gran Canaria, Arucas, Las Palmas, Spain.*

Self-suckling, an animal suckling on its own teats, is an abnormal behavior observed in dairy livestock. To investigate the effect of feeding management on self-suckling, the occurrence of this behavior was recorded in 21 dairy goats during periods of 20 min at 3 different times per day (immediately after milking and the first feed (10:30), immediately after the second feed (13:30) and in the afternoon (17:00)) along 3 consecutive experimental periods of 9 d each. During the first (PRE) and the third (POST) periods goats were fed with corn, soy 44, dehydrated lucerne, dehydrated beetroot, lucerne hay and a vitamin-mineral corrector. During the second period goats were supplemented ad libitum with wheat straw in addition to their ordinary diet. Statistical analyses were conducted using Wilcoxon Matched Pairs Tests and a Friedman ANOVA (a nonparametric alternative to one-way repeated measures ANOVA). During each 20 min period, an average of 6.9 ± 2.5, 5.1 ± 1.9 and 7.5 ± 2.9 goats suckled on their own teats during the PRE, ad libitum and POST periods respectively. During each 20 min period, a lower number of self-suckling goats were observed during ad libitum than during both PRE ($Z = 3.26$; $P = 0.001$) and POST periods ($Z = 3.74$; $P < 0.001$). Moreover, during PRE, ad libitum and POST experimental periods, each goat suckled on their own teats at least one time during an average of 8.9 ± 8.7, 6.6 ± 7.4 and 9.6 ± 8.6 20 min periods respectively. These differences reached significance (n = 21; Chi Sqr. = 9.34; d.f. = 2; $P < 0.01$) with a lower self-suckling frequency during ad libitum than during POST period ($Z = 2.66$; $P <$ 0.01). The same trend was found comparing PRE and ad libitum periods ($Z = 1.91$; $P = 0.06$). Overall, this study strongly supports the role of feeding management as a major factor affecting the occurrence of self-suckling in dairy goats.

Key words: behavior, feeding management, self-suckling

W414 Withdrawn

W415 Finishing performance of lambs fed fresh or dehydrated spineless cactus (*Opuntia ficus-indica*). M. I. Aguilar-Yañez[1], O. Hernadez-Mendo[1], G. Aranda-Osorio*[2], J. E. Ramirez-Bribiesca[1], S. S. Gonzalez-Muñoz[1], and M. M. Crosby-Galvan[1], *[1]Colegio de Postgraduados, Montecillos, Estado de Mexico, Mexico, [2]Universidad Autonoma Chapingo, Chapingo, Estado de Mexico, Mexico.*

The objective of this study was to evaluate the effect of cactus (*Opuntia ficus-indica*) supplementation on finishing lambs performance, during an 11-week period. For this purpose, 27 male commercial crossbred lambs were used, with initial body weight (BW) mean of 21.4 ± 2.18 kg. They were distributed homogeneously into 3 groups of 9 each (each lamb being an experimental unit), and randomly assigned to the following treatments: (T1) control diet (representative lambs finishing diet for the central region of Mexico), (T2) diet with 17% dehydrated cactus (dry basis), and (T3) diet with 17% fresh cactus (dry basis). Variables were in situ dry matter digestibility (ISDMD), dry matter intake (DMI), average daily gain (ADG), feed:gain ratio (F:G) and gain:feed ratio (G:F), backfat depth (BFD), hot and cold carcass yield (HCY and CCY), biological hot and cold carcass yield (BHCY and BCCY), and carcass pH at slaughtering and 24 h post mortem. The experimental design was completely ramdomized, analyzed under the Proc GLM of SAS, and means were compared with Tukey test ($P \leq 0.05$). There ISDMD was higher (42.0%) for T1 at 6 h and for the T3 (88.6%) at 48 h ($P \leq 0.001$). No differences ($P \geq 0.05$) were found between treatments for average final BW (37.7 ± 1.21 kg). Backfat (BFD) was lower ($P \leq 0.001$) in lambs fed dehydrated (4.1 mm) or fresh (3.3 mm) cactus diets, compared with those fed the control diet (7.8 mm). Average values for hot and cold carcass yield, biological hot and cold carcass yield, and carcass pH at slaughtering and 24 h post mortem, were 50.6 and 47.0%, 55.4 and 49.5%, and 6.6 and 5.8, respectively ($P \geq 0.05$). Feeding lambs a diet including cactus seems to be a viable alternative for finishing systems in Mexico where cactus is readily available all around the year at a low cost. Besides, cactus could have a beneficial effect on meat traits.

Key words: cactus, sheep, productivity

W416 Finishing performance of Pelibuey sheep fed with different levels of alfalfa. V. Resendiz-Cruz[1], O. Hernadez-Mendo[1], J. Gallegos-Sanchez[1], P. A. Martinez-Hernandez[2], G. Aranda-Osorio*[2], C. Sanchez-Del Real[2], and S. S. Gonzalez-Muñoz[1], *[1]Colegio de Postgraduados, Montecillos, Estado de Mexico, Mexico, [2]Universidad Autonoma Chapingo, Chapingo, Estado de Mexico, Mexico.*

The objective of this study was to evaluate the effect of feeding different levels of alfalfa to sheep on animal performance, during a period of 11 weeks. For this purpose, 36 Pelibuey male sheep were used indoors, with initial body weight (BW) mean of 22.3 ± 0.3 kg. They were distributed homogeneously into 4 groups of 3 each, with 3 replicates per group, and then randomly assigned to each of the following treatments:

0, 20, 30 and 40% alfalfa (dry basis). Dry matter intake (DMI), average daily gain (ADG), feed:gain ratio (F:G) and gain:feed ratio (G:F), hot and cold carcass yield (HCY and CCY), biological hot and cold carcass yield (BHCY and BCCY), and carcass pH at slaughtering and 24 h post mortem, and in situ dry matter digestibility (ISDMD), were evaluated. A completely random design under Proc GLM of SAS was used, and a mean comparison using the Tukey test was done. There were not differences ($P \geq 0.05$) between treatments on animal performance, except on dry matter intake, which increased ($P \leq 0.05$) from 1.2 to 1.4 kg DM per animal when increasing alfalfa level from 20 to 40%, even though diets including alfalfa had less ($P \leq 0.05$) digestibility compared with the control one. ADG, F:G and G:F averaged 271 g animal^{-1} d^{-1}, 4.7 and 0.212, respectively($P \geq 0.05$). The average for hot and cold carcass weight, and hot and cold carcass yield, were 19.3 and 18.8 kg, and 54.4% and 53.0%, respectively ($P \geq 0.05$). Including alfalfa to sheep diets offers no benefits on animal performance; however, including up to 40% of it, could be a viable feeding strategy, since it increases dry matter intake, which in a way, could have a positive effect if alfalfa is fed as meal or whole plant.

Key words: lambs, alfalfa, productivity

W417 Evaluation of feedlot male lamb performance receiving repeated doses of Zeranol. L. Carlos-Valdez*, A. Grado-Ahüir, L. González-Aguilera, D. Barron-Limón, P. García-Montoya, G. Villalobos-Villalobos, and D. Domínguez-Díaz, *Universidad Autónoma de Chihuahua, Facultad de Zootecnia y Ecología, Chihuahua, Chih., México.*

The objective of this study was to evaluate the effect of repeated doses of zeranol implant on the performance of male lambs. Fifty 5, post-weaning Charollais crossbred male lambs (BW = 25.2 ± 5.42 kg) were randomly allocated into 3 treatments: no implant (0ze, n = 15), 12 mg of zeranol (Ralgro, Schering-Plough) on d 0 (12ze, n = 15), and 12 mg of zeranol on d 0 with a second implant at d 28 (24ze, n = 15). The lambs had a 10 d acclimation period to a new diet and individual pens. During this time they were also vaccinated (Bobact-8, Intervet) and de-wormed (Baymec 1% Hidrofilico, Bayer). The diet was formulated to equal or exceed the nutrient requirements (NRC Sheep, 1985). The lambs were fed ad libitum twice a day (0800 and 1300h) with a TMR (85:15, concentrate:forage) that contained 2.9 Mcal/kg of ME and 13.7%CP, with free access to fresh water all day. Offered feed and refusals were weighed and recorded daily to estimate feed consumption. The lambs were weighed every 14 d for 70 d. All data was analyzed adjusting a linear model with treatment as the fixed effect. There were no differences found among treatments for final weight and DM intake ($P = 0.8$). However, numerically, 24ze had the greatest final weight (51.5kg). The ADG was greater for 24ze ($P < 0.03$; 0.37 ± 0.023kg) compared with 0ze and 12ze lambs (0.31 ± 0.020, 0.31 ± 0.020kg, respectively). For G:F 24ze lambs were more efficient ($P < 0.05$; 0.34 ± 0.02) compared with 0ze lambs (0.28 ± 0.03) but not different from 12ze lambs. These results show that repeated doses of zeranol implant increase the feed efficiency and ADG in male lambs post-weaning.

Key words: zeranol, lamb, performance

W418 Effect of using different performance traits to estimate residual feed intake. R. R. Cockrum*, R. H. Stobart, S. L. Lake, and K. M. Cammack, *University of Wyoming, Laramie.*

Predictive models for residual feed intake (RFI) have used ADG, feed intake, ME, mid-body weight (MWT), metabolic mid-body weight (MMWT$^{0.75}$), and various carcass traits. For RFI to become adopted by producers as an indicator of feed efficiency, relevant performance traits should be incorporated into the model to increase accuracy. Carcass traits typically measured in a ram performance test include back fat (BF) and loin eye area (LEA); scrotal circumference (SC) is another typical measurement that is indicative of growth. We hypothesized that incorporation of these biological measures into the prediction model would provide a more accurate measurement of feed efficiency in sheep. Our aim was to determine if the use of BF, LEA, and SC in the predictive equation affected RFI ranking. Individual feed intake measurements were collected on rams submitted to the University of Wyoming Western Whiteface Ram Test (n = 62) for 140 d using the GrowSafe System, an automated system that collects individual feed intake data from group-housed animals. Feed samples were collected and analyzed for DM, ADF, and IVDMD to determine ME, a measurement often preferred over actual feed intake as it accounts for individual digestibility. Using the GLM procedure in SAS, predictive equations were generated to estimate RFI, and the CORR procedure was used to evaluate relationships among these alternative predictive equations. An α of 0.05 was assumed. The base model used was $Y = \beta_0 + X_1\beta_1 + X_2\beta_2 + e$ where Y = ME, X_1 = ADG, and X_2 = MMWT$^{0.75}$ or MWT. An R^2 of 0.43 was generated for this equation regardless of use of MMWT$^{0.75}$ or MWT. Further analyses used only MWT for estimating RFI. When BF and LEA predictors were added to the equation, R^2 increased to 0.45, and SC further increased R^2 to 0.46. Additional performance traits in the model had no effect ($P = 0.985$) on individual RFI ranking, and the predictive equations analyzed were highly and positively correlated ($P < 0.001$). Adding performance data to the RFI predictive equation had limited effect on accuracy, and did not produce rankings different from the base model.

Key words: efficiency, predictive models, residual feed intake

W419 Increased nutritional level positively influences the onset of the breeding season and the reproductive performance of native male goats in northern Mexico. A. Olán-Sánchez[1], E. Carrillo[2], L. M. Tejeda[1], J. M. Guillén-Muñoz[1], P. A. Robles-Trillo[1], C. A. Meza-Herrera[3], F. G. Véliz[1], R. Rodríguez-Martínez*[1], and M. Mellado[4], *[1]Universidad Autónoma Agraria Antonio Narro, Torreón, Coahuila, México, [2]Instituto Tecnológico de Torreón, Torreón, Coahuila, México, [3]Universidad Autónoma Chapingo, Unidad Regional de Zonas Áridas, Bermejillo, Dgo., México, [4]Universidad Autónoma Agraria Antonio Narro, Buenavista, Saltillo, Coahuila, México.*

To determine whether feeding influences the onset of sexual activity in native bucks in northern Mexico (26° N), adults native bucks (n = 10) were divided into 2 homogeneous groups in relation their body condition (1.5, scale 1–4) and body weight (27 kg). Before the trial, bucks were kept in an extensive production system with predominant native vegetation consisting of *Prosopis glandulosa*, *Acacia farnesiana*, *Atriplex acantocarpa*, *Agave scabra*, *Mimosa biuncife*, *Heliantus ciliaris*, *Salsola kali*, *Solanum elaeagnilolium* as well as *Chloris virgata*, *Setaria verticillata*, *Eragrostis pectinacea*, *Bouteloua curtipendula*, *Aristida purpurea* and *Bouteloua barbata*. Sometimes, bucks had available some agricultural crop residues such as sorghum (*Sorghum vulgare*) and corn (*Zea mays*), among others. On May 19, 2010, a group of males (Well fed, n = 5) received a diet to cover 150% of their nutritional requirements for maintenance, while another group of males (Control, n = 5) was fed a maintenance diet. At the end of the

trial (June 19) a sexual behavior test was carried-out, in which males of both groups were exposed to 2 females in estrus during 15 min, for 2 consecutive days. Percentage of anogenital sniffing, nudging, mounting attempts, and complete mounts were compared with Chi-squared test, while the ejaculation latency time was compared with a Student *t*-test. All the tests were performed by means of the statistical package SYSTAL 12. Well-fed bucks had more anogenital sniffing, nudging, mounting attempts, and full mount than controls (Table). In addition, ejaculation latency time in well-fed bucks was shorter (57.8 ± 7.1 s) than Control bucks (419 ± 116 s). These results show that feed supplementation of range mixed-breed goat bucks in spring elicits a strong sexual behavior.

Table 1. Sexual behavior of native bucks, well and poorly fed, exposed to estrogenized females for two days during 15 min, at the onset of sexual activity season in northern Mexico (26° N)

Groups	Anogenital sniffing	Nudging	Mounting attempts	Complete mounts
Poorly fed	69[a]	258[a]	13[a]	27[a]
Well fed	102[a]	378[b]	22[a]	65[b]

Different superscripts within column indicate statistical differences ($P < 0.05$).

Key words: goats, feeding, sexual behavior

W420 Response of sexually inactive French Alpine bucks to the stimulus of estrous goats. L. M. Tejada*[1], E. Carrillo[2], R. Rivas-Muñoz[2], M. Guillén-Muñoz[1], C. A. Meza-Herrera[3], G. Arellano-Rodríguez[1], M. Mellado[1], and F. G. Véliz[1], *[1]Universidad Autónoma Agraria Antonio Narro, Torreón, Coahuila, México, [2]Instituto Tecnológico de Torreón, Torreón, Coahuila, México, [3]Universidad Autónoma Chapingo, Unidad Regional Universitaria de Zonas Áridas, Bermejillo, Durango, México.*

This study was designed to investigate whether sexually inactive French Alpine bucks stimulated with estrous does are capable to induce estrus and ovulation in anestrous does. Two goats were subcutaneously injected, every 2 d, with 2 mg estradiol cypionate (Estradiol, Qro., México) in 1 mL vegetable oil. These goats in permanent estrus were placed with 2 sexually inactive bucks (stimulated) in May and another 2 bucks in June, during 3 weeks before breeding. Fifty-nine adult anestrous French Alpine goats were randomly assigned to one of 4 treatment groups: exposure to stimulated (n = 14) or nonstimulated (n = 15) bucks in March, or with stimulated (n = 15) or nonstimulated (n = 15) bucks in June. All goats received a single I.M. injection of 25 mg progesterone (Progestelas E, Qro., Mexico) before the buck exposure. Does were considered in estrus when copulation occurred. Once bred, goats were removed from the breeding pens and pregnancy was diagnosed by transrectal ultrasonography using a 5.0 MHz transducer (Supply, Inc., Tequesta, FL) 50 d after mating. Additionally, the sexual behavior exhibited by bucks in contact with penned does was recorded during 2 consecutive observation sessions lasting one h each. The estrus response was 79 and 100% for goats exposed to stimulated bucks in March and June, but none of the goats joined with the nonstimulated bucks showed estrus in both breeding seasons. Pregnancy rate based on ultrasonography 50 d post copulation was lower ($P < 0.01$) in goats joined to stimulated bucks in March (50%) compared with goats bred in June (80%). For both breeding seasons none of the goats joined to nonstimulated bucks kidded. Interval to estrus was shorter (68 ± 2 vs 141 ± 13 h) and more synchronized in goats exposed to stimulated bucks in June than goats exposed to bucks in March. Frequency of flehmen, nosing, and approaches were higher ($P < 0.01$) for simulated bucks than nonstimulated bucks. It was concluded that the exposure of sexually inactive bucks to estrous goats is an inexpensive, practical and efficient way to elicit sexual active in bucks, which subsequently triggers breeding activity of anestrous goats.

Key words: male effect, goat, estrous goats

W421 Contact with estrogenized female goats influences the end of sexual activity of young bucks but not adult bucks in northern Mexico. A. Olán-Sánchez*[1], E. Carrillo[2], R. Rivas-Muñoz[2], L. M. Tejeda[1], J. M. Guillen-Muñoz[1], R. Rodríguez-Martínez[1], P. A. Robles[1], C. A. Meza-Herrera[3], F. G. Véliz[1], and G. Arellano-Rodríguez[1], *[1]1Universidad Autónoma Agraria Antonio Narro, Torreón, Coahuila, México, [2]Instituto Tecnológico de Torreón, Torreón, Coahuila, México, [3]Universidad Autónoma Chapingo, Unidad Regional Universitaria de Zonas Áridas, Bermejillo, Durango, México.*

In the present study it was determined if the contact of estrogenized female goats with bucks promotes the end of sexual activity of young or adult Alpine bucks in northern Mexico (26° N). Alpine adult (n = 8, 4-yr-old) and young bucks (n = 10, 1-yr-old) were divided into 2 homogeneous groups regarding their body condition score and body weight. All animals were reared in an intensive system and had free access to alfalfa hay and 200 g commercial concentrate (14% CP). On January 15, 2010, a first group of adult bucks (Experimental-Adult, n = 4) was daily exposed during 4 weeks to 2 goats permanently in estrus (does received 2 mg estradiol cypionate every 3 d). During this period, another group of adult bucks (Control-Adult, n = 4) had no contact with estrogenized does. A third group of young bucks (Experimental-Young, n = 5) was daily exposed during 4 weeks to 2 estrogenized does. A fourth group of young bucks (Control-Young, n = 5) did not have contact with does in estrus. At the end of the study (16 February, 2010) a sexual behavior test was carried out; males of both groups were exposed to 2 females in estrus for 15 min, for 2 consecutive days. Percentage of anogenital sniffing, nudging, mounting attempts, and complete mounts were compared with the Chi-squared test, whereas latency to ejaculation was compared with a Students *t*-test. All statistical tests were performed with the statistical package SYSTAL 12. The results of sexual behavior tests are indicated in Table 1. These results indicate that exposure of young bucks to estrogenized does elicited a strong sexual response in these animals; on the other hand, nonstimulated adult bucks displayed the same sexual performance as that showed by adult bucks in contact with estrogenized does.

Table 1. Sexual behavior of adult or young French Alpine bucks, previously isolated or exposed to goats permanently in estrus during two evaluations at the end of the breeding season

Groups	Anogenital sniffing	Nudging	Mounting attempts	Complete mounts	Latency to ejaculate	Aggression
Control-Young	28[a]	18[a]	1[a]	0[a]	901[a]	16[a]
Experimental-Young	66[b]	47[b]	23[b]	7[a,b]	484[b]	2[b]
Control-Adult	35[a]	37[a,b]	0[a]	9[b]	15[c]	0[b]
Experimental-Adult	38[a]	23[a]	1[a]	9[b]	26[c]	0[b]

[ab]Different superscripts within columns, indicate statistical differences ($P < 0.05$).

Key words: bucks, females in estrus, breeding season

W422 NCSynch: A protocol for ovulation synchronization and timed artificial insemination in goats. E. C. Bowdridge*, W. B. Knox, C. S. Whisnant, and C. E. Farin, *North Carolina State University, Raleigh.*

The study objective was to compare overall pregnancy rates achieved using a combined ovulation synchronization-timed artificial insemination protocol (NCSynch-TAI) with those obtained using estrus synchronization and artificial insemination (AI). Multiparous Boer and Boer-cross does (n = 132) were randomly assigned within age (Year 1) or parity (Years 2, 3) to one of 2 treatments. Control does received 15 mg prostaglandin F (PGF; Lutalyse®) on Days 1 and 10 of treatment. Estrus onset was checked twice daily with separately penned, intact bucks (Year 1) or a vasectomized buck penned with the does (Years 2, 3). Controls were bred by AI 12 h after estrus onset using frozen semen. NCSynch-TAI does received 15 mg PGF on Day 1 of treatment. On Day 8, does received 50 μg GnRH (Cystorelin®) and on Day 15, 15 mg PGF was given. On Day 18, NCSynch-TAI does were appointment bred (TAI) using frozen semen and received 50 μg GnRH at breeding. All AI/TAI procedures were performed in late September by experienced inseminators using a transcervical technique. Pregnancy was monitored by transabdominal ultrasonagraphy at 50 and 85 d after insemination. In Year 1, 13 of 15 control does (87%) were detected in estrus with 8 pregnant to AI (53% overall pregnancy rate). For NCSynch-TAI, 15 does were bred and 11 (73%) became pregnant. In Year 2, 24 of 26 controls (92%) were detected in estrus with 19 pregnant to AI (73% overall pregnancy rate). For NCSynch-TAI, 26 does were bred and 20 (77%) became pregnant. In Year 3, 21 of 25 controls (84%) were detected in estrus with 8 pregnant to AI (32% overall pregnancy rate). For NCSynch-TAI, 25 does were bred and 14 (56%) became pregnant. Across Years 1–3, the overall pregnancy rate for NCSynch-TAI does (45/66, 68%) did not differ ($P = 0.075$, Chi^2 df = 1) compared with controls (35/66; 53%). In summary, overall pregnancy rates using NCSynch-TAI were comparable to those for does bred by AI based on estrus detection. Use of NCSynch-TAI eliminates the need for heat checking before AI and allows breeding to be scheduled on a predetermined date. Supported by NC Ag Research Service.

Key words: ovulation synchronization, estrus synchronization, timed artificial insemination

W423 Comparison of two ovulation synchronization methods for timed artificial insemination in goats. N. C. Whitley*[1], C. E. Farin[2], W. B. Knox[2], L. Townsend[3], J. R. Horton[3], K. Moulton[1], and S. Nusz[4], *[1]North Carolina A&T State University, Greensboro, [2]North Carolina State University, Raleigh, [3]NCDA, UMRS, Laurel Springs, NC, [4]Redlands Community College, El Reno, OK.*

The objective of this experiment was to compare 2 potential estrus and ovulation synchronization protocols for timed artificial insemination (TAI) in goats. Thirty-eight mixed parity meat goat does (Spanish and Boer-crossbred) were used at 3.4 ± 0.3 years of age and 47.4 ± 1.3 kg body weight. Half of the does underwent the "NCSynch" protocol in which does were injected with 15 mg dinoprost tromethamine (3 mL Lutalyse) im on d 0, or start of the protocols, and d 14 and 50 μg gonadorelin diacetate tetrahydrate (1 mL Cystorelin) im on d 7 as well as on d 17 at TAI. Remaining does were administered a CIDR protocol in which sheep CIDRs were inserted on d 4 and removed on d 15. The CIDR group received 3 mL Lutalyse and a combination of 200 IU eCG and 100 IU hCG (2.5 mL PG600) im at CIDR removal; TAI occurred on d 17. Does were housed together throughout the study and were allowed fence-line access to an intact buck on d 15. Trans-cervical insemination was conducted by 2 experienced technicians alternating between groups such that equal numbers of does from each treatment were inseminated by each technician. One doe from the CIDR group was removed at insemination due to an unknown physical problem making it impossible to penetrate the cervix. An intact buck wearing a marking harness was introduced at 21 d after TAI. Blood samples were collected via jugular vein puncture at 31 d after insemination to determine pregnancy status (bioPRYN®; BioTracking, LLC). Pregnancy rates were higher ($P < 0.009$) for animals treated with the CIDR protocol (50%) than the NC-Synch protocol (10.5%) based on Chi-Square analysis. However, bioPRYN levels for one of the CIDR treated does was indicative of an early pregnancy loss and the doe was later marked by the buck. The buck marked more ($P < 0.005$) NCSynch treated does than CIDR-treated does (84% vs 39%, respectively). Previous use of the NCSynch protocol with the same inseminators resulted in higher pregnancy rates than seen with either protocol in this study; however, because both protocols are costly and labor intensive to use, more research will be required.

Key words: estrus synchronization, goat, timed artificial insemination

W424 Effect of flushing and (or) exposure to estrogenized does upon reproductive performance of anovulatory range goats exposed to male effect. M. A. De Santiago-Miramontes*[1], J. R. Luna-Orozco[1], F. G. Véliz-Deras[1], R. Rodríguez-Martínez[1], P. A. Robles-Trillo[1], C. A. Meza-Herrera[1], and M. Mellado[1], *[1]Universidad Autonoma Agraria Antonio Narro, [2]Centro de Bachillerato Tecnologico Agropecuario N° 1, [3]Universidad Autonoma Chapingo, Unidad Regional Universitaria de Zonas Aridas.*

The objective is to determine if flushing around mating or the stimulus of estrogenized goats is necessary to achieve a high reproductive response in anestrous mixed-breed rangeland goats (arid region of Mexico; 26° N). On May 21, 78 goats grazing on natural rangeland (1.6 ± 0.2 points, BCS, 1–4 scale) were randomly assigned to 1 of 4 experimental groups: (1) Flushed (F; n = 20) does received nutritional supplementation 1 week prior joining and 2 weeks after, receiving 1.0 kg of alfalfa hay (17% CP), 310 g rolled corn grain (8.5% CP) and 220 g soybean meal (48% CP) per animal. (2) Stimulated (S; n = 20) does was exposed to 4 estrogenized females. (3) Stimulated-Flushed (S-F; n = 20) does was supplemented and stimulated as mentioned. (4) Control (C; n = 18) does only grazed on the rangeland. All the does were exposed to 2 bucks/group. Regardless of treatment, 100% of does showed luteal activity. S and S-F groups depicted estrus during the first 5 d of joining (45 and 60%, respectively) compared with C or F group (11 and 5%, respectively; $P < 0.05$). Hours to estrus was greater ($P < 0.01$) in C (225 ± 18 h) and F (271 ± 19 h) groups than in S (130 ± 22 h) and S-F group (104 ± 16 h). Pregnancy rate did not differ at d-70 post-breeding among groups ($P > 0.05$; C, 72%; F, 80%; S, 70%; S-F 65%). However, kidding rates were lower ($P < 0.05$) in F and S-F groups, (40% and 35% respectively) compared with C (67%) and S (55%) groups. These results demonstrate that the presence of estrogenized does shortens the interval to estrus induced by the male effect. Nonetheless, the short-term nutritional supplementation around joining promoted the fertilization-implantation, did not improve the reproductive performance because of the failure to maintain gestation, probably due to the adverse nutritional conditions in the rangeland after the 2/3 of gestation. Therefore, alternative food resources must be offered to those supplemented-goats showing an increased ovulatory outcome around breeding once these females arrive to the 2/3 and 3/3 of gestation, if abortions or stillbirths is tried to be avoided.

Key words: feed supplementation, rangeland, kidding rate

W425 Exposure of does in estrus to bucks subsequently induces estrus in anestrus females. S. Marcelino-León*[1], J. R. Luna-Orozco[1], F. G. Véliz-Deras[1], L. Gaytán-Alemán[1], C. A. Meza-Herrera[1], R. Rodríguez-Martínez[1], M. Mellado[1], and M. A. De Santiago-Miramontes[1], *[1]Universidad Autonoma Agraria Antonio Narro, [2]Centro de Bachillerato Tecnologico Agropecuario N° 1, [3]Universidad Autonoma Chapingo, Unidad Regional Universitaria de Zonas Aridas.*

The objective of the present study was to determine if the stimulus exerted by the exposure of estrogenized does to bucks would stimulate the estrous behavior in mixed-bred anovulatory goats in the arid region of northern Mexico, also, determine if an increased percentage of estrogenized does would modify such response. A total of 93 pluriparus anovulatory goats were divided in 3 experimental groups (n = 31, each) and exposed to 2 males per group. Thereafter, one group was also exposed to 6 estrogenized does (G20%), a second group was exposed to 3 estrogenized does (G10%), and the third group was exposed to 6 non-estrogenized does (G0%). Proportions of does in estrus were analyzed with chi-squared test while hours to estrus was compared with a Student *t*-test. Systat 12 statistical package was used. The proportion of does displaying estrous behavior during the study was similar in both the G10% and G20% groups (93%, 90%, respectively; $P > 0.05$), although different in the G0%, where no female demonstrated estrous behavior (P 0.01). In addition, hr to estrus was greater in G10% (167.8 ± 17 h) than in G20% (142 ± 20 h; $P < 0.001$). These results indicate that estrogenized does exposed to "effected" male goats positively affected the percentage of goats depicting estrous behavior of anovulatory goats exposed to the male effect. In addition, an increased percentage of anovulatory goats depicting estrous behavior of female goats during the anestrous season.

Key words: female effect, seasonal anestrous, sexual activity

W426 Influence of sexually inactive bucks subjected to either long photoperiod or testosterone upon the induction of estrus in anovulatory goats. J. M. Guillén-Muñoz*[1], J. R. Luna-Orozco[2], L. M. Tejeda-Ugarte[1], M. A. De Santiago-Miramontes[1], M. Mellado[1], F. G. Véliz[1], R. Rodríguez-Martínez[1], and C. A. Meza-Herrera[3], *[1]Universidad Autónoma Agraria Antonio Narro, Torreón, Coahuila, México, [2]Centro de Bachillerato Tecnológico Agropecuario No 1, Torreón, Coahuila, México, [3]Universidad Autónoma Chapingo, Unidad Regional de Zonas Áridas, Bermejillo, Dgo., México.*

The objective of this study was to evaluate the efficacy of exposing sexually inactive bucks to either artificial long photoperiod or testosterone upon the induction of estrus of anovulatory goats under rangeland conditions. Multiparous mixed breed anestrous goats (n = 91) were randomly assigned to one of 3 treatment groups: I. Joining with bucks subjected to 2.5 mo of artificial long days (16 h of light/d; PHOTO; n = 31), II. Joining with testosterone-treated bucks (TESTO; n = 30), and iii. Joining with untreated bucks (CONTROL; n = 30). Two bucks were assigned to each treatment group. The breeding season was from August to February and estrus response was measured twice a day (0800 to 1000 and 1800 to 2000 h). Percentages of goats in estrus and conception rates were analyzed with the Fisher exact test, interval to estrus was analyzed by PROC-GLM, and buck sexual behavior was analyzed with the Fisher exact test. While no differences where observed ($P > 0.05$) between the light-treated (100%) and testosterone-treated (93%) bucks in their ability to induce estrus of anovulatory does, none of the goats exposed to the CONTROL-buck exhibited estrus behavior ($P < 0.05$). The interval from the onset of mating to estrus was shorter ($P < 0.05$) in those goats exposed to the light-treated bucks (37.9 ± 4.8 h) as compared with those exposed to the TESTO-treated bucks (58.3 ± 8.7 h). Overall pregnancy rate in goats joined to PHOTO, TESTO and CONTROL bucks was 84, 77, and 0%, respectively, with no differences ($P > 0.05$) between the first 2 groups. Ano-genital sniffing, approaches, mounting attempts and mounts were highest ($P < 0.01$) in the PHOTO-group and lowest in CONTRO-group. Both PHOT and TESTO treated bucks were equally effective in synchronizing estrus in anovulatory goats and resulted in similar levels of fertility under rangeland-extensive conditions.

Key words: male effect, photoperiod, reproductive outcomes

W427 Nutritional supplementation before or after the breeding season does not improve the productive and reproductive response of goats managed under a marginal production system in Northern Mexico. C. G. Orta-Castillón[1], C. A. Meza-Herrera[2], G. Arellano-Rodríguez[1], P. A. Robles-Trillo[1], M. A. De Santiago-Miramontes[1], R. Rodríguez-Martínez[1], M. Mellado[3], and F. G. Véliz*[1], *[1]Universidad Autónoma Agraria Antonio Narro, Torreón, Coahuila, México, [2]Universidad Autónoma Chapingo, Unidad Regional Universitaria de Zonas Áridas, Bermejillo, Durango, México, [3]Universidad Autónoma Agraria Antonio Narro, Saltillo, Coahuila, México.*

The aim of this study was to determine if feed supplementation before or after the breeding season improves both productive and reproductive performance of mixed-breed goats under rangeland conditions in northern Mexico. Three groups of goats grazed (11:00 to 17:00 h) on rangeland and field crop residues. Goats in one group were offered feed supplement 5 d before and 20 d after breeding (SS, n = 37; 2.2 ± 0.1, CC scale 1.4, and 39.7 ± 1.2, kg BW), other group (SS-After, n = 40; 2.2 ± 0.1, CC and 39.9 ± 1.0 kg) received feed supplement only 5 d before breeding. Both groups were fed a ration which provided 75% of their energy and protein requirements for maintenance. The control group (n = 24; 2.3 ± 0.4, CC and 39.5 ± 0.9 kg BW) received no feed supplementation during the experimental period. On March 20th 2010, experimental groups were exposed to 4 bucks which were induced to an intense sexual activity by means of a photoperiodic treatment of 2.5 mo of long day photoperiod scheme (16 h light/day) starting on November first. Differences in the proportion of does showing estrus activity and diagnosed pregnant were detected by using the exact probability test of Fisher. Differences in litter size were compared with the Kruskal-Wallis test. The statistical analyses were carried out with the Systat 10 program (Evenston, IL, USA). The results are shown in Table 1. Overall 83% of goats showed estrus during the experimental period with no difference between groups ($P > 0.05$). Percentage of pregnancy (mean 70% across groups) and ovulatory rates (1.5 ± 0.1 across groups) were similar between groups ($P > 0.05$). These results suggest that mixed-breed multiparous goats in good body condition under extensive-range production systems in northern Mexico, did not benefit from feed supplementation before or after breeding in spring.

Table 1. Reproductive performance of mixed-breed goats supplemented before or after breeding[1]

Goats	Estrus activity (%)	Pregnancy rate (%)[2]	Kidding rate (%)	Litter size (mean±SD)
CG	(88) 38/43	(70) 30/43	(63) 27/43	1.4 ± 0.1
SS-After	(85) 33/39	(74) 29/39	(69) 27/39	1.4 ± 0.1
SS	(79) 33/42	(67) 28/42	(60) 25/42	1.6 ± 0.1

[1]For all variables no statistical differences were detected among groups ($P > 0.05$).

[2]Pregnancy rate at 50 days after the last copulation.

Key words: nutritional supplementation, goat, reproduction

587 Comparison of porcine cathelicidin expression between Jinhua and Landrace pigs. Y. Gao*, S. An, Y. Xie, Y. Liu, F. Han, C. Luan, and Y. Wang, *Institute of Feed Science, Zhejiang University, Hangzhou, Zhejiang Province, China.*

Cathelicidins are important antimicrobial peptides with both antimicrobial and immunomodulatory functions in porcine innate immunity. However whether the expression levels of cathelicidin genes contribute to the disease resistance capabilities between different pig breeds still remains unclear. Therefore the present study was aimed to investigate the tissue-specific and developmental expression of Protegrin-1, Prophenin-2 and PR-39 genes in Jinhua pigs, in addition compare the baseline differential expression of these 3 cathelicidin genes between Chinese local Jinhua pigs and foreign landrace pigs at 20-d of age (before weaning) and 40-d of age (after weaning) by using quantitative real-time PCR. The results showed that cathelicidin genes were expressed in bone marrow, spleen, liver, lung, mesenteric lymph node, kidney and duodenum in both Jinhua and landrace pigs at 20- and 40-d of age. Bone marrow is the major expression site for the above 3 cathelicidin genes and the expression levels in bone marrow were significantly higher than in other tissues ($P < 0.05$). Spleen, liver, mesenteric lymph node and lung had moderate expression of cathelicidin genes. Jinhua pigs showed higher expression of Protegrin-1, Prophenin-2 and PR-39 in bone marrow, spleen, liver, mesenteric lymph node compared with landrace pigs at 20- and 40-d of age, and the difference were significant in bone marrow between breeds ($P < 0.05$). Moreover, cathelicidin genes were developmentally regulated in Jinhua pigs from neonatal to 120-d of age. Taken together, those results indicated that bone marrow was the major expression site of cathelicidin genes in both Jinhua and Landrace pigs, and the higher baseline expression of cathelicidin in Jinhua pigs may contribute to the better disease resistance capabilities, suggesting the expression of cathelicidin genes could relate to the disease resistance capabilities between different pig breeds.

Key words: cathelicidin, gene expression, Jinhua pigs

588 The effect of prenatal stress and dominance order on immune function in response to a DTH and LPS challenge in pigs. B. L. Davis*[1], M. A. Sutherland[1,2], and M. A. Ballou[1], *[1]Texas Tech University, Lubbock, [2]Ruakura Research Centre, AgResearch, Hamilton, New Zealand.*

Prenatal stress (PNS) is caused by elevated maternal glucocorticoid concentrations crossing the placenta to the fetus, resulting in potentially long-term physiological, immunological and behavioral changes in the offspring. The objective of this research was to determine the effects of PNS and dominance order on the cell mediated and acute-phase immune responses. Sows were either injected with adrenocorticotropic hormone or sham handled 3 times a week, from d 76 to 115 of gestation. At weaning, barrows from the stressed (PNS; n = 15) and sham (PNS; n = 15) sows were housed in groups of 3 within the same treatment. At 28 d of age, a food deprivation test was used to determine the dominance order of pigs within each pen. Pigs were denoted as being dominant (DOM), intermediate (INT) or submissive (SUB). A delayed-type hyperresponsivity (DTH) test was performed to assess the cell mediated immune response. One week after the DTH test, each pig was injected intraperitoneally with (include the dose) lipopolysaccharide (LPS) to stimulate an acute phase response. Blood samples were collected from pigs before and 60, 120, 360 min and 24 h after the LPS challenge to measure complete leukocyte counts and differentials; as well as plasma concentrations of cortisol and C-Reactive protein. Rectal temperatures were taken at the same time blood samples were collected. Data were analyzed using the MIXED procedures of SAS. Prenatally stressed pigs had a greater ($P < 0.05$) DTH response than CON pigs and DOM pigs had a lower ($P < 0.05$) DTH response than SUB pigs. Rectal temperature and total leukocyte counts changed ($P < 0.05$) over time in response to the LPS challenge; however, neither prenatal stress nor dominance order influenced the response. Cortisol concentrations following the LPS challenge were greater ($P < 0.05$) in DOM compared with INT pigs and tended ($P = 0.084$) to be greater than SUB pigs. The neutrophil to lymphocyte ratio was greater ($P = 0.05$) in SUB pigs than INT pigs. In conclusion, prenatal stress and dominance order affected both cell mediated immune function and the physiological response to an LPS challenge in barrows.

Key words: pigs, prenatal stress, immune

589 Effects of *Lactobacillus fermentum* I5007 on the redox state of healthy and oxidative-stressed piglets. C. J. Cai*, A. N. Wang, L. C. Chu, S. Y. Qiao, and D. F. Li, *China Agricultural University, Beijing, China.*

The study was conducted to investigate the effects of *Lactobacillus fermentum* I5007 (LF) on the redox state of healthy and oxidative-stressed piglets. A total of 24 weaned barrows (7.19 ± 0.22 kg) were randomly assigned to 1 of 4 treatments: control group (T1), stress group (T2), control group orally administrated LF (T3), and stressed group orally administrated LF (T4). The trial period lasted 21 d. Pigs in T3 and T4 were orally administrated with 20 mL/d (10^8 cfu/ml) LF. On d 8, pigs in T2 and T3 were injected intraperitoneally with diquat at 10 mg/kg body weight, while pigs in T1 and T4 were injected the same volume of isotonic saline. Following the injection, blood was collected at 0.5 h, 1.5 h, 3.5 h, 7.5 h and 14.5 h. At the end of the experiment, all pigs were killed and the liver was sampled. Data were analyzed using the GLM procedure of SAS. The effects of diquat, LF and their interaction were included in the statistical model. The results showed that compared with saline-injected pigs, the diquat-injected pigs had decreased growth performance ($P < 0.05$) during 2 wks after injection, and the increased levels of cortisol (26.90 vs 144.72 pg/ml, $P < 0.01$), adrenaline (3.68 vs 27.90 ng/ml, $P < 0.01$), the free fatty acid (67.02 vs 186.75 μmol/L, $P < 0.01$), glucose (26.90 vs 144.72 mg/dl, $P < 0.01$), malondialdehyde (MDA, 3.67 vs 4.03 nmol/ml, $P < 0.01$), and carbonyl (0.93 vs 1.06 nmol/mg protein, $P < 0.05$) in the plasma from 1.5 h to 14.5 h. Regardless of diquat, supplementation of LF improved the ADG (416 vs 446 g, $P < 0.05$) and ADFI (630 vs 667 g, $P < 0.05$); increased superoxide dismutase (105.23 vs 120.89 U/mg protein, $P < 0.05$), glutathione peroxidase (93.94 vs 103.54 U/mg protein, $P = 0.05$) and the ability to inhibit superoxide anion production (AISP, 316.90 vs 351.34 U/g protein, $P = 0.05$), and reduced the levels of MDA (3.66 vs 3.45 nmol/mg protein, $P < 0.05$) in pig liver. In conclusion, this study indicated that LF increased the growth performance of pigs, improved the antioxidative defense system, and alleviated the oxidative damage caused by oxidative stress.

Key words: *Lactobacillus fermentum*, piglet, oxidative stress

590 In vitro antibacterial activity, cytotoxicity and mechanisms of cathelicidin peptides against enteric pathogens in weaning pig-

lets. Y. Liu*, S. An, C. Luan, and Y. Wang, *Institute of Feed Science, Zhejiang University, Hangzhou, Zhejiang Province, China.*

In the last few decades, long-term and high-dose usage of antibiotics in livestock diets induces the emergence of antibiotic resistance bacteria, antibiotics residues in animal products and environmental pollution, which have adverse effects on animal health and well-being. This study investigated 5 cathelicidin peptides from different animal origins (i.e., protegrin-1[PG-1], PMAP-23, LL-37, indolicidin and cathelicidin-BF[C-BF]) as antibiotic replacements with higher antimicrobial activity and lower cytotoxicity and to study their mechanisms of action toward enteric pathogens in vitro. The antibacterial activity was evaluated via minimum inhibitory concentration (MIC) determinations, killing kinetics and synergy assays. The morphology of peptide-treated bacteria was observed by transmission electron microscopy and intracellular function was determined by DNA binding and cell-free protein synthesis assays. Finally, cytotoxicity was assessed by hemoglobin release, cell viability and lactate dehydrogenase release assays. PG-1 from porcine and C-BF from snake had the most effective bacteriocidal properties and widest spectra of activity, with the MIC values equal to or lower than commonly used antibiotics toward several *Escherichia coli* isolates and Salmonella strains, and showed a synergistic effect with aureomycin. Mechanism studies for PG-1 and C-BF suggested the C-BF killing mechanism was based on membrane permeability, while multiple targets existed for PG-1, including membrane and intracellular biomacromolecules. Cytotoxicity tests showed PMAP-23 and C-BF exhibited the lowest cytotoxic effects, while PG-1, LL-37 and indolicidin displayed cytotoxicity by dose. Although PG-1 showed strong cytotoxic activity, there was less than 20% lysis at 8 Î1/4g/mL at which there was remarkable antimicrobial activity. This study demonstrated that C-BF has the capacity to inactivate enteric pathogens with lower cytotoxicity and is potentially a novel anti-bacterial agent. The activity of PG-1 is highly efficient, with the potential to reduce cytotoxicity using molecular design.

Key words: cathelicidin peptides, antibacterial activity, mechanism of action

591 Microbial transmission and assembly of the gut microbiota in neonatal pigs on day 7 and 14 postfarrowing. E. E. Hinkle*, I. Martinez, J. Walters, P. S. Miller, and T. E. Burkey, *University of Nebraska-Lincoln, Lincoln.*

The gastrointestinal microbiota (GM) effects gut maturation, nutrient metabolism, host immunity, and protection from pathogens. We employed 454-pyrosequencing of 16S rRNA tags to evaluate 1) effect of dam parity (P) on microbial ecology, and 2) microbial transmission from sows to their progeny. Fecal samples were collected from P1 and P3 sows (n = 6/P; d 7 postfarrowing) and 1 piglet/litter on d 7 and 14 postfarrowing. Microbial DNA was extracted and pyrosequenced (Roche Genome Sequencer GS-FLX Titanium). Quality controlled, chimera checked sequences were taxonomically assigned (Classifier, Ribosomal Database Project). An α diversity (Shannon) measure was determined using Qiime. Phylogenetically blasted β diversity was obtained (UniFrac). There were no P effects on GM composition or diversity. The phyla Firmicutes and Bacteroidetes dominated in P1 (83.8% and 5.6%, respectively), and P3 sows (91.0% and 3.1%, respectively). A parity × d ($P < 0.05$) interaction was observed within the phylum Firmicutes. Specifically, P1 sows (83.8%) and d 7 progeny (81.48%) had increased Firmicutes compared with their d 14 progeny (61.7%), and P3 sows (91.0%) had increased Firmicutes compared with their d 7 (60.8%) and 14 (63.0%) progeny. Time effects ($P < 0.05$) were observed for Bacteroidetes, Fusobacteria, and Proteobacteria among progeny from both parities. Bacteroidetes were increased ($P < 0.001$) in piglets compared with sows (11.0 and 25.4% vs. 5.6% for P1, 22.8 and 27.4% vs. 3.1% for P3; respectively, for d 7 and 14 vs. sows on d 7). Fusobacteria and Actinobacteria in progeny were greater on d 7 compared with d 14 (Fusobacteria, 4.13 and 0.17%, Actinobacteria, 4.49 and 0.45%; respectively). Proteobacteria in progeny was increased on d 14 (5.8 and 7.4% for P1 and P3 piglets, respectively) compared with d 7 (0.76 and 3.70% for P1 and P3 piglets, respectively). Sows had increased ($P < 0.001$) Shannon's index compared with progeny. The GM of progeny had greater β diversity than sows ($P < 0.001$). These results represent an initial investigation into transmission and establishment of microbial populations from sows to their progeny.

Key words: parity, gut microbiota, swine

592 Viability of *Parascaris equorum* eggs intermittently exposed to the interior of a windrow composting system. J. C. Gould*, E. T. Lyons, L. M. Lawrence, and M. G. Rossano, *University of Kentucky, Lexington.*

Parascaris equorum generally infects horses less than 18 mo; its pathological effects can be severe. The purpose of this study was to examine the effects of windrow composting on the viability of *P. equorum* eggs intermittently exposed to the interior of a windrow. ANKOM F57 filter bags were used as sentinel chambers and spiked with manure confirmed positive for *P. equorum* eggs. Starting on d 0, chambers were placed within the center of the windrow at 5 different locations, then alternated between resting on top of, or inside, the windrow whenever it was turned. Chambers from each location and control chambers were removed at d 2, 4, 6, 8, 10, 12, 14, and 18; chambers incubated for 21 d at room temperature (24°C). After incubation, chamber material was diluted with a 10% bleach solution, subsampled, and eggs were recovered using double centrifugation with Sheather's solution. Eggs were evaluated using a microscope and classified as viable or nonviable. Efficacy was assessed by 2-tailed *t*-test; a *P*-value of <0.05 was deemed to be significant. The average % viability of *P. equorum* eggs exposed to composting were 10.77, 0.31, 0.00, 0.00, 0.00, 0.00, and 0.00 on sampling d 2, 4, 6, 8, 10, 12, 14, and 18 respectively. The average % viability of control *P. equorum* eggs were 91.34, 79.97, 90.37, 89.93, 81.30, 86.74, 83.29, and 86.94 on sampling d 2, 4, 6, 8, 10, 12, 14, and 18 respectively. Intermittent windrow composting treatment reduced the percent viable eggs compared with the control on d 2 and 4 ($P < 0.000002$). By d 6, percent viable eggs for sentinel containers under the intermittent windrow composting treatment dropped to 0.00 and remained this way for d 8, 10, 12, 14, and 18. The results of this study demonstrate that a well maintained windrow composting system is capable of rendering *P. equorum* eggs nonviable even under intermittent exposure within the windrow.

Key words: parasite, *Parascaris equorum*, compost

593 Effect of a yeast nucleotide product on performance and health status of broilers. A. Ganner*, S. Schaumberger, J. Uhlik, and G. Schatzmayr, *BIOMIN Research Center, Tulln, Lower Austria, Austria.*

Nucleotides are involved in various essential biochemical processes; in animal studies dietary nucleotide supplementation has been shown to exert positive effects on performance, growth, gut health and the immune system. Yeasts as feed additives are an economical and practi-

cal way to provide concentrated nucleotides to the animal. The present study was conducted to evaluate the efficacy of a product, consisting of purified nucleotides, on performance and health status of broilers. The nucleotide product contained 27% RNA-monomers (AMP 9%, GMP 6%, CMP 5%, UMP 4%, nucleosides 3%). In a 35-day study, 675 1-d-old mixed sexed broilers were distributed into 3 experimental groups with 8 replicates: control group A, group B and C with 0 kg, 0.2 kg and 2 kg of nucleotide product per ton feed. Directly after housing the chicks were supplied with the experimental diets. Feed and water were provided ad libitum, feeding was done manually several times a day. Chicks were group weighed at day 1, day 14 and single weighed at day 35. On day 14, statistical significant differences ($P < 0.05$) for weight and average daily weight gain could be observed in group C (2 kg per ton feed) compared to group B (0.2 kg per ton feed) and the control group. At the end of the trial no more statistical differences could be observed in group C ($P > 0.05$), but group B showed positive trends over all parameters (weight day 35, $P = 0.5$; average daily weight gain (ADWG) day 15-35, $P = 0.1$; ADWG d 1-35, $P = 0.5$; FCR d 15-35, $P = 0.09$; FCR d 1-35, $P = 0.2$) compared to group C and the control group. Mortality was slightly reduced in both trial groups with 1.3%, compared to the control (1.8%). Our results indicate that proper nucleotide dosage and supplementation period may have beneficial effects on broilers growth and performance; however over-dosage of nucleotide additives which could cause loss in performance through potential over-reaction of the immune system should be avoided.

Key words: yeast nucleotides, broiler performance, growth

594 The effect of *Vernonia amygdalina* leaf extract on Alloxan-induced diabetic rats. A. H. Ekeocha*, P. C. Ekeocha, and T. Fashola, *University of Ibadan, Ibadan,Oyo,Nigeria.*

The hypoglycaemic or sugar reducing effect of the bitter leaf extract (BLE) was determined using Alloxan-induced diabetic rats. Thirty male Albino rats were divided into 6 groups of 5 rats. Four groups with basal blood sugar levels of 38 ± 0.16, 39.2 ± 0.23, 35.2 ± 0.27, and 35.8 ± 0.25 mg/dl were injected with 10% alloxan in saline to make them diabetic (277.6Â ± 6.55, 284.8 ± 3.80, 256.4 ± 1.39 and 265.6 ± 4.41 mg/dl fasting blood sugar (FBS) respectively). The 4 diabetic groups were then treated with different doses (g/kg body weight, BW) of an aqueous extract of dried bitter leaf herein referred to as BLE. A fifth group (non diabetic) was treated with 400mg BLE /kg BW. BLE was administered twice daily for 2weeks using an oral cannula. The sixth group (non-diabetic) received no BLE as a positive control. Blood was collected from the tail to determine blood on a glucometer. The FBS levels of the 6 albino rat groups were recorded every 2 days for 2 weeks. At the end of wk 2, the rats were slaughtered and their liver, kidney and pancreas examined. Data were analyzed using ANOVA (SAS, 1999). All the rats injected with alloxan became diabetic as their fasting blood sugar (FBS) levels exceeded the normal range of between 80 and 100 mg/dl. The FBS of the diabetic albino rats significantly ($P < 0.05$) decreased as BLE levels increased from 50 to 400 mg/kg BW on days 2, 4, 6, 8, 10, 12 and 14 (Table 1). The plant extract was observed to have a hypoglycemic effect on each group of diabetic rats as it reduced FBS levels (mg/dl) from 277.6 ± 6.55 to 92.0 ± 1.68 (Group 1), 284.8 ± 3.80 to 68.8 ± 0.41 (Group 2), 256.4 ± 1.39 to 55.8 ± 0.49 (Group 3) and 265.6 ± 4.41 to 38.4 ± 0.21 (Group 4) over a period of two weeks. The extract reduced the level of damage to the kidney, liver and pancreas when administered on diabetic rats. The rats were considered treated when their FBS returned to almost their basal blood sugar (BBS) levels. *Vernonia amygdalina* has anti-diabetic properties as it reduced the blood sugar level of albino rats.

Table 1. Fasting blood sugar (mg/dl) of normal and induced-diabetic albino rats administered with varying doses of *Vernonia amygdalina* leaf extracts

No of days	Gp1	Gp2	Gp3	Gp4	Gp5	Gp6	SEM
2	237.4^{a}	226.6^{b}	203.2^{c}	201.8^{c}	65.6^{d}	54.4^{e}	2.1
4	231.2^{a}	200.0^{b}	151.6^{c}	94.0^{d}	60.0^{e}	46.0^{f}	2.1
6	196.0^{a}	176.0^{b}	94.0^{c}	72.0^{d}	55.0^{e}	44.0^{f}	1.3
8	163.4^{a}	132.0^{b}	89.0^{c}	62.0^{d}	47.6^{e}	41.8^{f}	1.6
10	142.2^{a}	102.0^{b}	75.0^{c}	50.8^{d}	42.2^{e}	41.2^{e}	1.5
12	110.4^{a}	80.0^{b}	61.0^{c}	44.0^{d}	42.2^{de}	40.0^{e}	1.7
14	92.0^{a}	68.8^{b}	55.8^{c}	38.4^{d}	38.0^{d}	40.0^{d}	1.6

Means on the same row with different superscripts differ significantly.

Key words: *Vernonia amygdalina* leaf extract, Alloxan-induced diabetic rats

Breeding and Genetics Symposium: Is There Space for Genomic Selection in Small Populations?

595 Is genomic selection a one size fits all? I. Misztal*, *University of Georgia, Athens.*

Several methods are used for genomic selection (GS). A multi step method in dairy involves a regular BLUP, creation of pseudo-observations for animals with genomic information, genomic prediction (GP) for genotyped animals, and creation of an index with parent average. This method is successful when models for prediction are simple, genotyped animals include high accuracy bulls, and the number of genotypes is >2000. When genotyped animals have low or variable accuracy, approximations in pseudo-observations, GP and the index reduce the accuracy of prediction and create biases. Lack of the index results in lower accuracy especially for animals farther from the reference population. Another method of GS applies GP directly to phenotypes and genotypes of reference populations. The resulting equations are used for prediction, either directly or as a correlated pseudo-trait in a regular evaluation. This method is simple but less accurate because it ignores information from ungenotyped ancestors and from correlated traits. Also, accuracy of predictions for animals far from the reference populations may be very low. The newest method for GS is single-step GBLUP (ssGBLUP), which is conventional BLUP except that the pedigree-based relationship matrix is modified by SNP-derived relationships. In tests, ssGBLUP seems to be the most accurate one as it utilizes all the information with few approximations. Issues implicitly present in the other methods but explicit in ssGBLUP are proper scaling of genomic relationships, removal of genotype and pedigree conflicts, realistic approximation of accuracies, and optimal selection of animals for genotyping to minimize costs. The additional accuracy due to GS is approximately $\sim\sum[(a^{ij}-g^{ij})^2\ acc_j^2]$, where a_{ij} (g_{ij}) are pedigree (genomic) relationships between animal i and j, and acc_j is accuracy for animal j. The additional accuracy is maximized by selection of reference animals with high accuracy who are strongly related to candidates for selection. In populations where an individual is inexpensive, expanding progeny sizes may be more cost effective than extra genotyping.

Key words: genomic selection, accuracy, single step

596 Is there value in maintaining small populations? Example of the Dual-Purpose Belgian Blue breed. N. Gengler*[1,2], H. Soyeurt[1,2], C. Bastin[1], B. Buske[1], S. Vanderick[1], and F. Colinet[1], *[1]Ulg - GxABT, Gembloux, Belgium, [2]FNRS, Brussels, Belgium.*

Current status of thinking on genomic selection in dairy cattle is mostly major breed centric (e.g., Holstein) and only for traditional traits (e.g., milk yields). Once you depart from this, it becomes obvious that different, often related, issues appear (e.g., lack of large training populations, need for expensive recording of new phenotypes). Also, there is an urgent need to rethink issues that are important for sustainability of dairy production (e.g., added value foods, animal robustness). In this context, small populations (breeds/lines) could represent a potential source of extra information to justify their maintenance. As marker densities increase, efficient dissection of different selection histories of divergent breeds or lines, potentially identifying pockets of unexploited variability will increase. A current example from the Belgian (Walloon) perspective is the Dual Purpose (DP) line of the Belgian Blue Breed (BBB), with presently around 4500 breeding females, for historical reason of which only 1500 have good pedigrees, and which is present in Belgium and northern France. Recent research, done on this line, showed its tendency to produce less saturated milk fat and to have better fertility. Results indicated that it could stay competitive in specific markets, especially because of largely increased meat value. Currently, the myostatin mutation is largely used for breeding purposes. To assess the genetic diversity of the breed, recently, over 200 genotypes (SNP50K) for nearly all breeding bulls of the last 20 years became available. HD genotypes should be available in the near future, also allowing to access selection history of this breed as being in between the 2 extreme breeds: Beef BBB (with which it shares a recent history) and Holstein-Friesian (which is related through its geographic proximity over centuries). Finally, genomic selection for DP-BBB will need to consider a single step type approach without the need of reference population and potentially relying heavily on SNP3K of cows, also with the objective to recreate relationships between animals of interest.

Key words: genomic selection, milk quality, robustness

597 Overview of genomic selection in dairy cattle populations. P. M. VanRaden*[1] and J. R. O'Connell[2], *[1]Animal Improvement Programs Laboratory, ARS, USDA, Beltsville, MD, [2]University of Maryland School of Medicine, Baltimore.*

Genomic selection is most successful for traits recorded over many years in large populations. Holstein breeders have reference populations >10,000 proven bulls via cooperation among major countries, and countries with smaller Holstein populations can contribute additional bulls. Scandinavian red dairy cattle breeders have 8,000 reference bulls, and Brown Swiss breeders have a global population of 4,500 reference bulls at Interbull. Jersey breeders have genotyped but have not yet merged their 6,000 reference bulls. Denser chips can transfer genomic information across breeds if all breeds are in the same data set. Less dense chips with imputation to higher densities allow affordable selection for smaller populations or more recently recorded traits. The North American database now includes Illumina 2,900 marker (3K) or 50,000 marker (50K) genotypes for 74,389 Holsteins, 8,905 Jerseys, and 2,008 Brown Swiss, plus 777,000 marker (HD) genotypes for 435 animals. To determine how many HD animals within each breed may be needed for imputation, 600,000 marker genotypes were simulated for either the youngest animals or for older bulls with highest reliability, and the other animals had 40,000 markers. After imputation using findhap.f90 version 2, percentages of estimated genotypes that matched true genotypes ranged from 96.1 to 98.7% when numbers of HD genotypes ranged from 250 to 1000 within each of the 3 breeds. Imputation accuracy was about 1% less if the youngest animals instead of the older bulls had HD. The value of matching cow phenotypes to their own genotype instead of to their sire's genotype was demonstrated by excluding bulls and using only the 13,935 cows in the Holstein reference population instead of all 25,131 reference bulls and cows (official). For milk yield of young animals, the correlation was 0.86 between cow-only and official evaluations vs. 0.71 between parent average and official. Smaller populations can increase genomic reliability by exchanging information with large populations and by lower cost genotyping.

Key words: genomic evaluation, reference populations, breeds

598 Overview of genomic selection in small populations of beef cattle. G. L. Bennett*, W. M. Snelling, R. M. Thallman, J. W. Keele, and L. A. Kuehn, *USDA, ARS, US Meat Animal Research Center, Clay Center, NE.*

Efficiency and reproduction are important to beef production and are enhanced by using breeds adapted to specific management strategies and environments and by crossbreeding. Thus dozens of breeds are currently used in the US Genomic prediction of breeding value (MBV) needs large trait and genotypic data sets which favors breeds with many cattle. Breeds with small effective population sizes have longer blocks of linkage disequilibrium which they should exploit. Using equations for MBV trained in one population and applied in another has had limited success. New sources of data and analyses are needed to improve MBV. New genotyping assays with more than 10 times the SNP on current assays are expected to yield more robust associations across breeds but this is not proven yet. Using multi-breed data to train MBV predictions identifies markers with consistent associations across breeds but limits the proportion of variation that can be predicted within populations because population specific associations are often not detected. Analyses that utilize both general and breed specific marker associations need to be developed. Identifying the breed origin of an allele is a prerequisite for these analyses and haplotypes may have stronger associations across breeds than SNP alleles. Phenotypic data, especially for expensive or difficult traits, is particularly limiting in less numerous breeds. Breeds that are genetically less diverse (e.g., European Continental) are more likely to have consistent marker associations and might benefit from combining SNP data and expensive phenotypes. Some traits are difficult because they are measured on commercial animals that are not usually genotyped. A strategy of genotyping pools of cattle in from the tails of a trait distribution and using genomic relationships to these pools may be useful for some traits, particularly disease and reproduction, measured in unpedigreed progeny. Basic research to develop and use MBV has been done and is being used in the beef cattle industry, but there is a strong need for innovations that will make this progress accessible to more of the industry.

Key words: breeds, genotype, phenotype

599 Overview of genomic-assisted selection in swine populations. S. Forni*, *Genus Plc, Hendersonville, TN.*

Swine breeders have been successfully using genetic markers since the early 1990s. Marker assisted selection has been applied in the past 20 years and genetic gain was increased for several performance traits. Recent studies have shown that a relatively small number of markers can improve the predictive ability of breeding values by 40–60% for challenging traits such as scrotal hernia, mortality and litter size. Genomic information on a large reference population of swine is not available. Genomic-assisted selection in swine imposes large computational and statistical challenges because information is accumulated and selection decisions are made as often as weekly. The single-step genomic evaluation proposed recently for dairy cattle has appealing features for the swine industry. The method allows for the use of an unrestricted number of markers independent of the trait and accounts for non-genotyped animals in the population. Increases in accuracy of 30% for genotyped selection candidates have been observed in lowly heritable traits with the single-step evaluation. Accuracy improvement was also obtained when only the parents of selection candidates were genotyped. Different weights for specific markers can be incorporated in the method, and this is expected to improve predictive ability. Kernel-based methods can have similar properties regarding computational efficiency and can be used to include the effects of gene interactions in genomic-assisted evaluation. The outcomes of blending genomic information from different lines or swine breeds have not yet been well exploited. Results with simulated data have indicated that genomic information on parental lines could significantly impact the evaluation of performance in the commercial level, if non-additive effects are contemplated. Multi-breed genomic evaluation may also benefit from genotype imputation procedures because higher marker density is important for increasing evaluation accuracy. Methods to reduce genotyping costs and computation time are imperative for the full implementation of genomic-assisted selection in the swine industry.

Key words: genomic-assisted selection, single-step genomic evaluation, swine

600 Delivering livestock genetic improvement in a genomics era: Evolving roles and responsibilities. W. Herring* and K. Andersen, *Pfizer Animal Genetics, Kalamazoo, MI.*

Genomic usage in the genetic improvement business has rapidly evolved over the past 5 years. Until recently the research pipeline has been funded by government/university sources and commodity groups. However, due to the delivery of genetic improvement in each of these species and regional differences in the livestock production structure, the timeline of genomic utilization has and is varying differently. Poultry breeding companies have pursued a consortium approach involving breeding companies and university partners to provide their initial products. Retail swine genetics providers have relied primarily on their own funding to add value to their products. Dairy and beef represent the most diverse examples of utilization of genomic technologies. In the US, U.S.D.A. has heavily funded dairy genetic improvement and is also the source of the industry's genetic evaluations. Due to the heavy use of A.I. and recent efforts of aggressive genotyping, dairy has provided the most visible utilization of genomic technologies into genetic improvement platforms available to dairymen in North America. Conversely, beef cattle genetic evaluations are managed by breed societies and service providers that have been challenged with limited budgets and relatively small resource populations from which to grow their knowledge base. As a result, the largest beef breed societies maintain a position of more advanced execution, with smaller societies struggling to keep pace. Entrance of animal health companies as providers of genomic-based evaluations (primarily beef and dairy), into a space traditionally occupied only by societies and academic institutions that provide genetic evaluation services, is causing shifts in the culture and delivery of genetic improvement. These companies bring networks of expertise across disciplines, customer service, access to development funding and relationships with livestock producers. As shifts in regional production competitiveness are occurring in real-time, all with collaborative influence should be motivated to deliver the most rapid access to genetic improvement such that constraints to its utilization are removed.

Key words: genomics, genetics

Dairy Foods: Impact of Salt Reduction on Cheese

601 Influence of salt-in-moisture of full fat and low fat Cheddar cheese on microflora and flavor. D. J. McMahon*[1], C. J. Oberg[2], L. V. Moyes[2], R. E. Miracle[3], and M. A. Drake[3], *[1]Western Dairy Center, Utah State University, Logan, [2]Department of Microbiology, Weber State University, Ogden, UT, [3]Southeast Dairy Foods Research Center, North Carolina State University, Raleigh.*

Low fat (LF) cheddar cheese develops flavor during aging uncharacteristic of full fat (FF) cheese, such as rosey and burnt/brothy flavors and bitter taste. Our objective was to determine if this is a function of differences in salt-in-moisture (S/M) content. Full fat and LF curd was made (in triplicate) using 700 kg of milk and salted to produce cheese with S/M typical of LF cheese. Half the curd was pressed into blocks, and further salt was added to the remainder to make cheese with S/M typical of FF cheese. For FF cheese, high salt (HS) levels were 2.1–2.5% salt (5.4–6.4% S/M) and low salt (LS) levels were 1.4–1.6% (3.5–4.0% S/M). For LF cheese, HS levels were 2.4–3.1% (4.3–5.6% S/M) and LS levels were 1.6–2.0% (3.0–3.6% S/M). Cheese was stored at 6°C and analyzed monthly for total lactic acid bacteria (LAB), lactococci, and nonstarter LAB (NSLAB) using selective media. Sensory profiles and volatile compounds of cheeses were analyzed after 2, 5 and 7 mo using descriptive sensory analysis and gas chromatography mass spectrometry. In general, initial NSLAB levels were $< 10^4$ and NSLABs became dominant after 3 mo storage. The HS cheeses had the expected die-off of lactococci during storage to $< 10^4$ cfu/g, with this occurring faster at the highest salt level (6.4% S/M) and slower at 4.3% S/M. For LS-FF and LS-LF cheeses, lactococci remained at ~10^5 cfu/g throughout storage. All flavor attributes except milkfat were impacted by age ($P < 0.001$). Both FF and LF cheese with LS levels tended to have higher flavor attributes of sulfur, brothy, rosy, and bitter flavors. In general, LF cheese with HS level had similar flavor scores (except for milkfat flavor) to the FF cheese with LS levels. Volatiles were generally higher in FF than LF cheeses. When comparing salt levels, both LF and FF cheeses had higher concentrations of phenyl and furanone compounds known to be sources of rosy and burnt off flavors. Thus, development of undesirable flavor attributes in LF cheese was not just a function of its lower S/M content but fat content also played a role in sensory perception of flavorants.

Key words: Cheddar, low fat, flavor

602 Manufacture and sensory analysis of reduced and low sodium Cheddar cheeses. B. Ganesan*, K. Brown, D. Irish, C. Brothersen, and D. J. McMahon, *Western Dairy Center, Department of Nutrition, Dietetics and Food Sciences, Utah State University, Logan.*

Salt is used for moisture control during Cheddar cheese manufacture and also restricts off flavors from bacterial metabolism during aging. To address the technical challenges associated with making acceptable reduced salt Cheddar cheese, we made Cheddar cheese in triplicate with final salt levels of 0.75%, 1%, 1.25%, 1.5% and 1.75% (w/w) with similar post press moisture and pH ($P > 0.05$) by altering current manufacture protocols. We conducted texture profile analysis at 0 and 6 mo and initially, cheeses at different salt levels varied in hardness, springiness, and chewiness, but exhibited similar properties by 6 mo of age. The changes in properties however varied at different salt levels. For example, cheese containing 1.8% salt was initially ~40% harder ($P < 0.05$), but became softer and comparable to the others ($P > 0.05$) at 6 mo. In contrast, the 0.75 and 1.5% salt cheeses did not soften during aging. Cheese adhesiveness decreased with salt content between 1.25% and 0.75% and with age ($P < 0.05$), but varied at higher salt levels. Consumer preference (9 point hedonic scale) and descriptive (15 point intensity scale) sensory panels were conducted to evaluate liking and flavor attributes as a function of salt content, respectively. Cheese was served in the consumer panel on separate occasions either cold as cubes or melted as a quesadilla. Cubed Cheddar cheese containing 0.75% salt received ($P < 0.05$) lower liking scores at 0 or 6 mo than the other cheeses. Consumers were able to distinguish cheeses at alternate salt levels at 0 and 6 mo age ($P < 0.05$) irrespective of serving style. Salty and buttery attributes were perceived more ($P < 0.05$) with increasing salt levels by the descriptive panel at 0 mo, whereas bitter, brothy and umami attributes were perceived less ($P < 0.05$) at the higher salt levels. However, this trend reversed at 6 mo, when salty, sour, bitter, buttery, lactone/fatty acid, and umami attributes' perception all increased ($P < 0.05$) along with salt level. Our study highlights that salt plays a multi-faceted role in shaping the physical attributes and flavor perception of Cheddar cheese.

Key words: Cheddar cheese, reduced sodium, flavor

603 Growth and metabolism of *Lactobacillus casei* in a ripening Cheddar cheese model varying salt, lactate, and lactose concentrations. J.-H. Oh*[1], M. F. Budinich[1], M. A. Drake[3], R. E. Miracle[3], J. R. Broadbent[2], and J. L. Steele[1], *[1]Department of Food Science, University of Wisconsin-Madison, Madison, [2]Department of Nutrition, Dietetics, and Food Sciences, Utah State University, Logan, [3]Department of Food Science, North Carolina State University, Raleigh.*

This study focused on how varying the composition of a cheese ripening model system affects the growth and metabolism of *L. casei* M36, UW1, UW4, 32G, and 12A. The conditions that were varied included salt (1.2% and 4.8%), lactate (2.7% and 4.3%), and lactose (0.2% and 1.0%). The Cheddar cheese ripening model system employed a water extract of Cheddar cheese, Cheddar cheese extract (CCE), as the growth media, and 10-week incubation was conducted at 8°C and pH 5.2 in the absence of oxygen. During the 10-week ripening period, there were 12 time points during which the culture was enumerated and the pH determined. At select time points, organic acids and volatile compounds were quantified by high performance liquid chromatography (HPLC) and gas chromatography (GC), respectively. *L. casei* UW4 reduced the concentration of phenylacetaldehyde, a compound responsible for rosy and metallic off-flavors in Cheddar cheese, 78% relative to the control. *L. casei* M36 enhanced the accumulation of diacetyl and sulfur containing volatiles, compounds thought to enhance Cheddar cheese flavor development. Additionally, these 2 strains exhibited fast growth in CCE under the conditions examined. The results obtained suggest that UW4 and M36 strain may have utility in enhancing the flavor of reduced-sodium and reduced-fat Cheddar cheeses. This study has demonstrated that salt in the moisture is a key variable in determining the volatiles produced by non-starter lactic acid bacteria and identified 2 strains to be examined in subsequent Cheddar cheese trials with reduced salt in the moisture. Screening of a collection of genetically diverse *Lactobacillus casei* strains will allow us to select a subset of strains to be examined for their ability to dominate the microbiota and positively influence flavor development in ripening reduced-fat and reduced-sodium Cheddar cheeses.

Key words: *Lactobacillus casei*, reduced-fat Cheddar cheese flavor, volatile compounds

604 Manufacture and sensory analysis of reduced and low sodium pasta filata style Mozzarella cheeses. B. Ganesan*, K. Brown, D. Irish, C. Brothersen, and D. J. McMahon, *Western Dairy Center, Department of Nutrition, Dietetics and Food Sciences, Utah State University, Logan.*

High sodium intake negatively impacts consumer health, thus there is active interest in lowering sodium levels in dairy foods. Toward developing a healthier cheese and tackling the challenges associated with reduced sodium cheese manufacture, we made low moisture part skim Mozzarella cheese with total salt levels at 0.7, 0.9, 1.25, 1.35, and 1.8% (w/w) in triplicate, thus reducing sodium by 25 to 60%. Our manufacturing protocols yielded cheeses with similar moisture and pH ($P > 0.05$) independent of the final salt levels in cheese that allowed us to study the effect of salt on cheese properties. Further, we evaluated mozzarella cheese functionality by characterizing stretch and melt properties, and also studied flavor and acceptance using descriptive (15-point intensity scale) and consumer (9 point Hedonic scale) taste panels. At wk 2, all Mozzarella cheeses melted similarly, but by wk 8, the meltability of all cheeses increased by ~2-fold ($P < 0.05$), with the 0.9% salt cheese showing the greatest increase. Stretchability also increased 4 to 8-fold ($P < 0.05$) with storage, but varied with salt content. At wk 2, 1.8% salt cheese required the greatest stretch force, while other cheeses had similar stretch properties. Taste panels conducted at 3 wks with cold shredded cheese showed that consumers liking for Mozzarella cheese was low at 0.7 and 0.9% salt, but equally ($P > 0.05$) preferred all cheeses containing higher salt levels (1.25, 1.35, and 1.8% salt). All cheeses had acceptable liking scores when served as pizza toppings, and consumers were able to differentiate cheeses ($P < 0.05$) at alternate salt levels, e.g., 1.8% and 1.5% salt cheeses scored similar ($P > 0.05$), as did cheeses at 1.5% and 1.35% salt, but 1.35% salt cheese scored lower ($P < 0.05$) than and was discernible from 1.8% cheese. Descriptive panelists identified salty, sour, umami, bitter, brothy, lactone/fatty acid, and sulfur attributes as different across the cheeses, with the perception of each significantly ($P < 0.05$) increasing along with salt level. To our knowledge, this is the first study that investigates the role of salt as the chief variable in mozzarella cheese physical properties and flavor attributes.

605 Informatic prediction of alterations to Cheddar cheese flavor reactions and pathways due to sodium substitution. B. Ganesan* and K. Brown, *Western Dairy Center, Department of Nutrition, Dietetics and Food Sciences, Utah State University, Logan.*

Increased interest in reduced and low sodium dairy foods due to health implications generates novel issues for product manufacture. As an alternate to reduction, Na may be partly replaced with potassium or calcium, but the role played by the substituting cations in flavor development is unclear. For example, NaCl addition to Cheddar cheese induces a general stress response at the gene level in lactic acid bacteria and restricts microbial outgrowth and metabolism and consequently reduces off flavors. Once Na is reduced or replaced the metabolic routes and the resulting flavors may also be altered. For example, Ca substitution beyond 10% total salt causes bitterness in Cheddar cheese. The roles of other cations in bacterial stress are unknown, but the effect of some cations on metabolic enzymes has been characterized. K, for example, is an activator of over 40 enzymes and inhibits 25 enzymes. Similarly Ca activates 29 enzymes but also inhibits 55 enzymes. Currently we can visualize the effects of these cations only as lists inside metabolic databases. By visualizing the impact of these activating and inhibitory activities as biochemical pathways inside a metabolic database we can analyze, predict, and eventually dictate the aging process of cheeses with non-sodium cations. Henceforth, we reconstructed new metabolic databases that illustrate the effect of different salt cations on flavor-related enzymes as microbial pathways. After metabolic reconstruction and analysis we found that nearly 100 pathways of lactic acid bacteria are affected due to enzymes likely to be activated/inactivated by K and Ca. These pathways are primarily linked to sugar metabolism, acid production, and amino acid biosynthesis and degradation. Notably, some pathways controlled by K also link to assimilation of other minerals such as magnesium and iron, suggesting that K addition will also affect additional cation inclusions currently being considered. This approach will allow us to identify and tackle metabolic routes induced and inhibited by cation replacements and their effects on Cheddar cheese flavor.

Key words: reduced sodium, Cheddar cheese, flavor

606 The effect of NaCl substitution with KCl on Nabulsi cheese: Chemical composition, total viable count, microstructure and texture profile. N. P. Shah* and MM Ayyash, *School of Biomedical and Health Sciences, Victoria University, Melbourne, Victoria, Australia.*

Sodium chloride is traditionally added to cheeses as a preservative and to improve flavor. However, a positive correlation between high level of sodium and osteoporosis, kidney stones and hypertension has been found. Hence, there has been an increased interest to reduce salt in foods. This study aimed at examining the impact of NaCl substitution with KCl on characteristics of a high brined white cheese (Nabulsi). Nabulsi cheese was made and kept in 4 different brine solutions at 18% including NaCl only (A; control); 3NaCl: 1KCl (w/w; B); 1NaCl: 1KCl (w/w; C); and 1NaCl: 3KCl (w/w; D) and stored for 5 mo. Chemical composition, proteolysis, total viable count (TVC) and texture profile analysis (TPA) were assessed at monthly intervals for 5 mo. No significant effect was found among experimental cheeses in terms of chemical composition and TPA profiles. Proteolytic activities were higher in cheeses kept in brine solutions that contained higher KCl (B, C, and D) as compared with the control. At the end of the storage period, water soluble nitrogen (WSN) and 12% trichloroacetic acid (TCA)-SN in Nabulsi cheeses stored in B, C and D was higher than the control (A). Also, TVC increased significantly after 1 mo of storage for all salt treatments. Hardness and gumminess decreased significantly during storage at the same salt treatment. ESEM micrographs showed a compact and closed texture for cheeses at same storage period. Microstructure of all cheeses became more closed and compact with storage period. Calcium content negatively correlated with hardness and sodium and potassium contents during storage at same salt treatment. The results showed that KCl could partly replace NaCl without any significant effect on the general characteristics of Nabulsi cheese.

Key words: salt substitution, TPA, TVC

607 The effect of NaCl substitution with KCl on low moisture mozzarella cheese: Chemical composition, organic acid profile, soluble calcium content, functional properties, proteolysis, lactic acid bacterial population, and ACE-inhibitory peptides. N. P. Shah* and M. M. Ayyash, *School of Biomedical and Health Sciences, Victoria University, Melbourne, Victoria, Australia.*

NaCl is traditionally used as a preservative and is added to cheeses to control bacterial growth, enzymatic activities, and to improve flavor. The recommended daily intake for sodium is 2.4 g, which is equivalent to 110 mmol Na or 6.0 g NaCl; the daily sodium intake in developed countries is substantially higher than the RDI. There is a positive asso-

ciation between hypertension and salt which in turn causes cardiovascular diseases. The effect of NaCl substitution with KCl on chemical composition, organic acids profile, soluble calcium and functionality of low moisture Mozzarella cheese LMMC) was investigated. Four batches of LMMC were made, and after milling cheeses were dry salted using 4 combinations of NaCl and KCl (only NaCl (A; control), 3NaCl:1KCl (B), 1NaCl:1KCl (C), and 1NaCl:3KCl (D) at 46 g/Kg. Functionality (meltability and browning), organic acids profile and chemical composition, proteolysis, lactic acid bacteria, and ACE-inhibitory of LMMC were measured. Chemical composition showed no significant difference between experimental cheeses at same storage period, and same salt treatment. Meltability of LMMC with treatment B, C and D was higher compared with the control. The amount of soluble Ca and P increased significantly during storage with no significant difference between salt treatments. There was no significant difference in organic acid profile between salt treatments at same storage period. Substitution of NaCl with KCl had similar effect on chemical composition, organic acids profile and functional properties. In addition, LMMC salted with NaCl/KCl mixture (treatments C and D) improved functionality of LMMC compared with the control. pH value of LMMC salted with NaCl/KCl mixture (C and D) was generally higher compared with the control. ACE-inhibitory peptides in treatment D increased significantly compared with other batches. WSN, TCA-SN showed no significant difference between experimental cheeses; however, PTA-SN significantly differed.

Key words: LMMC, substitution of NaCl, functionality

608 The impact of pectin types on the rheological and physical properties of yogurt. S. S. Mohamed*[1,2] and J. A. Lucey[1], [1]*University of Wisconsin, Madison,* [2]*University of Kafrelsheikh, Egypt.*

Pectin is commonly used as a gelling agent in the manufacture of yogurt. The objective of our study was to evaluate the impact of 4 different types of pectin that had different degrees of esterification (DE) and amidation (DA), on the physical properties of set type yogurt. The pectin samples included 2 types of low methoxyl (LM) pectin with 38% and 45% DE, one type of low methoxyl amidate (LMA) with 39% DE and 14% DA, and one of high methoxyl (HM) with 72% DE. Other pectin types resulted in phase separation in milk. Pectins were added to heated reconstituted skim milk at various concentrations (0.005, 0.05, 0.1 and 0.2%). Gelation properties were monitored using dynamic low amplitude oscillatory rheology and infrared light backscatter. Microstructure was studied using fluorescence microscopy. Wheying off and permeability (porosity) were analyzed at pH 4.6. At pectin concentration of 0.005% no significant differences were observed in yogurts. Yogurt made with 0.05 or 0.1% LMA, LM with 38% DE, and LM with 45% DE, had significantly lower storage modulus (G'), light back scatter ratio at pH 4.6 (RpH4.6), wheying off and permeability compared with control yogurt (no pectin). Permeability and wheying off increased with increasing LMA concentration from 0.1 to 0.2%, while the G' and RpH4.6 values were reduced. Complete inhibition of wheying off was observed when 0.2% LM (38% DE) pectin was used in yogurt and this sample also had the lowest permeability. In yogurt made with 0.2% of HM pectin, the R value gradually decreased after gelation pH until pH 4.6. Wheying off and permeability increased with an increase in the concentration of HM (from 0.005 to 0.2%). HM pectin produced yogurt with the lowest G' and RpH4.6 values compared with other treatments. The microstructure results indicated that yogurt made with HM pectin had an open network, especially at 0.2% pectin, while yogurt made with LM (38% DE) had higher degree of interconnectivity of strands. In conclusion, pectin types greatly impact gelation behavior and yogurt texture. LM pectin with low DE value and without amidation gives the best gelation properties.

Key words: yogurt, pectin, rheology

609 Engineering yogurt texture: Interactions between texturing lactic acid bacteria and processing conditions in low fat stirred yogurt. K. B. Qvist*, C. Gilleladen, J. Trihaas, and C. Svane, *Chr. Hansen, Hoersholm, Denmark.*

Recent years has seen increasing use of highly texturizing cultures in yogurt manufacture, and also a rapid diversification regarding protein ingredients used. This caused us to question whether the current understanding of yogurt technology is adequate, given that most of it was derived before widespread use of new protein ingredients and highly texturizing cultures. To study effects and interactions of the following factors we executed a so-called D-optimal design experiment with 168 yogurts samples (representing 1134 samples of a full factorial): protein type used for fortification (skimmilk (SKM), or PM500G (fortified in whey protein compared to SKM, from IDI); protein addition level (0.7, 1.05, 1.4%); fat content (0.5, 1.0, 1.5%); back pressure during cooling in plate heat exchanger (0, 0.1, 0.2 MPa); filling temperature (12, 18.5, 24°C); and 7 commonly used yogurt cultures differing in EPS production and other properties. Shear stress assessed at a shear rate of 300 s^{-1}, and complex modulus at 1 Hz (StressTech rheometer), were used to represent mouth thickness and gel stiffness, respectively. Major variables determining shear stress and complex modulus were culture used, protein addition level and type, and back pressure. Shear stress and modulus increased substantially when raising protein addition from 0.7 to 1.4%, but decreased when back pressure was increased from 0 to 0.2 MPa. The most important new insight was that interactions between culture, protein type, and amount of protein added can be complex. For instance, the effect of amount of protein added on shear stress can depend strongly on which culture is used. Also, with some cultures, PM500G increased shear stress much more efficiently than SKM. Regarding the modulus, with a highly texturizing culture, adding SKM did little to increase the modulus, while addition of PM500G was highly effective. In conclusion, a much higher level of process optimization can be achieved by exploiting interactions between cultures, ingredients and technology, than by thinking of these factors independently of each other.

Key words: yogurt texture, cultures, interactions

610 Yogurts made from milk where heating was performed at different pH values. T. Ozcan[1,2] and J. Lucey*[1], [1]*University of Wisconsin-Madison, Madison,* [2]*Uludag University, Bursa, Turkey.*

It is well known that the pH of milk during heat treatment has significant effect on level/type of whey protein interaction with casein micelles. As the pH of heating decreases there is an increase in the proportion of denatured whey protein associated with casein micelles (bound aggregates) and less soluble denatured whey proteins. The objective of this research was to investigate the effects of heating milk at different pH values, with or without readjustment to pH 6.7 after heating, on the properties of yogurt gels. Reconstituted skim milk was adjusted to pH values 6.2, 6.7 or 7.2 and heated at 85°C for 30 min. Another set of milks were heated as above but readjusted to pH 6.7 after heating. Milks were inoculated with 3% yogurt culture and incubated at 40°C until pH 4.6. Gel formation was monitored using dynamic oscillatory rheology and light backscattering. Fluorescence microscopy was used to observe gel microstructure. The G′ values at pH 4.6 were highest in gels made from milk heated at pH 6.7 and lowest in milk heated at pH 6.2, with or without pH adjustment after heating. The G′ values at pH 4.6 were lower in samples adjusted to pH 6.7 after heating. No maximum in the loss tangent parameter was observed during gelation for yogurts heated at pH 6.2 but a maximum was observed at pH~4.8 for milks heated at pH 6.7 or 7.2, with or without pH adjustment after heating. Profiles for the light backscatter ratio (R) during gelation indicated that higher R values were observed in samples heated at higher pH values, with or without pH adjustment after heating. The first derivative of light backscatter ratio (R') also revealed differences between samples. The R' profiles for samples heated at pH 6.7 and 7.2 had 2 peaks during gelation but the pH 6.2 sample had only one. Higher peak values in the R' profiles were observed with an increase in the pH of heating. No clear differences were observed in the microstructures of gels between treatments. Heating milk at pH 6.7 created an optimum balance of bound and soluble denatured whey proteins, which resulted in yogurt with the highest gel stiffness.

Key words: yogurt, rheology, gelation

611 Dextran addition to model acid gels to explore the mechanism by which EPS influence yogurt texture. U. Pachekrepapol* and J. A. Lucey, *University of Wisconsin - Madison, Madison.*

Exopolysaccharides (EPS) are biopolymers produced by lactic acid bacteria and EPS production can impact the rheological properties of yogurt. It is not clear when EPS is produced during the yogurt fermentation process. We believe that the point in the fermentation process when EPS are produced could greatly impact gelation and rheological properties of yogurt. Our objective was to use a model acid gel system to explore the impact of biopolymer addition at various pH values. High molecular weight dextran (2×10^6 Da) was used as a simple model biopolymer instead of bacterial EPS. Reconstituted skim milk was acidified to pH 4.4, 4.6, 4.8 and 4.9 at ~0°C by addition of 3N HCl. Dextran solution was then added into cold acidified milk to give a dextran concentration of 0.5% (w/w). Milk was then warmed up in a rheometer at a rate of 0.5°C/min until the temperature reached 30°C and it was held for 17 h at 30°C. The cold acidified milks gelled as they were warmed to 30°C. The rheological and microstructural properties of these gels were determined by small amplitude oscillation rheology and confocal scanning laser microscopy (with image analysis), respectively. No significant difference in the gelation time or storage modulus (G′) was observed in gels with or without dextran addition for gels made at the same pH value. Image analysis was used to determine the percentage of area of the protein aggregates in gels. Image analysis indicated that there was no significant difference in protein aggregate area in gels made at the same pH with or without dextran. However, gels made at different pH levels had different area of protein aggregates. At pH 4.4 and 4.6, the areas of protein aggregates were similar and higher than those of gels made at pH 4.8 and 4.9. In conclusion, we did not find that the addition of dextran had any significant impact on gel properties. Although, we added a high concentration (0.5%) of a high molecular weight dextran, possibly other physical characteristics of EPS (e.g., branching or charge) could be important in the ability of EPS to impact yogurt texture.

Key words: EPS, yogurt, Dextran

612 Effect of the addition of glucose/glucose oxidase and packagings with different permeability oxygen rates on some characteristics of probiotic yogurts. A. Cruz[1], J. Assis*[1], D. Granato[2], S. Bogusz Junior[1], and H. Godoy[1], *[1]University of Campinas (UNICAMP), [2]University of São Paulo (USP).*

The use of the enzymatic complex glucose/glucose oxidase has been presented as a potential option for removal of the dissolved oxygen in stirred probiotic yogurt. In this research, the stability of probiotic yogurt packaged in plastic material with different values of oxygen permeability was investigated during 28 d. Probiotic yogurts supplemented with *Lactobacillus acidophilus* La14, *Bifidobacteria longum* BL05, 62.32 ppm of glucose oxidase and 4.35 ppm glucose were manufactured and packaged in conventional polypropylene cups (PP) or PP coextrused with different levels of vinyl ethylene alcohol (VEOH), presenting the following permeability oxygen rates (TPO2): 0.09 (P1), 0.20 (P2), 0.39 (P3) and 0.75 (P4) ml O2/cup*day. Postacidification, dissolved oxygen, proteolysis, viable count of yogurt and probiotic bacteria, carbohydrate consumption (glucose and lactose), organic acid production (acetic and lactic acid) and aroma compounds (diacetyl and acetaldehyde) were monitored weekly (1, 7, 14, 21, and 28 d). A significant ($P < 0.05$) effect of the packaging system was observed for all analyzed parameters. P1 and P2 presented the lowest values of dissolved oxygen, reflecting in an increased metabolism of probiotic cultures. These samples also presented a greater postacidification, proteolysis, carbohydrate consumption, organic acid levels and aroma compounds, suggesting a continuous performance of the enzymatic system. P3 and P4 had the opposite trend, maybe due to the difficulty of the enzymatic complex in removing the oxygen in the product. As a conclusion, if plastic materials with a low barrier to oxygen are used a higher concentration of glucose should be added into the yogurt to guarantee the best enzymatic efficiency and, hence, the functionality of the stirred probiotic yogurt during the shelf life.

Key words: probiotic yogurt, glucose oxidase, stability

613 Effect of increased concentration of glucose oxidase in probiotic stirred yogurt on functionality, proteolytic pattern, and metabolic products. A. Cruz, W. Castro, and J. Assis*, *University of Campinas (UNICAMP).*

The addition of increased concentrations of glucose oxidase, a potential oxygen remover, in probiotic stirred yogurt was evaluated. Probiotic yogurts supplemented with *Lactobacillus acidophilus* La-14 and *Bifidobacteria longum* BL 05, added with 0, 200, 400, 600, 800 and 1000 ppm glucose oxidase were manufactured and packaged in 200 mL polypropylene cups. Post acidification, dissolved oxygen, proteolysis, viable count of yogurt and probiotic bacteria, carbohydrate consumption (glucose and lactose) and organic acid production (acetic and lactic acid) were monitored weekly during 1, 7, 14, 21, and 28 d refrigerated storage. Independent of the amount of added enzyme, a rapid consumption of the substrate (glucose) was observed and also an increase of dissolved oxygen during the storage time, probably because of the high oxygen permeability of the package. Consequently, the count of viable probiotic microorganisms (mainly *B. longum*) decreased as function of storage time as well as lower carbohydrate consumption, lower proteolysis and lower ph values ($P < 0.05$). No effect was observed in the lactic acid production ($P > 0.05$). However, at the of shelf life the counts of *Lactobacillus acidophilus* and *Bifidobacteria longum* were still 7 and 6 log cfu/g, respectively. Based on such results it was concluded that it is necessary to improve the oxygen barrier of the package to benefit from the use of glucose oxidase and prolonging the shelf life of probiotic stirred yogurt.

Key words: probiotic yogurt, glucose oxidase, stability

614 Impact of adding galactooligosaccharides on the physical and optical characteristics and sensory acceptance of vanilla ice cream. A. Cruz, J. Faria*, W. Castro, R. Cadena, and H. Bolini, *University of Campinas (UNICAMP).*

Prebiotic and conventional dairy foods should present similar technology and sensory performance. The research aimed to evaluate the effect of adding galactooligosaccharide (GOS) on the physico-chemical and optical characteristics and sensory acceptance of ice cream. Vanilla ice creams supplemented with 0, 1.5% and 3.0% w/w (0G, 1.5G, 3G) galactooligosaccharides (GOS) were subjected to physico-chemical analysis (pH, firmness, melting rate, and overrun) and optical analysis (instrumental color). Simultaneously, vanilla ice creams supplemented with 1.5% or 3% w/w (1.5F, 3F) fructooligosaccharides (FOS) were also produced and submitted to the same analyses. In addition, a consumer test (30 consumers, triangular test) was performed. The 3G ice creams were characterized as firmer and with lower melting rates as compared with the others samples ($P < 0.05$) while absence of effect was observed in the pH and instrumental color values. The results from the consumer test indicated that the 3G ice creams were perceived as different from the 0G ice creams ($P < 0.05$), whereas the 1.5G, 1.5F, and 3F ice creams were perceived as similar ($P > 0.05$) to the control sample. The findings suggest it is possible to manufacture ice creams

supplemented with 1.5% GOS, which presented more stable and with a sensory perception similar to the conventional ice creams.

Key words: ice cream, galactooligosaccharides, stability

615 Physical properties and functionality of probiotic vanilla ice creams manufactured with different overruns levels. A. Cruz, J. Faria*, W. Castro, R. Cadena, and H. Bolini, *University of Campinas (UNICAMP)*.

The effect of different overrun levels on the physical properties and functionality of probiotic ice creams was investigated. Vanilla ice creams supplemented with *Lactobacillus acidophilus* were manufactured with 45, 60 and 90% (O45, O60, O90) overruns levels. Physical analysis (pH, viscosity, melting rate) were performed. In addition, *L. acidophilus* counts were performed during 60 d of frozen storage at −20°C. Probiotic ice creams manufactured with higher overrun levels showed better stability ($P < 0.05$), presenting lower melting rate and improved viscosity, while no effects on pH were observed. Overrun levels also influenced the survival of *L. acidophilus* ($P < 0.05$). O60 presented viable probiotic counts ranging from 8.10 and 8.02 log cfu/g while for O90 this parameter ranged from 7.00 to 6.06, respectively. However, O45 presented viable probiotic counts ranging from 8.06 to 8.04 log cfu/g ($P > 0.05$), during storage. These findings suggest it is important to optimize the overrun levels during the probiotic ice cream processing to keep its functionality, without negative impact on its intrinsic parameters of quality.

Key words: probiotic ice cream, overrun, functionality

616 Withdrawn

Extension Education Symposium: Enhancing Educational Approaches for Future Changes in Biosecurity and Antibiotic Use in Animal Agriculture

617 Overview–The importance of biosecurity and animal production. E. R. Jordan*, K. J. Lager, and R. G. Bruno, *Texas AgriLife Extension Service, College Station.*

Many factors, including religion, personal income, commodity price, traditions and personal preference, influence demand for animal protein provided by livestock production. Frequently, as affluence in developing countries improves, demand for animal protein expands. According to the World Health Organization worldwide per capita consumption of livestock products increased from 24.2 kg/yr in 1964–66 to 36.4 kg/yr in 1997–1999 and was projected to reach 45.3 kg/yr by 2030. During the same period worldwide per capita milk consumption increased from 73.9 to 78.1 kg/yr and was projected to reach 89.5 kg/yr in 2030. Yet, despite increases in total caloric intake and animal protein intake, the Food and Agriculture Organization (FAO) of the United Nations estimated that 925 million people were undernourished in 2010. The world population is expected to grow from 6.8 billion today to 9.1 billion in 2050, requiring 200 million tonnes of additional meat production. As the world has become more intertwined, disruptions to food production, processing and distribution as a result of natural disasters, disease, economic constraints or terrorist actions can have far reaching effects on food insecurity, further destabilizing the World. For example, the 2001 Foot and Mouth Disease Outbreak in Britain resulted in 6 million animals (4.9 million ovine, 0.7 million bovine and 0.4 million porcine) being culled, resulting in an economic loss of £3.1 billion to agriculture and the food chain plus a significant loss of animal protein to the food supply. A global threat for poultry as well as humans is the H5N1 highly pathogenic avian influenza virus, which emerged in 1997 in SE Asia and has subsequently infected the wild bird population. To protect the food supply for an expanding world population, increased emphasis has been placed on biosecurity, which encompasses the various measures taken to secure a population from exposure to harmful biological agents. Preventing animal disease and the spread of those diseases once introduced into an animal population is one of the keys to fighting hunger, malnutrition and poverty. Furthermore, having biosecurity measures in place so that food supply chain disruptions resulting from a disease outbreak can be minimized is imperative for the well-being of the animal industry, as well as to the human population to which it provides nourishment.

Key words: biosecurity, livestock

618 Biosecurity at the farm level: The role of extension in preventing animal disease introduction. R. Daly*, *South Dakota State University, Brookings.*

Biosecurity can be defined as interventions that prevent the introduction of novel infectious diseases into an area such as a farm, state or country. While extension personnel should be aware of and assist state and federal disease control programs where appropriate, it is at the farm level where extension programming has potential for great impact. A wealth of publications that address biosecurity have been published and distributed by extension and other groups. These publications are primarily directed toward general livestock, dairy, beef and poultry operations. Common subjects addressed are use of footbaths/disposable boots, quarantine of new animals, equipment disinfection and visitor/vehicle access. A recent review of these resources revealed that there are discrepancies among recommendations. For example, recommended isolation time for new animals entering beef operations varied from 14 to 60 d. Producers may become discouraged when trying to account for these differences, and may "cherry-pick" procedures that are most convenient for them or avoid them entirely. Another pitfall of many biosecurity recommendations is that they are often too general to be useful. An individual, farm-specific approach to biosecurity is more desirable than dependence on general recommendations. Tools are available to extension personnel for conducting individual risk assessments, in concert with herd veterinarians, regarding infection control practices. Practical and effective biosecurity measures can then be developed for the operation. Comprehensive materials for beef, dairy and equine facility risk assessment are available through the Center for Food Security and Public Health at Iowa State University. Extension personnel have a unique role in educating youth about biosecurity measures. Animal exhibitions present ideal opportunities to emphasize infection control practices and proper management of animal movements to prevent novel disease back at home. Assisting producers in development of biosecurity plans is an appropriate function of extension personnel. Tools are available to formulate specific, useful recommendations for farms and ranches.

Key words: biosecurity, extension

619 Extension and outreach programs that address contemporary issues in food animal production. P. D. Ebner*, *Purdue University Department of Animal Sciences, West Lafayette, IN.*

Most Americans are far removed from animal agriculture. There is an increasing demand by the general public, however, for information regarding various technologies used in modern livestock production. Both consumers and non-consumers of animal products have questions on topics ranging from antimicrobial use to manure application and its potential environmental impact. The land-grant universities, where many of these technologies were developed, are uniquely positioned to provide these individuals with research-based information. In recent years, the Department of Animal Sciences at Purdue University has focused on the development extension programs that examine contemporary topics in food animal production, but target less traditional audiences. These programs have mixed traditional media such as fact-sheets and symposia with newer media including YouTube-hosted educational videos, social networking sites and other web-based tools. Examples of such programs include the Purdue University Concentrated Animal Feeding Operation Team (www.ansc.purdue.edu/CAFO) which brought together experts in various fields to identify and research public health, environmental and social/economic issues surrounding the expansion of animal agriculture in Indiana. The team developed a series of educational materials and programs targeted to the state and local officials charged with making decisions regarding proper siting of larger livestock facilities. Purdue University more recently developed the Food Animal Education Network (www.ansc.purdue.edu/FAEN), which is targeted to individuals who may have no connection to livestock production, but have questions or concerns regarding how their meat is produced. The program answers a wide range of questions from 'why are antibiotics used in livestock production?' to 'who is in charge of meat inspection?' and provides the information in accessible and appropriate forms. Together, these programs provide information to all of our stakeholders so that they can better determine the impact that food animal production has on their lives and their communities.

Key words: contemporary issues, extension, livestock production

620 Novel approach to measuring internal scrotal temperature in stallions utilizing a thermal sensory device. J. D. Mawyer*, R. K. Gordon, C. A. Cavinder, M. M. Vogelsang, C. C. Love, S. P. Brinsko, T. L. Blanchard, and S. R. Teague, *Texas A&M University, College Station.*

Past studies investigating testicular heat stress due to exercise or insulation in the stallion have utilized thermistor probes to measure scrotal surface temperatures (SST). Although such devices are effective, a more efficient measurement of testicular thermal stress would be subcutaneous scrotal temperature (SQST). The objective of this study was to utilize a thermal sensory device to measure SQST in the stallion during exercise and correlate it with subcutaneous neck (SQNT), rectal (RCT), and ambient temperatures (AMBT), as well as % humidity (HUM), and temperature-humidity index (THI). Thermal sensory microchips (Digital Angel, Inc., St. Paul, MN) were surgically implanted into the subdermis of the necks and scrotums of 8 miniature stallions. Stallions were assigned to a non-exercised (Non-Ex; control; n = 4) or exercised (Ex; n = 4) group. A motorized equine exerciser was used to work stallions 30 min/d for 4 d/wk during a 12-wk period from July–October. Temperatures (SQST, SQNT, RCT, and AMBT) were recorded before exercise, immediately after intense exercise, and 1 and 2 h post-exercise. Humidity data was obtained later to determine THI. Data were not normally distributed; therefore, a Spearman′s Rank Order correlation analysis was used. No deleterious effects were observed from implantation of thermal sensory microchips. Subcutaneous scrotal and RCT showed the highest correlation (R = 0.761). Scrotal temperature was also correlated to SQNT, AMBT, and THI ($P < 0.0001$) (Table 1). Thermal sensory microchips are a safe and effective way to measure SQST to monitor testicular heat stress.

Table 1. Mean correlations (Rs) of SQST, SQNT, RCT, AMBT, HUM, and THI

	SQST (°C)	SQNT (°C)	RCT (°C)
SQNT (°C)	0.476*		
RCT (°C)	0.761*	0.453*	
AMBT (°C)	0.625*	0.513*	0.558*
HUM (%)	−0.074*	−0.263*	−0.025
THI (°C)	0.629*	0.453*	0.573*

* indicates $P < 0.0001$.

Key words: stallion, subcutaneous scrotal temperature, exercise

621 Electrolyte and pH response to submaximal training in Quarter and Miniature Horses. R. M. Legere* and J. S. Pendergraft, *Sul Ross State University, Alpine, TX.*

Plasma electrolyte concentration and pH response was compared in Quarter Horses (QH) and Miniature Horses (MH) to evaluate the miniature horse as an exercise physiology model for full size horses during submaximal exercise and training. Four QH, 8 to 16 yr of age (439 ± 14 kg), and 4 MH, 10 to 17 yr of age (95 ± 16 kg), with each size consisting of 2 mares and 2 stallions, were blocked within breed by age and initial body weight. Horses were subjected to 2 standardized exercise tests (SETs) in a 2 × 2 factorial design. Between SETs horses performed 6 weeks of biweekly submaximal training bouts, with 3 2-week stages of increased training time. The SET and training bouts were scaled using the Froude pendulum model to provide equivalent workouts for all horses at customized speeds, based on height at the withers, and performed on the Kagra Mustang 2200 high speed equine treadmill. Whole blood was sampled via jugular venipuncture into lithium heparin treated tubes at 11 points before, during, and in recovery after each SET. Plasma was immediately separated using the Iris Statspin centrifuge and analyzed by the Idexx VetStat Electrolyte and Blood Gas Analyzer. Differences in plasma pH, bicarbonate (HCO_3), chloride (Cl), potassium (K), and sodium (Na) were analyzed using a PROC MIXED procedure for repeated measures (SAS Inst. Inc., Cary, NC). No sex effect or horse size difference was observed for pH, HCO_3, Cl, K, or Na. As expected, all parameters varied ($P < 0.001$) over time before, during, and after exercise bouts. No difference was seen for Cl between SETs. Na was higher ($P < 0.001$) and K was lower ($P < 0.001$) for SET2 than SET1. Both pH and HCO_3 were numerically higher ($P < 0.001$) for SET2 compared with SET1, which suggests adaptations to training. Results suggest that miniature horses could be used as a research model to measure electrolyte and pH response during submaximal training for full size horses.

Key words: miniature, submaximal, electrolyte

622 Effects of intra-articular lipopolysaccharide injection on circulating leukocyte population in yearling horses. C. L. Mueller*, D. H. Sigler, J. A. Coverdale, N. D. Cohen, M. M. Vogelsang, C. A. Cavinder, and J. L. Lucia, *Texas A&M University, College Station.*

The immature skeletal structure of a young horse in training is subject to repeated stress which induces inflammation and may ultimately lead to articular degradation. Further characterizing this process may allow for development of preventative strategies to improve future performance and longevity. Intra-articular injection of lipopolysaccharide (LPS) has been used successfully as a method of inducing temporary inflammation in skeletally mature horses to mimic progression of joint disease. However, little information exists regarding its application to the young equine. The objective of the current study was to evaluate the circulating leukocyte population in yearling horses following an intra-articular LPS injection. Nineteen yearling Quarter Horses were utilized in a randomized complete block design. Horses were blocked by age, sex, and BW and treatments were randomly assigned within block. Treatments were an injection of 0.25 ng (n = 7) or 0.5 ng (n = 6) of LPS or sterile lactated Ringer′s solution (n = 6; control). The LPS was obtained from *Escherichia coli* 055:B. Blood was collected at pre-injection hr 0 and at 2, 6, 12, and 24 h post aseptic injection of the left radial carpal joint. Peripheral blood smear slides accompanied plasma samples for determination of total leukocyte count and differential. Leukocyte analysis was performed by Texas Veterinary Medical Diagnostic Laboratory (College Station, TX). Data were analyzed using PROC MIXED (SAS v 9.1; SAS Inst. Inc., Cary, NC). No treatment effects were observed; however total circulating leukocytes increased over time ($P = 0.04$) with highest values at 6 and 12 h post injection. Similarly, an increase over time was observed in subpopulations of monocytes ($P = 0.002$) beginning at 12 h post injection and in platelets ($P = 0.01$) at 12 and 24 h post injection. The results indicate that regardless of treatment a mild immune response was elicited, likely due to repeated arthrocentesis. Future experiments need to consider effects of arthrocentesis, even in control animals, and dosage of LPS injections for young horses.

Key words: joint inflammation, leukocyte, horse

623 Role of cellular sodium transport in nonglandular equine gastric ulcer disease. F. Andrews*[1], A. Peretich[2], R. Reese[2], L. Abbott[2], and M. Dhar[2], [1]*Louisiana State University, Baton Rouge,* [2]*University of Tennessee, Knoxville.*

Gastric ulcers are common in horses. Volatile fatty acids (VFAs), from bacterial fermentation of carbohydrates, decrease sodium transport (NAT), by inhibiting NA-K ATPase (NAKA) across nonglandular (NG) mucosa, which leads to ulceration. The purpose of this study was to determine the role of NAT and NAKA in NG ulcers. NG gastric mucosa were collected from 10 euthanatized horses. NG tissue bioelectric properties were measured in Ussing chambers while exposed to normal Ringer's solution (NRS, control), a VFA mixture containing concentrations found 2 h after feeding sweet feed (0.5 Kg/Kg BW) (VFA-AF) and a VFA mixture containing high acetic acid (40 mM) (VFA-HAc) at pH 1.5, 4, or 7 for 330 min. Tissues were removed and examined under light microscopy and frozen in liquid nitrogen for determination of NAKAβ1 subunit gene mRNA-expression RT-PCR. Unpaired *t*-tests were used to determine differences in relative expression of NAKA using standard software. $P < 0.05$ was considered significant.NG mucosa exposed to the VFA mixture-AF, showed a decrease in bioelectric properties (PD and Isc), similar to tissue exposed to NRS at the same pH. However, NG mucosa exposed to VFA mixture-HAc showed an immediate decrease in bioelectric properties and NG cell swelling was noted in tissues exposed to the VFA mixture-HAc. When tissues were grouped together there was no difference in relative expression of mRNA for NAKA. However, relative expression of mRNA for NAKA was significantly decreased in horses (n = 5) < 5 years of age when compared with horses (n = 5) > 12 years of age and controls. Results suggest that VFAs present in gastric juice from excessive grain feeding, at pH ≤4.0, result in changes in barrier function and may be related to alternations in NAKA and may be age-dependent. This may account for the age bias in NG gastric ulcer disease.

Key words: horse, gastric ulcers, volatile fatty acids

624 Effect of concentrate form on gastric ulcer syndrome in horses. L. R. Huth*, D. H. Sigler, C. A. Cavinder, and N. D. Cohen, *Texas A&M University, College Station.*

Equine gastric ulcer syndrome (EGUS) is common among equine athletes of various disciplines and has been linked to decreased performance. Incidence among racehorses has been reported to be over 90%, performance horses at 60%, and endurance horses at 67%. In swine, concentrate form and smaller particle size increase ulceration; thus, the objective of this study was to investigate the effect of concentrate type on EGUS. Quarter Horse yearlings (n = 19; 12–18 mo) were blocked by initial EGUS score on a scale of 0 to 4 (0 = no ulceration or hyperkeratosis, 4 = extensive, deep ulceration) and sex, and utilized in a 77-d crossover design with 2 28-d periods separated by a 21-d washout period. During the first 28-d period, horses were separated into 1 of 2 treatment groups that were all fed Bermuda grass hay and either pelleted or textured concentrate. After the initial 28-d period, horses were all fed pelleted feed and Bermuda grass hay for a 21-d washout period and then treatment groups were switched for the final 28-d period. The rations were a commercially available, pelleted 14.3% CP concentrate and 14.4% CP textured concentrate formulated for this study. Data were analyzed using PROC MIXED (SAS) and effects of horse, treatments (pelleted or textured), period (1st vs 2nd; switchback) and all interactions were considered. Results were considered significant at $P < 0.05$. At the beginning of the study, baseline EGUS scores were not different between horses assigned to either treatment (mean EGUS scored of 1.1); however, upon treatment, horses fed textured feed acquired a reduced incidence of ulceration as compared with those fed pelleted (mean EGUS score of 1.1 vs 1.6, respectively; $P = 0.02$). Degree and incidence of ulceration was influenced by concentrate form as yearlings fed pelleted feed had higher mean ulcer scores then those fed textured feed. Textured feed reduced the EGUS score, possibly due to larger particle size. Also, EGUS scores for both groups in the second period (switchback) were lower, which may be attributed to yearlings being accustomed to the housing, feeding, and management practices during the second period.

Key words: horse, ulcer, diet

625 Development of a nutritional model to predict digestible energy requirements for broodmares based on body condition changes. V. V. Cordero*, C. A. Cavinder, L. O. Tedeschi, and D. H. Sigler, *Texas A&M University, College Station.*

Nutritional models have been developed for beef and dairy cattle to estimate energy balance based on changes in body condition score. These models have not been developed or fully evaluated in horses to date. The objective of this study was to develop a model to predict changes in body weight (BW), rump fat (RF) thickness, and overall % body fat (BF) to maximize profitability and productivity by accurately predicting energy balance of mares. The evaluation of the model was performed using non-lactating Quarter Horse mares (n=20; 4 to 18 yr of age). The initial BW ranged from 376 to 553 kg, with an initial body condition score (BCS) of 3.5 to 7.0 (scale of 1 - 9; 1 = emaciated, 5 = moderate, and 9 = obese). The BCS, RF thickness, and BW were measured for each mare prior to the commencement of the feeding trial and once/wk thereafter for the duration of a 30 d feeding trial. The pre-trial BCS was used to assign mares to 1 of 4 treatment groups (n=5/group) and fed to alter BCS by 1 unit as follows: Group 1, 4 up to 5; Group 2, 5 down to 4; Group 3, 6 up to 7; and Group 4, 7 down to 6. Initial BCS, target BCS, %BF, and BW data was collected from each mare and input into the model. Mares (non-lactating; 10 open, 10 early gestation) were individually fed according to the DE suggestions proposed by the model in order to achieve the targeted BCS change within 30 d. The forage provided was a Coastal Bermudagrass hay and the concentrate was a 12% CP pelleted horse feed (Brazos County Producer's Co-Operative Association, Bryan, Texas). Results showed a 79.8% correlation between BCS and BF in which for every change in 1 BCS (either increasing or decreasing) a change in the same direction of 1.05 percentage units of BF can be expected. All mares' observed final %BF values finished with less than a 20% variation from the model-predicted values (r2=0.61), less than 10% variation from BCS values (r2=0.91), and less than 32kg variation from final EBW values (r2=0.94). An equine nutritional model will enhance feeding management and also reduce the costs of unnecessary overfeeding while maintaining broodmares at a nutritional level to achieve optimum reproductive efficiency.

Key words: body condition score, digestible energy, broodmares

626 Equine grazing preferences of twelve cool season grasses. K. Martinson*, E. Allen, and C. Sheaffer, *University of Minnesota, St. Paul.*

The objective was to evaluate the relationship between equine grazing preferences and forage quality of 12 perennial, cool season grasses. The experimental design was a randomized complete block with 4 rep-

licates. Grasses included tall fescue (*Schedonorus phoenix*), meadow fescue (*Festuca pratensis*), quackgrass (*Elytrigia repens*), smooth bromegrass (*Bromus inermis*), meadow bromegrass (*Bromus biebersteinii*), reed canary grass (*Phalaris arundinacea*), perennial ryegrass (*Lolium perenne*), timothy (*Phleum pretense*), Kentucky bluegrass (*Poa pratensis*), creeping foxtail (*Alopecurus arundinaceaus*), and orchardgrass (*Dactylis glomerata*). Four adult horses were grazed on May 18, June 16, July 19, August 16, September 14, and October 11. Horses grazed 2 replicates (21 × 31-m) for 8-h on day one, and 2 replicates for 8-h the following day. Forage subsamples were harvested to a 9 cm height from duplicate 0.25 m square areas to assess crude protein (CP), neutral detergent fiber (NDF), acid detergent fiber (ADF), and non-fiber carbohydrates (NFC). Grass removal on a scale of 0 (no grazing) to 100 (100% grazed) was visually assessed by 2 trained researchers to determine preference. Forage quality and removals were averaged throughout the season. Data were analyzed using MIXED, ANOVA or PROC REG procedures of SAS. Grasses differed in ADF, NFC ($P < 0.01$) and in palatability ($P < 0.01$). Timothy was most preferred (82%), while orchardgrass and meadow bromegrass were least preferred (47 and 38%, respectively). Timothy had lower ADF (240 g/kg) and higher NFC values (217 g/kg), while orchardgrass and meadow bromegrass had higher ADF (281 and 298 g/kg, respectively) and lower NFC values (142 and 154 g/kg, respectively). To investigate the relationship between grass removal and forage quality, univariate regressions of percent grass removal on forage quality components were performed. ADF ($P < 0.01$) was negatively and NFC ($P = 0.02$) was positively associated ($R^2 = 0.53$ and 0.43, respectively) with horse preference. Grasses differed in forage quality and palatability to grazing horses. Horse preference for specific grasses was partially explained by lower ADF and higher NFC forage levels.

Key words: forage quality, horse, preference

627 A comparison of two conventional horse feeders with the Pre-Vent feeder. M. Carter*, T. Friend, J. Coverdale, S. Garey, A. Adams, and C. Terrill, *Texas A&M University, College Station.*

Feed waste, choke, and sand colic are economic and health issues that present concerns for horse owners across the industry. A new feeder on the market claims to reduce these issues by reducing the speed at which a horse can eat, and the amount of feed dropped and eaten off the ground by the horse. This study compared the Pre-Vent feeder (PV) with commonly used rubber tub (T) and hanging bucket (B) feeders. The PV has 8 cup-like structures 12.7 cm in diameter with a depth of 8.89 cm molded into the bottom of the feeder. It is claimed that the cups will make the horse use its lips and tongue to retrieve the feed, and hence reduces the amount of feed that a horse can eat at one time. Nine Quarter Horse geldings were used to determine time spent eating and feed wastage from the 3 types of feeders. Each horse was fed a 12% crude protein pellet diet at 0.75% bodyweight per day from one of the 3 feeders twice a day for 3 d, and then switched to the next feeder following a 3 × 3 replicated Latin square design (n = 9). The horses were brought from pasture twice daily, and placed in individual 3 × 3 m concrete-floored feeding stalls. Data were analyzed using a GLM with individual animal, day fed, time fed, and feeder type as independent variables to predict time spent eating and feed wastage (dropped on stall floor), followed by pair-wise comparisons. Horses spent more time eating (31.15 ± 0.72 min, $P < 0.0001$) from PV than B (19.39 ± 0.72 min), and T (18.87 ± 0.72 min) feeders. When fed from PV, horses wasted significantly less feed (3.2 ± 0.98% of their ration) than when fed from B (10.2 ± 0.98%, $P < 0.0001$), and from T (7.0 ± 0.98%, $P < 0.007$). One of the 9 horses was particularly wasteful, losing 22.6 ± 1.7% of his feed overall. When fed from the PV, he lost a mean of 8.7% of his ration, compared with 32.8% when fed from B, and 26.2% when fed from T. Residual feed left in PV could not be compared statistically with the other treatments because PV had the only recoverable residuals, which averaged 0.20 ± 0.04% of each horse's ration. The PV is a useful device for increasing time spent eating and reducing feed wastage.

Key words: Pre-Vent feeder, horse, time eating

628 Evaluation of a granulated paper waste product as a suitable bedding material for horses. A. G. Youngblood*[1], B. J. Rude[1], J. D. Davis[1], D. L. Christiansen[1], C. Mochal[1], P. M. Ward[2], and P. L. Ryan[1], *[1]Mississippi State University, Starkville, [2]Rutgers University, New Brunswick, NJ.*

Twelve mares (BW = 540 ± 46.8 kg) were used for three 14 d trials comparing granulated paper-clay mix (GP) to pine pellets (PP) and wood shavings (WS) as a bedding for horses. After each trial, mares were re-randomized for each subsequent trial. During d 1 through 5 stalls were cleaned daily of feces only. On d 6 stalls were re-bedded with clean bedding and feces and saturated bedding (wet spots) were removed daily through d 14. If needed, clean bedding was added to maintain depth of bedding. Additional GP and WS were needed, but not PP. Due to apparent decreased absorptive capacity, WS were added; however, GP was added mostly because of loss of bedding during the removal of feces and wet spots. Horse and stall (AM and PM) cleanliness scores were assigned daily (1 to 5; 1=clean and 5=heavily soiled). Horses were subjected to a nasal swab (d 5 and 14) and tracheal wash (d 14) during each trial. Tracheal washes were scored from 1 to 5 (1=none and 5=chronic) for cytology, aerobic bacteria and fungal growth. Piled bedding was used to acquire NH3 and pH (5 d and 14 d). Individual horse was considered the experimental unit, and data was analyzed as a complete random design, using the GLM procedures of SAS. Horse cleanliness was not different ($P > 0.10$) among bedding types. For A.M. and P.M. stall cleanliness, PP (2.79, 3.12; respectively) was cleaner ($P = 0.0014$) than both GP (3.30, 3.74; respectively) and WS (3.09, 3.47; respectively). Initial pH was greater ($P = 0.0001$) for both GP and WS compared to PP and all bedding types increased with use. No differences ($P > 0.10$) were found for ammonia on d 5 (between 3.3 and 88.5 ppm) or d 14 (between 7.3 and 42.7 ppm). Amount of bacteria (cfu) found in the nasal cavity was not different ($P > 0$ .05) among bedding types on d 5 (between 107,413 and 148,575 cfu) or d 14 (between 152,500 and 191,775 cfu). No differences ($P > 0.05$) were found for cytology and aerobic bacteria scores within the tracheal wash. However, WS (1.67) and PP (1.67) had less ($P = 0.0474$) fungal growth than GP (2.17). Results indicate the use of GP as a bedding material for horses has potential.

Key words: equine, bedding material, granulated paper-clay mix

629 Evaluating varying dietary energy levels for optimum growth and early puberty in Sahiwal heifers under sub tropical environment. M. Abdullah*[1], M. Fiaz[2,1], M. Nasir[1], M. E. Babar[1], J. A. Bhatti[1], T. N. Pasha[1], and M. A. Jabbar[1], *[1]University of Veterinary & Animal Sciences, Lahore, Punjab, Pakistan, [2]Buffalo Research Institute, Pattoki, Pattoki, Punjab, Pakistan.*

To study the effects of different energy levels for optimum growth and early puberty, 20 Sahiwal heifers (Age = 12 ± 2 mo and wt = 120 ± 10 kg) were assigned to 4 dietary treatments having 5 animals on each treatment. Iso-nitrogenous (CP = 13.7%) diets having varying energy, viz; ME 100% (Control), ME 88%, ME 112% and ME 124% of NRC recommended level for small breed non bred heifers were fed to the respective groups until onset of puberty. The collected data was analyzed through ANOVA techniques using SAS 9.1.3 potable software. Average daily gain (ADG) during the time phase from 13 to 18 mo of age was found optimum. The overall ADG was higher (571 ± 15 g/d) in ME 124% than of ME 100, 88 and 112%, whereas ADG was lowest in ME 88% (397 ± 07 g/d). Similar trend was observed in feed efficiency for different treatment groups. Heifers fed dietary level of ME 124% of NRC acquired higher body length, height and heart girth as compared with those fed other dietary energy levels. The digestibility of nutrients, age at puberty, age at 1st conception and serum progesterone were not influenced by dietary treatments ($P > 0.05$). It is concluded that higher dietary energy level (ME 124% of NRC) enhanced growth parameters and feed efficiency but reproductive performance of Sahiwal heifers in terms of age at puberty and age at 1st concenption was optimum even at lower dietary energy level (ME 88% of NRC recommended level) under sub tropical regions.

Key words: dietary energy, Sahiwal heifers, puberty

630 Performance of Sahiwal calves raised on whole milk, blend or milk replacer with or without calf starter supplementation. M. Abdullah*[1], J. A. Bhatti[1], Z. Iqbal[1], and K. Hayat[2], *[1]University of Veterinary and Animal Sciences, Lahore, Pakistan, [2]Livestock Experiment Station, Jahangirabad, Khanewal, Pakistan.*

Young dairy calves are severely deprived of the milk allowance during pre-weaning period for obvious monetary reasons. This leads to stunted growth, high mortality and ultimately late age at puberty. The objective of the present study was to compare the performance of Sahiwal calves fed whole milk, blend or milk replacer with or without calf starter. The study was conducted using 40 8 newly born Sahiwal calves, maintained at Livestock Experiment Station Jahangirabad, having mean birth weight of 20.40 ± 0.18 kg to determine the affect of feeding whole milk, milk replacer or blend of whole milk and milk replacer with or without calf starter supplementation on their performance. At 14 d age the calves were randomly allotted to whole milk (W), WM+ calf starter (WC), W+ Milk replacer (WR), WM+MR+CS (WRC), Milk Replacer (R) and MR+CS (RC) diets up to 120 d of age. Data thus obtained were analyzed using ANOVA technique under completely randomized design (CRD) and differences among treatment means were compared through least significant difference (LSD) test. Mean daily intake was highest ($P < 0.05$) in calves on treatment WC (2.33 ± 0.21 kg) followed by W, R, WR, WRC and RC, respectively. Highest daily weight gain ($P < 0.05$) was observed in the calves on treatment WRC (0.38 ± 0.02 kg). Fortnightly mean body height increase in calves on W, WC, WR, WRC, R and RC was 0.70 ± 0.07, 1.08 ± 0.10, 0.75 ± 0.09, 1.14 ± 0.09, 0.74 ± 0.09and 1.13 ± 0.10 inches, higher ($P < 0.05$) in the groups fed either whole milk, milk replacer or blend but supplemented with calf starter. Similar trend was observed in body length and heart girth increase at fortnightly intervals. Differences in mean WBCs, RBCs values and hemoglobin level varied ($P < 0.05$) between treatments and differences among total protein and albumin contents were non-significant. Cholesterol and triglyceride levels were highest ($P < 0.05$) in calves fed R. Cost to gain ratio was lowest on treatment RC. It was concluded that early introduction of calf starter during pre-weaning period improved the growth performance of Sahiwal calves

Key words: milk replacer, calf starter, weight gain

631 Withdrawn

632 Financial and energy analysis spanning the first decade of the pioneer organic beef enterprise in the Mexican tropics. P. Fajersson*[1] and P. Parada[2], *[1]EcoAgroPec, Hueytamalco, Puebla, Mexico, [2]Carnes La Rumorosa, Poza Rica, Veracruz, Mexico.*

Ten years ago a strategic alliance was formed between academia, a certification agency and a rancher to establish the first organic beef enterprise in the Mexican tropics. The sustainability and rentability of a 761 ha pasture based 550 head traditional beef cattle system (TBCS) converted to an organic beef cattle foodchain (OBF), with 685 head of cattle and marketing beef in 8 states in 2010, was evaluated using a financial and energy analysis. Continuous collaboration and interviews with the rancher and a questionnaire were used to obtain production costs, quantify inputs and collect data from yrs 2000, 2006 and 2010. In the energy analysis, the inputs used were identified, quantified, each assigned a value and transformed into energy units, compared and also used to determine critical points of the foodchain to identify opportunities to improve resource use. An analysis of 6 future economic scenarios identified strengths and weaknesses in a dynamic environment. The fixed costs were similar, USD 460933–466603 over time, while variable costs were less in the TBCS than in the OBF, USD 25123, 59608 and 75778 respectively. The marginal gain of the fixed costs remained negative, while the difference between return on investment, 16.6% in the TBCS and 36.6% and 31.2% in the OBF, represents the real gain from the conversion. Using only the variable costs, the marginal gain was USD 43912 for the TBCS and USD 132725 and 93339 for the OBF over time. The OBF remained profitable in all future scenarios, USD 37139–144074.The organic certification and integration of the foodchain increased production and commercialization costs, but guarantee the product quality and access to value added markets. The energy flow reflected the use of natural resources and their direct and indirect use in generating beef for society. The OBF was more energy efficient, 37.9% and 49.6% in yrs 2006 and 2010, than the TBCS with 18.3%. The efficiency and stability, indicating improved sustainability of the OBF, have increased as external inputs have declined. Increased beef production is possible without deterioration of natural resources in this low input organic agroforestry system, but economic gain depends more on the value added, 25% in 2010, to the organic beef.

Key words: organic beef, profit margin, energy efficiency

633 Expansion of meat rabbit projects in disaster-stricken Haiti. S. D. Lukefahr*[1], M. Kaplan-Pasternak[2], J. I. McNitt[3], and B.

Migny Jasmin[4], *[1]Texas A&M University, Kingsville, [2]PO Box 587, Nicasio, CA, [3]Southern University Agricultural Research and Extension Center, Baton Rouge, LA, [4]PO Box 80, Cap Haitian, Haiti.*

Following the recent devastating earthquake in Haiti in January of 2010, humanitarian efforts have been made to expand small-scale rabbit farming enterprises to over 1,000 resettled rural families. The rabbit program was initiated in the mid-90s. The study objective was to evaluate rabbit program status, based on a USAID consultancy visit in July–August, 2010. In the townships of Cap Haitian and Grand Boulage, several farms were visited to determine production status. In general, farmer enthusiasm toward the project was perceived to be high. Shed and cage designs as promoted by the host organization (Makouti Agro-Enterprises; MAE) were sound. Rabbit health problems associated with pathogens were minor. Contrary to the objective of farmer's achieving low-cost, on-farm feed security, only one feed species was typically fed each day, rather than a broad variety of grass and legume forages and garden and kitchen "wastes." With one exception, poor feeding practices were observed on all farms visited. In response, reproductive performance on farms was low and body condition of does was poor to fair. Average litter size was 3.71 kits, well short ($P < 0.05$) of the target standard of 5.5 fryers at market age per litter. Also, fryer body weights were light considering age. A frequency distribution of does on farms that were present with litter revealed a mode of 0%, a mean of 23.3%, and a median of 22.2%. Further, the distribution was sharply skewed to the right with one-third of farmers having no does with litters. Over one-half of farmers fell short of the 50% target (based on 6 litters per doe per annum). During the visit, rabbit training that emphasized proper feeding practices was conducted in both townships involving a total of 63 students, professionals, and farmers from many project locations. Several recommendations were made including that MAE make more frequent routine visits to farmers and also explore rabbit meat market opportunities. In conclusion, despite the discouraging present status, good progress has been made since project initiation, and people have accepted the practice of rabbit farming and the consumption of rabbit meat in their diets.

Key words: rabbits, development, international

Meat Science and Muscle Biology Symposium: Biochemical Mechanisms influencing Postmortem Proteolysis and the Identification of Protein Markers for Predicting Tenderness

634 The role of the muscle cell microenvironment on postmortem proteolysis. E. Huff-Lonergan* and S. Lonergan, *Iowa State University.*

Muscle cell metabolism reacts quickly to stimuli in living muscle and in the early postmortem period, thus the microenvironment of the muscle cell is very dynamic. Some of the changes in microenvironment that occur include loss of energy stores, a decline in pH, an increase in ionic strength, and a change in the oxidative status. The postmortem development of these changes can be influenced by genetics, ante mortem metabolism state, and postmortem handling of carcasses and muscle/meat. The resulting interplay between the intracellular environment and muscle enzymes and structural proteins is a large factor governing the amount and extent of postmortem proteolysis and meat tenderness that occurs. One family of enzymes in muscle that is sensitive to changes in pH and oxidative conditions is the calpain family. Both the rate and the extent of pH decline have a significant influence on the activity of μ- and m-calpain. In addition, oxidative changes in their environment can modify the activity of the calpain enzymes as well as their interactions with specific proteins, including their inhibitor, calpastatin. Structural proteins are also susceptible to oxidation and to denaturation by alterations in early postmortem pH. For example, oxidation of myosin, particularly the heavy chain region, has been shown to promote its aggregation and may potentially lead to cross-linking with other proteins in the myofibril, most notably titin. These changes in myosin may promote toughening of meat. Another microenviromental factor that may play a role in governing tenderness is the process of protein nitration. Nitrosylation is a potent signaling mechanism in living muscle and its effects are still evident in postmortem muscle. For instance, the activity of the protease μ-calpain is influenced by nitrosylation events. This posttranslational modification is among many that need to be examined in detail in early postmortem muscle. Understanding how the microenvironment of muscle cells influences changes like protein degradation, denaturation, oxidation and nitration is key to ultimately developing methods to predict and potentially control meat quality

Key words: calpain, skeletal muscle, meat tenderness

635 Orchestration of postmortem proteolysis following apoptosis onset. B. Yasmine[2], B. Samira[2], G. Mohamed[2], and O. Ahmed*[1], *[1]INRA de Clermont-Theix, St Genes Champanelle, France, [2]Unversity of Constantine, Constantine, Algeria.*

Meat tenderness variability is still a major problem for meat industry. All scientists agree that tenderization of meat upon storage results from a proteolytic degradation of myofibrils and associated components by endogenous muscle proteases. Progress in that domain thus followed the discovery of different proteolytic systems and their ability to mimic biochemical and structural changes affecting postmortem muscle. Despite the large controversy about the nature of the major proteolytic system responsible of meat tenderization, accumulating evidences support that this process is mutienzymatic in nature and involves a large set of endogenous proteolytic enzymes acting in a synergistic manner. The recent proposal that the first step of the conversion of muscle into meat is the onset of apoptosis is a real revolution in the meat science field. Apoptosis is a finally regulated process allowing elimination of excessive, damaged or potentially dangerous cells from an organism without damaging surrounding cells and contributing to the normal development of a multicellular organism during embryogenesis and the maintenance of tissue homeostasis in adults. Apoptosis is mediated by a particular group of cysteine peptidases called caspases, an acronym of cyteine aspartyl proteases. In that presentation we will overview different aspect of the apoptotic process: 1) how we came to that conclusion; 2) mechanisms and regulation of the process; 3) apoptosis is an energy dependent process but how the cell can provide enough energy for the onset of apoptosis in postmortem muscle?; 4) we will finely overview the consequences of apoptosis on muscle structure and how proteolytic systems may act all together.

Key words: apoptosis, muscle, proteolysis

636 Understanding postmortem proteolysis and identification of protein markers for tenderness using proteomics approaches. E. Veiseth-Kent* and K. Hollung, *Nofima Mat AS, Ås, Norway.*

Tenderness is a critical factor determining consumer acceptance of meat. Despite substantial research efforts aimed at revealing the critical factors determining meat tenderness, today′s level of understanding remains unable to explain a significant amount of the observed variation. Historically, research into postmortem proteolysis was conducted using techniques such as Western blotting and protease activity assays. While sensitive and specific, these techniques only provide insight into the actions of those specific proteins. A proteomics approach allows for a more global analysis of the dynamic process occurring with postmortem proteolysis. By expanding our focus beyond a limited set of candidates, new relationships and key players can be identified. Proteomics approaches in meat science have provided us with a better understanding of postmortem proteolysis and its relation to meat tenderness. This includes discovery of degradation products from proteins thought to be unaltered during postmortem storage and the involvement of heat shock proteins. Not surprisingly, proteomics has also been used by several groups to identify potential protein markers for tenderness. The power of these candidate markers to explain variation remains unclear, but it is certain that they will contribute to building a better picture of this complex process. However, applying this new knowledge to improve tenderness is a significant challenge. It is unlikely that online measurements of protein markers will ever be introduced as standard into meat processing plants. Fortunately, recent advances in technology and reduction in costs mean that today′s potential sires are routinely genotyped and data is being used to improve stock by genomic and marker-assisted selection. The success of genetic breeding programs is dependent upon access to high-resolution phenotype data, and if our efforts to detect potential protein markers for tenderness are successful and they have a sufficient genetic contribution, then it should be possible to associate these with genetic markers and improve breed and meat tenderness through selective breeding.

Key words: proteomics, proteolysis, tenderness

637 Growth and physiological responses of growing pigs to co-fermented wheat and corn distillers dried grains with solubles. D. Ayoade*, E. Kiarie, B. Slominski, and CM Nyachoti, *University of Manitoba, Winnipeg, Manitoba, Canada.*

Gaining a detailed knowledge on the impact of a feedstuff on pig growth and physiological responses is critical for its effective utilization in swine nutrition. Thus, the purpose of this study was to investigate the effect of distillers dried grains with solubles derived from co-fermentation of wheat and corn (wcDDGS) on performance, carcass and viscera organ weights, whole body O_2 consumption and heat production (HP) in growing barrows. The experimental diets were: (1) corn-soybean meal diet (Basal) (2) Basal + 15% wcDDGS, and (3) Basal + 30% wcDDGS. All diets were formulated to meet the NRC 1998 nutrients specification for 20–50 kg pigs. In Exp. 1, 48 pair-housed pigs (18.5 kg BW) were alloted based on BW to the 3 diets (n = 8). Pigs had free access to water and feed for a 28-d period during which ADG and ADFI were monitored weekly. On d 28, 1 pig/pen was killed to measure carcass and viscera organ weights. Overall, wcDDGS linearly decreased ($P < 0.001$) ADFI and ADG but had no effect on G:F ($P > 0.10$). The ADFI was 3.1, 2.9 and 2.7 kg/d for diets 1, 2 and 3, respectively; corresponding values for ADG were 0.79, 0.75 and 0.67 kg/d. A linear decline ($P = 0.04$) in eviscerated hot carcass weight was observed as wcDDGS increased, specifically, pigs fed 30% wcDDGS had 11.2% lower carcass weight relative to the pigs fed the basal diet. However, diet had no effect ($P > 0.10$) on the weights of any of the viscera organs. In Exp. 2, 18 pigs (20.4 kg BW) individually housed in metabolism crates were fed the 3 diets (n = 6) at 550 kcal ME/kg $BW^{0.60}$/d for a 15-d period followed by measurement of O_2 consumption and CO_2 production over a 24-h period using an indirect calorimeter system. There was no effect of diet ($P > 0.10$) on whole body O_2 consumption and CO_2 production and HP. In conclusion, increasing wcDDGS content in growing pig diets linearly reduced ADFI, ADG, and eviscerated hot carcass weight but had no effect on G:F, viscera organ weights and heat production.

Key words: co-fermented wheat and corn DDGS, physiological responses, pigs

638 High-protein distillers dried grains can replace soybean meal in the diets for growing-finishing pigs. L. Ma*[1] and G. Allee[2], *[1]Chia Tai Investment Co., Ltd., Beijing, China, [2]University of Missouri, Columbia.*

The information on the use of high-protein distillers dried grains (HP-DDG) to replace soybean meal (SBM) in swine diets is limited. Additionally, previous studies from our lab determined that the optimal SID Trp:lys ratio of pigs fed diets containing HP-DDG was 16%. Thus, the objectives of this study were to determine the effects of HP-DDG replacing SBM in grower-finisher diets on growth performance and to evaluate the validity of 16% SID Trp:Lys ratio for pigs. Pigs (n = 108; initial BW = 29.1 kg) were blocked by BW and allotted to one of 3 dietary treatments: 1) Corn-SBM control diet, 2) diet with HP-DDG replacing 37% of SBM, 3) diet with HP–DDG replacing 70% of SBM, in a 4-phase study (21 d/phase). Each treatment had 6 replicate pens with 6 pigs per pen. In this study, the SID Trp:Lys ratios of the control diets were above 17%. The diets including HP–DDG contained SID Trp:Lys ratios of 16%. In phase 4 (99–123 kg), ractopamine (Paylean, Elanco Animal Health) was added in the diets. At the beginning and the end of each phase, pigs were individually weighed and feed disappearance was recorded. There were no differences in ADG, ADFI, and G:F ($P > 0.05$) during any phase and the entire 84 d among the 3 treatments. In conclusion, HP–DDG (35.5% CP) can be used to replace up to 70% of SBM in growing-finishing pigs diets without any detrimental impact on performance. In addition, 16% SID Trp:Lys ratio is suitable for growing-finishing pigs fed diets containing HP–DDG.

Table 1.

	Control	2	3	SE	*P*-value
D 0 WT, kg	29.13	29.00	29.37	0.66	0.65
D 84 WT, kg	124.94	123.52	124.04	1.36	0.56
D 0 to 84					
ADG, kg	1.14	1.13	1.13	0.01	0.61
ADFI, kg	3.05	3.01	3.03	0.06	0.85
G:F	0.37	0.37	0.37	0.003	0.83

Key words: high-protein distillers dried grains, pigs, growth performance

639 Effects of including tallow, palm kernel oil, corn germ, or glycerol to diets containing distillers dried grains with solubles on pork fat quality of growing-finishing pigs. J. W. Lee*, B. D. Keever, J. Killefer, F. K. McKeith, and H. H. Stein, *University of Illinois, Urbana.*

Thirty 6 barrows and 36 gilts (initial BW: 43.7 ± 2.0 kg) were used in an 88-d experiment to determine effects of including tallow, palm kernel oil, corn germ, or glycerol to diets containing distillers dried grains with solubles (DDGS) on pork fat quality of growing-finishing pigs. Pigs were individually housed and randomly allotted to 1 of 6 dietary treatments using a 2 × 6 factorial design with 2 genders and 6 diets and 12 replicate pigs per diet. A corn-soybean meal control diet with no added fat and a diet containing corn, soybean meal, and 30% DDGS were formulated. Four additional diets were formulated by adding 15% corn germ, 3% tallow, 3% palm kernel oil, or 5% glycerol to the DDGS-containing diet. At the end of the experiment, pigs were slaughtered, belly characteristics were measured, and backfat and belly fat samples were collected. Fatty acids were analyzed in all ingredients, diets, and fat samples, and iodine value (IV) was calculated. Dietary IVP was calculated using either the sum of the analyzed IVP of each ingredient in the diet (IVP 1) or the analyzed IVP of dietary fat (IVP 2). There were no effects of diet on belly length, width, and weight. Pigs fed the control diet had greater ($P < 0.05$) flop distance than pigs fed the DDGS-containing diets. There were no differences in flop distance among the diets containing DDGS. Barrows had greater ($P < 0.05$) flop distance and heavier ($P < 0.05$) bellies than gilts. Diet did not affect belly fat IV. However, gilts had greater ($P < 0.05$) belly fat IV than barrows. Dietary IVP 1 was positively correlated (r = 0.80; $P = 0.06$) to backfat IV; however, there was no correlation with belly fat IV. Dietary IVP 2 was not correlated with either backfat or belly fat IV. Back fat IV can be predicted using the following equation: IV = 0.11 × dietary IVP 1 + 70.29 (R2 = 0.63, $P < 0.06$). In conclusion, the negative effects of DDGS on pork fat quality were not ameliorated by supplementing diets with corn germ, tallow, palm kernel oil, or glycerol.

Key words: fat quality, DDGS, pigs

640 The impact of feeding corn distillers dried grains with solubles to sows on plasma and milk vitamin E and selenium levels. S. A. Crowder* and M. E. Johnston, *JBS United Inc., Sheridan, IN.*

Corn distillers dried grains with solubles (DDGS) were fed to gestating and lactating sows to determine the impact on milk and plasma vitamin E (vit E) and selenium (Se) levels. One hundred thirty-eight sows (PIC-C29) were blocked by parity and body condition score and allotted to 1 of 4 treatments. Diet 1 (Control) contained 0% DDGS in gestation and lactation, diet 2 contained 15% DDGS in gestation and 7.5% DDGS in lactation, diet 3 contained 30% DDGS in gestation and 15% DDGS in lactation. Diets 1, 2, and 3 were formulated to contain 66 IU/kg of vit E. Diet 4 contained 15% DDGS in gestation and 7.5% DDGS in lactation with supplemental vit E (110 IU/kg total). Plasma samples were collected from sows on d 100 of gestation and at weaning. Milk samples were collected from sows and plasma samples from a subset of pigs at weaning. All samples were analyzed for vit E and Se levels. Sow performance was not affected by the inclusion of DDGS with or without added vit E; including number of pigs born live and weaned, birth and wean weight, and lactation feed intake ($P > 0.05$). There was no negative impact of DDGS inclusion with or without added vit E on plasma Se levels at d 100, weaning, in the pig, or the milk. There was no negative impact of DDGS inclusion on sow plasma vit E levels at d 100 (Control = 1.69 μg/ml, 15% DDGS = 1.90 μg/ml, 30% DDGS = 2.10 μg/ml, 15% DDGS + vit E = 2.35 μg/ml) or at weaning. Milk vit E levels for Control, 15% DDGS, 30% DDGS, and 15% DDGS + vit E were 3.57, 3.24, 3.35, and 3.90 μg/ml respectively. There was no difference in milk vit E level between the Control and the DDGS treatments ($P > 0.05$). The 15% DDGS + vit E had a higher milk vit E level ($P < 0.05$) compared with the 15% and 30% DDGS treatments. Pig vit E level was greatest for the 15% DDGS + vit E treatment ($P < 0.05$). There was no difference in pig vit E level between the Control and DDGS without added vit E treatments ($P > 0.05$). These data suggest the addition of up to 30% DDGS in gestation and 15% DDGS in lactation diets with 66 IU/kg of vit E had no negative impact on vit E and Se levels.

Key words: sow, DDGS, vitamin E

641 Evaluation of various corn distillers dried grains with solubles (DDGS) feeding strategies in nursery pigs. N. L. Horn*, C. R. Little, and J. D. Spencer, *JBS United Inc., Sheridan, IN.*

An experiment was conducted to determine the performance response of nursery pigs fed various corn DDGS feeding strategies. There were 11 replicates per treatment with 11 pigs per pen. Four hundred and eighty-four pigs (PIC C29 × 337, BW = 6.21 ± 0.16 kg, 19-d old) were blocked by gender and BW, and pigs within each block were randomly assigned to one of 4 dietary treatments. Pigs were fed a 4-phase nursery program with a common phase 1 pellet containing no DDGS from d 1 to 6 post wean and the phase 2, 3, and 4 experimental diets from d 7 to 13, d 14 to 20, and d 21 to 41 post wean, respectively. Dietary treatments were 1.) No DDGS throughout, 2.) 0, 10, and 20% DDGS d 7 to 13, d 14 to 20, and d 21 to 41 post wean, respectively (slow step-up), 3.) 10, 20, and 30% DDGS d 7 to 13, d 14 to 20, and d 21 to 41 post wean, respectively (moderate step-up), and 4.) 20 and 30% DDGS d 7 to 13 and d 14 to 41 post wean, respectively (aggressive step-up). Experimental diets were formulated to contain equivalent true ileal digestible lysine (1.36%) during phases 2 and 3 and an equivalent true ileal digestible lysine to ME ratio (3.75) during phase 4. Introducing DDGS to pigs in phase 2 did not affect ($P > 0.05$) growth performance. DDGS supplementation in phase 3 increased ($P < 0.05$) ADG and G:F compared with the no DDGS program. Furthermore, 20 and 30% DDGS supplementation increased ($P < 0.05$) ADFI compared with the no DDGS program during phase 3. In phase 4, the pigs fed the aggressive DDGS program gained less weight ($P < 0.05$) than the other dietary treatments. Cumulatively (6 wk), use of DDGS in diets for nursery pigs had no effect ($P > 0.05$) on final BW or ADG, but did result in reduced ($P < 0.05$) feed intakes and increased ($P < 0.05$) G:F, with no difference among the DDGS utilization strategies. These results suggest that 20% DDGS can be used as early as 7-d post weaning and up to 30% DDGS by 14 d post weaning without negatively affecting growth performance; however, all these results will depend on DDGS quality and accurate characterization of nutrient values.

Key words: DDGS, nursery, swine

642 Effects of distillers dried grains with solubles in the diet of gestating sows on nutrient excretion. H. J. Kim*, S. D. Carter, T. M. Walraven, M. R. Bible, and K. F. Coble, *Oklahoma State University, Stillwater.*

A total of 88 sows (212 kg; parity = 2.5) were used to determine the effects of distillers dried grains with solubles (DDGS) on nutrient excretion during the gestation period. Sows were stratified by BW, parity, and status of gestation, and housed in one of 2 identical environmentally-controlled buildings (experimental unit) with shallow pit, pull-plug systems. Dietary treatments were randomly assigned to one of 2 buildings in a 2 (trt) x 2 (building) crossover design. The control diet consisted of a fortified corn-soybean meal based diet formulated to 12% CP, 0.47% SID Lys and 0.39% digestible P. The experimental diet (DG40) contained 40% DDGS (89.2% DM, 26.1% CP, 0.8% P, and 2.2 ppm DON) and was formulated to 16% CP, 0.47% SID Lys and 0.39% digestible P. DDGS replaced corn, soybean meal and dicalcium phosphate and Lys HCl was used to adjust dietary levels of CP and SID Lys. Each of 2 phases consisted of a 6-wk period which included a 2-wk adjustment period followed by a 4-wk slurry collection period. At the end of the initial 6-wk period, treatments were switched between buildings to allow for another 6-wk period. There was no difference ($P > 0.10$) in feed intake (2.28 vs. 2.20 kg) for sows fed control vs. DG40. Also, slurry pH (7.66 vs. 7.65), temperature (16.6 vs. 17.2°C), and volume (38.4 vs. 42.7 L) were similar ($P > 0.10$). Daily intakes of DM, P, Ca, K, Fe, Zn, Cu, and Mn were similar ($P > 0.10$) for both dietary treatments. However, daily N intake (46 vs. 55 g) tended to increase ($P = 0.10$), but Mg (3.1 vs. 4.5 g), Na (4.8 vs. 7.5 g), and S (4.1 vs. 7.6 g) intake increased ($P < 0.05$) for sows fed 40% DDGS. Inclusion of DDGS in the diet increased ($P = 0.04$) daily excretion of DM (199 vs. 255 g) and S (2.7 vs. 4.4 g) by 28 and 68%, respectively. The daily excretion of Ca and Mg tended to increase ($P < 0.08$) with DDGS. Daily N excretion increased by 20% with inclusion of DDGS in the diet; however, this was not significant ($P = 0.12$). In conclusion, 40% inclusion of DDGS in the diet of gestating sows markedly increases DM and S excretion, and may influence N, Ca, and Mg excretion. This work was partially funded by NPB.

Key words: Sows, DDGS, nutrient excretion

Nonruminant Nutrition Symposium: Nutrition's Role in Environmental Management and Meeting Government Regulations

643 An update on current environmental regulations and standards for livestock facilities. D. Porter*, *Environmental Protection Agency, Region 7, Kansas City, KS.*

In 1972 Congress enacted the Clean Water Act which defined Concentrated Animal Feeding Operations or CAFOs as point sources. Subsequently, the EPA established National Pollution Discharge Elimination System or NPDES permit regulations for livestock facilities defined as CAFOs. These regulations created effluent limitation guidelines that permitted discharges from the CAFO production area during a 25-yr, 24-h rainfall event, assuming the CAFO was in compliance with the conditions of its NPDES permit. In 2003, EPA revised the regulations to require effluent limitation guidelines for land application areas through development of nutrient management plans (NMP) and require all CAFOs that discharge to obtain a permit. In 2005, the 2nd Circuit Court of Appeals Decision vacated the duty to apply for all CAFOs and required that all NPDES permits and NMPs must be available for public review and comment before issuance. In the CAFO Rule that became effective in December of 2008, EPA revised the duty to apply for an NPDES permit to CAFOs that discharge or propose to discharge to waters of the US; based on the CAFOs design, construction, operation, and maintenance. The 2008 CAFO Rule also established additional NMP-related requirements to be included as enforceable terms of the permit. Several site-specific terms to be included in the permit and NMP include: 1) fields available for land application, 2) outcome of a phosphorus risk assessment, 3) crops to be planted, 4) a realistic yield goal for each crop, and 5) nitrogen and phosphorus removal rates for each crop. Substantial revisions to the NMP, such as changes to land application fields, crops, and increases in the risk of phosphorus runoff, must be changed in the permit and public noticed.

Key words: CAFO regulation, nutrient management plan

644 Environmental management regulations in Europe. N. Penlington*, *BPEX, Warwickshire, UK.*

Environmental regulations in Europe are comprehensive and developed to address existing pollution issues such as water and air quality. Farmers and agri-businesses have to work within a complex regulatory framework including the need for some to have permits and licenses, minimum facilities, restrictions on how and when some activities can be carried out. Regulators and the public are demanding higher levels of performance from farmers and scrutinize proposals for new or expanding operations. Conflicts arise between regulations often developed in isolation for a specific purpose and economic viability. Cross media effects, factors including animal welfare, consumer requirements and local conditions become the issue rather than the Best Solution. Recent world events and significant rises in food costs, government focus on reducing greenhouse gas emissions, food security and a growing world population has changed the dynamic in which agri-businesses have to operate. The emphasis is shifting, the drivers being efficiency and increased production, but not at any cost. Businesses embracing this change are finding that environmental regulations become less of an issue, those who run their business to comply with regulation are unlikely to thrive. Regulations will change to allow pig and poultry producers working with processors to convert resources efficiently into meat and other products with minimal waste or loss from the system.

645 Nutritional practices that affect the environment-excretion of nitrogen, phosphorus, and sulfur; and emissions of odors and greenhouse gases from swine production facilities. B. J. Kerr*, *USDA-ARS-NLAE, Ames, IA.*

In growing swine, whole-body retention of nitrogen, phosphorus, and sulfur is approximately only 50% of total dietary intake. Consequently, excretion of these compounds in urine and feces (i.e., manure), and subsequently into the environment, can be relatively extensive, especially in areas where large numbers of livestock are produced on relatively small areas of land. Air, surface water, and ground water are 3 natural resource components that can be impacted by livestock production facilities. Although generally depicted separately, many avenues for nutrient or gaseous abatement in any of one these components are directly interrelated and can simultaneously increase, or decrease, the impact on the environment. From animal production facilities, release of nitrogen (NH3), carbon (CO_2 and CH_4), phosphorus, sulfur (H_2S), volatile organic compounds (primarily short chain fatty acids, SCFA), particulates, and greenhouse gasses (CH_4, CO_2, and N_2O) are of highest interest since reduction in any of these compounds have short-and long-term environmental impact. Because a reduction of these compounds from animal production facilities will have a multiplicative effect on the total excretion process, these compounds need to be evaluated simultaneously and methods to reduce these compounds must be considered in diet formulation, especially because feed costs account for approximately 70% of the total cost of livestock production. The bottom line is that undigested feed products, endogenous animal secretions, and nutrients in excess of the needs of the animal are ultimately the nutrient input (carbon, nitrogen, phosphorus, sulfur, etc.) in manure storage systems, and subsequently, are potential contaminants into the environment; either air or water. Data will be summarized and new data will be presented evaluating diet modifications (focusing largely on dietary carbon, nitrogen, and sulfur) relative to nutrient excretion and the impact that these nutrients on the environment.

Key words: environment, nutrient excretion, gas emissions

646 Practical application of manure management plans of a swine production system to row crop production agriculture. B. S. Borg*, *Murphy Brown LLC, Ames, IA.*

During the past several years there has been tremendous change in the methodology, equipment used for application and regulatory emphasis on the accurate use of animal waste. Farmers have always understood the "value" of manure being applied to crop land but this understanding has grown to include intricate detail about the inputs and outputs of the fine balance of crop nutrient requirements, current soil nutrient content and manure nutrient content. Sustainable agriculture programs circulate around the balance of nutrient application and nutrient use. Environmental concerns about the leaching of nutrients into underground water reservoirs as well as nutrient run off have led to regulations in many states that now monitor and direct the use of manure more intelligently than the use of more nutrient dense, commercially available nutrients. Murphy Brown LLC, and former ownership entities, have included manure management plans as an important part of our hog production system since the early 1990s. Historical records of soil nutrient content that span over a 17 year period, with every other year manure application, show phosphorus and potassium content of

the soil to be on a slight decline over time. During this period of time, significant changes have occurred in feeding programs to include a greater use of crystalline amino acids, phytase as well as other ingredients that have a direct impact on the nutrient content of the manure. Understanding and monitoring soil nutrient content, waste nutrient content and the changing requirements of the crop being raised allow for a balanced system to occur. Animal waste is an excellent source of highly available nutrients and can be very effectively used as a cost efficient source of nutrients while maintaining adequate focus on environmental concerns relating to nutrient loading of the land and surface waters.

Key words: swine, animal waste, soil nutrients

Physiology and Endocrinology II

647 Can prenatal social stress impact sex characteristics in piglets? L. A. Mack*[1], S. D. Eicher[2], A. K. Johnson[3], D. C. Lay Jr.[2], B. T. Richert[2], and E. A. Pajor[4], *[1]Purdue University, W. Lafayette, IN, [2]LBRU, USDA-ARS, W. Lafayette, IN, [3]Iowa State University, Ames, [4]University of Calgary, Calgary, AB, Canada.*

Prenatal stress (PNS) alters sex traits in rodents by androgenizing offspring resulting in reduced reproduction. In production, gestating sows are often exposed to social stress of mixing. This study examined if mixing gestating sows alters sexual development in piglets. At 34 ± 10 d of gestation, 6 groups of 18 sows (n = 108) were put in 1 of 4 treatments: stable (S), hydrocortisone acetate (HCA), unstable (U) or unstable companion (UC). In an incomplete block design, 18 sows were housed in 6 pens of 3 sows for 3 wk. Each pen contained 3 S, 3 HCA, or 1 U and 2 UC sows. Stable, HCA, and UC sows did not move; unstable sows moved weekly into a new pen with unknown UC sows. To simulate stress, 70 mg HCA was orally given twice daily to HCA sows for 3 wk. Data were analyzed in SAS using Mixed Model Procedure. Cortisol concentration was greatest in HCA sows ($P < 0.0001$) and after initial mixing ($P < 0.05$). Sows' progesterone level did not differ by treatment or time. Lesion scores increased after mixing in all treatments ($P < 0.05$). On wk 3, U sows had more head and upper leg lesions than the other treatments ($P < 0.05$). Sow's treatment had little effect on piglets: litter size, sex ratio, BW, and mortality did not differ. Pigs were weighed on d 1, d 3, weaning (d 19 ± 8), and 5 mo post-weaning (6 mo). There was no treatment effect on weight from birth to weaning but at 6 mo HCA and UC pigs tended to weigh more ($P < 0.10$) and from weaning - 6 mo had greater ADG than S pigs ($P < 0.05$). Testes weight, teat number, and teat asymmetry did not differ by treatment or gender. Males born from dominant sows, defined by feeding behavior, tended to have more teats than those of low ranked sows ($P < 0.10$). Anogenital distance (ANO) in male pigs was greater in UC than U pigs ($P < 0.05$) with the other treatments intermediate. Female ANO showed no differences. Social stress induced by weekly mixing had little impact on sexual, morphological measures of the offspring in this study.

Key words: prenatal stress, swine, reproduction

648 Heat stress increases small intestinal permeability and circulating endotoxin in growing pigs. S. C. Pearce*, V. Mani, L. H. Baumgard, and N. K. Gabler, *Iowa State University, Ames.*

Heat-stress causes a decreased intestinal integrity and induces "leaky" gut. This may lead to reduced growth performance and bacterial sepsis, but whether this occurs in pigs and the mechanisms responsible for it, are ill-defined. Crossbred gilts (n = 48; 35 ± 4 kg BW) were housed in constant climate controlled rooms in individual pens and exposed to 1) thermal neutral (TN) conditions (20°C; 35–50% humidity) with ad libitum intake (n = 18), 2) HS conditions (35°C; 20–35% humidity) with ad libitum intake (n = 24) or 3) pair-fed (PF in TN conditions [PFTN], n = 6: to eliminate confounding effects of dissimilar feed intake [FI]). Pigs were sacrificed at 1, 3, or 7d of environmental exposure and freshly isolated jejunum samples were mounted into modified Ussing chambers. Segments were then analyzed for transepithelial electrical resistance (TEER) and intestinal fluorescein isothiocyanate (FITC)-labeled lipopolysaccharide (LPS) transport expressed as endotoxin apparent permeability coefficient (APP). Additionally, circulating concentrations of endotoxins were measured in plasma blood samples. Irrespective of day, plasma endotoxin concentrations increased 46% ($P < 0.05$) in HS pigs compared with TN pigs, while TEER decreased 24% ($P < 0.05$) and endotoxin APP increased 81% ($P < 0.01$), respectively. Furthermore, d 7 HS pigs tended to have increased APP ($P = 0.06$) compared with PFTN controls. These data indicate that HS decreases intestinal integrity and increases endotoxin permeability. Together, this translated into an increase in circulating endotoxin. We hypothesize that these events lead to increased acute inflammation which is responsible for reduced pig performance during warm summer months.

Key words: heat stress, pig, intestinal permeability

649 The effect of naloxone on reproductive behavior and plasma prolactin levels in third lactation sows. V. O. Fuentes Hernadez*, R. Orozco Hernandez, and A. Bernal Canseco, *Centro Universitario de los Altos, Universidad de Guadalajara, tepatitlan Jalisco, Mexico.*

The present study was undertaken to study the effect of small doses of naloxone on behavior, prolactin plasma levels, interval of weaning to first estrus, and duration of estrus in third lactation sows. Thirty York × Landrace sows weaned at 25 to 27 d pospartum, were selected and separated at random in 2 groups of 15. One group served as control and the other received every 12 h 2 mg of naloxone im. Treatment with small doses of naloxone started 3 d before and continued for 3 d after weaning similarly the control group was injected with 2 mL of a saline solution. Naloxone treated sows showed estrus 88.8 ± 6.2 h after weaning ($P < 0.01$), control sows estrus was evident 102.37 ± 7.2 h after weaning. Duration of estrus in treated and nontreated was 85.6 ± 3.8 and 42.6 ± 3.7 h respectively. Prolactin levels decreased rapidly after weaning in both groups, but plasma PR in naloxone treated sows were below control levels (15 ± 2 and 7 ± 0.3 ng respectively $P < 0.1$). Behavior scores showed that naloxone treated sows accepted mounting with a significant reduction in aggressive behavior as compared with controls. It was concluded that endogenous opioids are important modulators of sow sexual behavior.

Key words: sow, naloxone, behavior

650 Differential expressed proteins in porcine follicular fluid during folliculogenesis. J. M. Feugang*[1], K. Pendarvis[2], S. T. Willard[3], and P. L. Ryan[1,4], *[1]Department of Animal and Dairy Sciences, Mississippi State University, Mississippi State, [2]Life Science Biotechnology Institute, Mississippi State University, Mississippi State, [3]Department of Biochemistry and Molecular Biology, Mississippi State University, Mississippi State, [4]Department of Pathobiology and Population Medicine, Mississippi State University, Mississippi State.*

Ovarian follicular fluid (FF) is a dynamic and suitable microenvironments for growth and acquisition of oocyte developmental competence. Disparities in oocyte quality of diverse follicle sizes are partly attributed to FF composition, whose changing contents during folliculogenesis are still not well-characterized. Follicular fluid is an optimal source for identifying determinants of oocyte and follicle growth. Therefore, we compared proteome profiles of porcine FF of various follicular developmental stages. Follicles were dissected from healthy sow ovaries and classified as small (SFF; ≤3mm), medium (MFF; 4-6 mm), and large (LFF;7-12mm). Follicular fluid was aspirated from individual follicles, centrifuged and collected for protein quantification and estradiol assay. All procedures were performed at 4°C and

repeated 4X. Samples with highest estradiol content were selected for a non-gel based proteome analyse. Peptides significantly detected ($P \leq 0.05$) were subjected to protein identification, and highly differentially detected (DD) proteins ($P \leq 0.05$) were selected for functional annotation. Approximately two thousand proteins were detected in each FF group. Significant protein numbers (1,493-1,656) were specific to each FF group, and 23-26% of proteins (558-570) were common amongst groups. Of these shared proteins, 28 to 33% were significantly differentially detected ($P \leq 0.05$). Gene ontology (GO) analyses of highly significantly DD indicated associations with various cellular components, molecular functions and biological processes. Pairwise comparisons indicated that MFF vs SFF had the highest total GO annotation number (184) compared to LFF vs SFF (61), and LFF vs MFF (48). Based on their abundance in FF, few proteins such as fibronectin 1, inhibitor of carbonic anhydrase precursor, and histidine rich glycoprotein were highly DD in LFF, MFF, and SFF, respectively. In conclusion, the study indicates important quantitative and qualitative changes in FF composition during folliculogenesis, and whose specific components may serve as candidate markers of follicle and oocyte growth. Work supported by USDA-ARS Biophotonics Initiative #58-6402-3-0120.

Key words: follicular fluid, proteome, oocyte growth

651 Effects of glucuronic acid supplementation on the in vitro maturation and fertilization of pig oocytes. A. R. Clark* and B. D. Whitaker, *The University of Findlay, Findlay, OH.*

The objective of this study was to assess the in vitro maturation and fertilization (IVF) of pig oocytes supplemented with glucuronic acid during the last 24 h of maturation. Oocytes were transferred after 20 h from the beginning of maturation into hormone-free maturation media containing glucuronic acid (0, 0.01, 0.1, 1 mM) for an additional 24 h of maturation. Oocytes (n = 300) were evaluated for thickness of the zona pellucida, size of the perivitelline space, fertilization characteristics at 12 h after IVF, and embryo development at 48 h and 144 h after IVF. There were no significant differences between treatment groups when comparing zona pellucida thickness, however supplementation of 0.1 and 0.01 mM glucuronic acid significantly increased ($P < 0.05$) the size of the perivitelline space compared with no supplementation. Supplementation of 0.01 mM glucuronic acid significantly increased ($P < 0.05$) the size of the perivitelline space compared with 1.0 mM glucuronic acid supplementation. There were no significant differences between the treatment groups when evaluating sperm penetration or male pronucleus development but 0.01 mM glucuronic acid supplementation significantly decreased ($P < 0.05$) polyspermic penetration compared with the other treatment groups. Although there were no significant differences in cleaved embryos at 48 h after IVF, there were significantly higher ($P < 0.05$) numbers of embryos derived from oocytes supplemented with 0.01 mM glucuronic acid (38.78 ± 5.50%) at the blastocyst stage by 144 h after IVF compared with 0 mM (22.00 ± 5.68%), 0.1 mM (25.00 ± 5.81%), and 1.0 mM (18.60 ± 5.87%). The results of this study suggest that there are positive effects of 0.01 mM glucuronic acid supplementation during the oocyte maturation on successful IVF and subsequent embryo development in pigs.

Key words: glucuronic acid, swine, embryo development

652 Vitrification versus freezing for cryopreserving bovine embryos. S. G. Kruse* and G. E. Seidel Jr., *Colorado State University, Fort Collins.*

Our objective was to compare vitrification and freezing for cryopreserving bovine embryos. Crossbred, nonlactating beef cows were superovulated and embryos recovered 7d post estrus. Embryos of quality #1 or #2 per IETS standards were cryopreserved via vitrification (VIT; n = 40) or slow freezing (SLF; n = 42). For VIT, embryos were exposed to 5 M ethylene glycol in SynGro for 3 min at 22°C and moved to 6.5 M ethylene glycol + 0.5 M galactose + 18% Ficoll in SynGro at 22°C, and in 20 µl, immediately loaded in 0.25 mL straws between 2 columns of 1 M galactose in SynGro. After 35 s, embryos were vitrified by cooling for 2 min via contact of straw walls with columns drilled into an aluminum block immersed in liquid nitrogen; straws were then plunged into liquid nitrogen. Embryos frozen via SLF were exposed to 1.36 M glycerol in modified Dulbecco′s PBS + 0.4% BSA (PBS) for 10 min at 22°C, loaded in 0.25 mL straws, and placed into a freezing machine. Straws were cooled to −6°C at 4°C per min, held at −6°C for 5 min, seeded, held at −6°C for 10 min, and cooled to −30°C at 0.5°C per min and plunged into liquid nitrogen. Embryos were warmed/thawed by holding straws in air at 22°C for 8 s and placing them in 37°C water for 20 s. VIT embryos were mixed with 1 M galactose in SynGro in the straw for 2 min and directly transferred. SLF embryos were expelled, and glycerol was removed in steps: 0.8 M glycerol + 0.3 M sucrose for 6 min; 0.4 M glycerol + 0.3 M sucrose for 6 min; 0.3 M sucrose for 6 min; and PBS for 2 min, then loaded in 0.25 mL straws. Embryos were nonsurgically transferred into cows culled for unknown reasons, but with normal-appearing reproductive tracts. Recipients were d 7 ± 0.5, and each received 2 embryos into the uterine horn ipsilateral to the CL. Pregnancy diagnosis was at d 37 ± 2 via ultrasonography. Survival rate per embryo (normal fetus with heartbeat) did not differ (Fisher′s Exact; $P \geq 0.1$) between methods (VIT = 47.5%; SLF = 38.1%; 16 of the 19 pregnant cows carried twins). Therefore, VIT was similarly efficacious to SLF for cryopreservation of bovine embryos, and simpler, requiring less equipment, time, and expense.

Key words: embryo transfer, vitrification, bovine

653 Effects of cyanocobalamin supplementation on frozen-thawed boar spermatozoa. A. M. Hyde, L. E. Elsea*, and B. D. Whitaker, *The University of Findlay, Findlay, OH.*

The objective of this study was to assess the in vitro fertilization (IVF) of pig oocytes using frozen-thawed boar sperm supplemented with cyanocobalamin to the incubation media. Frozen semen pellets were thawed and incubated for 1 h in fertilization media containing cyanocobalamin (0, 0.5, 1.0, 2.0 µM) then evaluated for forward progressive motility and viability. Forward progressive motility of the 0.5 and 1.0 µM cyanocobalamin supplements were significantly higher ($P < 0.05$) than the 0 and 2.0 µM cyanocobalamin supplements. Viability of sperm supplemented with 0.5 µM cyanocobalamin was significantly higher ($P < 0.05$) than all other groups. Oocytes were matured and fertilized with frozen-thawed boar semen that was previously incubated for 1 h in fertilization media containing cyanocobalamin (0 or 0.5 µM; 100 oocytes/treatment). Fertilization characteristics were evaluated 12 h after IVF of oocytes and embryo development was analyzed at 48 h and 144 h post-IVF. There were no significant differences between treatment groups when evaluating sperm penetration, polyspermic penetration, or male pronucleus development. Embryos derived from the oocytes fertilized with 0.5 µM cyanocobalamin supplemented sperm had a significantly higher percentage ($P < 0.05$) of cleaved embryos compared with those without cyanocobalamin supplementation at 48 h after IVF. There were no significant differences in the percent of embryos reaching the blastocyst stage by 144 h after IVF

between treatment groups. The results of this study suggest that there are positive effects of 0.5 μM cyanocobalamin supplementation during incubation of frozen-thawed boar semen on early development of IVF derived pig embryos.

Key words: cyanocobalamin, in vitro fertilization, swine

654 GnRH therapeutics to advance the timing of pregnancy in the seasonally anovulatory mare. J. F. Thorson*[1,2], L. D. Prezotto[1,2], R. D. Cardoso[1,2], B. R. C. Alves[1], M. Amstalden[1], and G. L. Williams[1,2], *[1]Texas AgriLife Research, Beeville, [2]Texas A&M University, College Station.*

Onset of the winter anovulatory period in mares is associated with a marked diminution in adenohypophyseal synthesis and release of LH. Native GnRH, unlike its synthetic agonists, stimulates the synthesis and secretion of LH in mares without pituitary refractoriness. Herein we tested the hypotheses that 1) the average Julian day of conception can be accelerated by up to 50 d in winter anovulatory mares treated continuously with native GnRH beginning on February 1 and 2) mares will sustain luteal function and pregnancy following treatment withdrawal. Forty-two winter anovulatory mares were stratified by age and BCS across 2 locations in a randomized block design and assigned to 1 of 3 groups (n = 14/group): 1) Control: untreated; 2) GnRH-14: GnRH delivered subcutaneously in saline at a rate of 100 μg/h for 8 wk (Feb. 1–Mar. 29) using 4 consecutive 14-d pumps (Alzet 2ML2), or 3) GnRH-28: GnRH delivered as in 2, but using 2, 28-d pumps (Alzet 2ML4). Upon development of a 35 mm follicle and expression of estrus, mares were bred the following day and treated with hCG. Pregnancies were confirmed by ultrasonography on d 14, 24, 33, and 45, with blood samples collected to assess luteal function. Mares treated with GnRH (GnRH-14 and GnRH-28) exhibited marked increases ($P \leq 0.04$) in the frequency of development of a 35-mm follicle, submission rate for live cover/AI, ovulation, and pregnancy compared with Control mares on treatment d 28 (March 1, 2010) and 56 (March 29, 2010). Interval to first 35 mm follicle was 51.8, 15.1, and 16.0 d for Control, GnRH-14 and GnRH-28, respectively, excluding 2 GnRH-28 mares that failed to develop 35-mm follicles during the treatment period. By the end of the treatment period (Mar. 29), only 14% of Control mares were confirmed pregnant compared with 75% of GnRH treated mares. Further, serum concentrations of progesterone were similar to ($P \geq 0.07$) or greater than ($P \leq 0.05$) that of Control mares from d 14 to 46 post-breeding for GnRH-28 and GnRH-14, respectively. These data illustrate that continuous administration of native GnRH is a practical and highly efficient option for managing seasonal anovulation in mares.

Key words: GnRH, mare, seasonality

655 Adaption of a kinetic chromogen LAL test system to investigate the incidence of endotoxins on pig farms. S. Schaumberger*, C. Ratzinger, L. Krüger, and G. Schatzmayr, *BIOMIN Research Center, Tulln, Austria.*

Endotoxins cause a stimulation of the immune system and since they are ubiquitous in the environment their contribution to pig diseases has been repeatedly discussed. The objective of this study was to evaluate a test for measuring endotoxins in the farm environment and to determine the incidence of endotoxins on swine farms. Feed, water and air samples were taken from 16 pig farms and 32 sows were sampled (milk, feces and urine) between the first and third lactating week. All samples were tested with the kinetic chromogen Limulus-Amoebycat-Lysat test (LAL). Feces, air and feed were extracted with Tween20 for 1 h and dilution rows of all samples were prepared within 12 h after sampling. Predefined dilutions were used for testing. Tests were evaluated valid with a r^2 of the calibration line > 0.97 and the recoveries ranging between 50 – 200% of added LPS. Data were statistically analyzed using PASW 18.0 (formerly SPSS Statistics). The first step was to identify the lowest valid sample dilution to use, since using high dilutions can lead to a rise in endotoxin activity in the sample. Reproduction of endotoxin measurements with the LAL test over a period of time revealed a deviation of 15% compared to the first measurement. Nevertheless, endotoxin values of the different matrices showed high variation among farms. Problems concerning the sensitivity of the test system and sample preparation could be overcome. Interferences in samples were inhibited by diluting and heat inactivation before testing. These steps in addition with routine handling led to valid and reproducible results. This study demonstrated the prevalence of endotoxins in pig farms; however, we were unable to draw any conclusions about the correlation between occurrence of endotoxins in the farm environment and impairment of pig health. Therefore, additional resarch is needed.

Key words: endotoxin, swine, environment

656 Effect of day of mixing gestating sows on measures of reproduction and animal well-being. M. Hopgood*[1], L. Greiner[2], J. Connor[2], J. Salak-Johnson[1], and R. Knox[1], *[1]University of Illinois, Urbana, [2]Carthage Veterinary Service, Carthage, IL.*

Available data provides limited evidence that mixing gestating sows during certain periods, including peri-implantation, disrupts pregnancy establishment and reduces litter size. We designed a study to test the effect of day of mixing on reproduction and measures of sow well-being. Mixing was conducted in replicates (n = 5) on a commercial farm in Illinois. Mixed parity (2–6) sows (n = 1,436) were assigned to treatment during June through August. At estrus sows were assigned to one of 4 treatments: 1) housed in crates from weaning until d 110 of gestation (Crate n = 20/replicate); 2) housed in crates after weaning and mixed in a pen at d 3 of gestation (D3 Mix, n = 58/pen/replicate); 3) housed in crates after weaning and mixed in a pen at d 14 of gestation (D14 Mix, n = 58/pen/replicate); and 4) housed in crates after weaning and mixed in a pen after d 35 gestation (D35 Mix, n = 58/pen/replicate). On d 3, 6, 9, 12 and bi-weekly after mixing until d 110, all sows were observed for lesion and body condition score. Sub-sample populations (n = 15/treatment) were identified from d 3 high, moderate, and low lesion score sows to collect serum for cortisol and progesterone. All sows were assessed on d 30 by ultrasound for pregnancy status. Binomial data were analyzed using GENMOD and continuous data by the MIXED procedures of SAS for the main effects of replicate and treatment. Conception rate differed ($P < 0.001$) by treatment with D3 (87%) and D14 (90%) reduced compared with D35 (94%) and Crate (95%). Preliminary data for the first 3 replicates indicates total born (12.2 pigs), born alive (11.6), mummies (0.1) and stillborns (0.6) were not affected by treatment ($P > 0.10$). Future data will include additional measures for reproduction and animal well-being. Our preliminary analyses suggests that mixing sows at d 3 and d 14 is associated with lower conception but not litter size. The effect of treatment on the key reproductive measures of farrowing and litter size in addition to the critical measures of animal well-being will be needed for accurate interpretation of this experiment.

Key words: reproduction, sow, well-being

657 A pig growth model for assessment of environmental footprint from swine operations: Effect of dietary energy and lysine supply. A. B. Strathe*[1], A. Danfaer[2], H. Jorgensen[2], and E. Kebreab[1], *[1]Department of Animal Science, University of California, Davis, [2]Department of Animal Health and Bioscience, Faculty of Agricultural Sciences, Aarhus University, Blichers Allé, Tjele, Denmark.*

In swine operations, greenhouse gas emissions are mostly from stored manure. Accurate prediction of manure composition is required to estimate environmental footprint from swine operations. Pig growth models are often used to optimize profitability of swine production facilities; however, their application may be more valuable through assessment of environmental footprint from swine production. The study aims to describe and evaluate nutrient partitioning and excretion in a pig growth model to be used in predicting manure volume and composition. From a biological perspective, nutrient excretion can be viewed as the "residual" and hence prediction of nutrient partitioning between protein (PD) and lipid deposition (LD) is central. The model represents the partitioning of digestible nutrients from intake through intermediary metabolism to body protein and body fat. The model contained 3 state variables: Amino acids, fatty acids and a central pool of metabolites that supplies substrate for lipid synthesis and oxidation. Body protein and fat represented the body constituent pools. It was assumed that fluxes of metabolites follow saturation kinetics depending on metabolite concentrations. The feed intake can either be defined by the user or ad libitum intake may be simulated by means of an algorithm for metabolic regulation. The model was developed using the open source software R. The data of Bikker et al. (1994, 1995 and 1996) [J. Anim. Sci. 72:1744–1753, 73:2355–2363 and 74:817–826] was used to evaluate model predictions. The data had 48 different feeding regimens with contrasting energy and lysine intakes at 2 different stages of growth. The overall observed and predicted mean were 109, 112, and 132 and 136 g/d for PD and LD, respectively, suggesting minor mean bias. The overall mean square prediction error was 2.2 g/d and 4.1 g/d for PD and LD, respectively.

Key words: simulation modeling, nutrition, sustainability

658 Evaluating the biological and economic differences between light- and heavy-birth weight piglets. D. A. Widmar*, N. J. Olynk, A. P. Schinckel, B. T. Richert, and K. A. Foster, *Purdue University, West Lafayette, IN.*

Not all piglets are created equal. A host of genetic and environmental influences create biological variation in the growth and production of hogs. Variation begins at birth and follows the piglet throughout its life, ultimately creating variation in the economic performance of individual hogs. The objective of this research was to evaluate how light-birth weight (birth weights less than 1.0kg) piglet's biological growth and economic performance differs from heavy-birth weight (birth weights greater than 1.0kg) piglets. A bioeconomic model was constructed to simulate individual piglet growth and performance. Implications resulting from sow parity, litter size, competition while nursing, crowing while in feeding pens, and survivability were included. The stochastic model simulated each piglet's daily bodyweights, daily feed intake, carcasses characteristics, and market value to track its unique revenues and costs. By tracking individual piglet performance, it was possible to analyze the average performance of different groups of piglets, in this analysis piglets sorted into light- or heavy-birth weight groups. Under the assumptions of the model, the initial difference in bodyweights for the average light- and heavy-birth weight piglet, or the difference at birth, between the two groups was relatively small. Over their lifespan however, the differences between the groups becomes increasingly pronounced. Costs, revenues, and returns on an individual piglet basis were calculated. Heavy-birth weight piglets were more profitable, on average, than light-birth weight piglets. Light-birth weight piglets were found to have a greater probability of zero or negative returns. However, it was observed that the relationship between the two groups is not static. The difference between the group's expected profitability, and the probability of achieving an expected level of return, was impacted by the growth curves of the piglets in the two groups and changing values of pigs at time of market. This research provides producers with insight about the biological and economic performance of piglets with varying birth weights.

Key words: farm management, stochastic modeling, piglet birth weight

659 Withdrawn

660 Withdrawn

661 Doe reproductive rates among Boer F_1 and four purebred genotypes including Myotonic in the southeastern United States. A. Nguluma*[1], R. Browning Jr.[1], A. Pellerin[1], J. Groves[1], and M. Leite-Browning[2], *[1]Tennessee State University, Nashville, [2]Alabama A&M University, Huntsville.*

This study evaluated primiparous does produced in a diallel of Boer (B), Kiko (K), and Spanish (S) meat goat breeds. An assessment was also made on Myotonic (M) purebred does. Straightbred and reciprocal BxK and BxS F_1 crossbred (BX) does (n = 192) born across 2 yr were evaluated. All does were exposed to M bucks. Rate of does kidding was higher ($P < 0.01$) for BX does than for B does but not different from S or K does. Kidding rate was affected by maternal grandsire breed ($P < 0.01$) and maternal granddam breed ($P < 0.05$). Kidding rate of daughters of B dams was lower (39.7 ± 21.0%) than for S (59.7 ± 21.3%) and K dams (61.7 ± 21.0%). Kidding rate of B-sired daughters was lower (34.0 ± 21.0%) than from K (63.3 ± 21.2%) or S sires (64.0 ± 21.0%). Rate of does weaning kids did not differ among BX, B, K, and S. Weaning rate was affected by maternal grandsire breed ($P < 0.05$) and maternal granddam breed ($P < 0.001$). More daughter of K (55.0 ± 17.4%) or S dams (50.6 ± 17.4%) weaned a kid than from B dams (29.1 ± 17.3%). Higher proportion of K-sired (55.9 ± 17.6%) and S-sired daughters (52.0 ± 17.4%) weaned a kid than from B sires (26.8 ± 17.3%). Stayability through 1 yr did not differ among BX, B, K, and S genotypes. A higher proportion ($P = 0.06$) of K-sired (78.1 ± 6.7%) and S-sired daughters (85.1 ± 6.2%) stayed in the herd than from B sires (63.7 ± 6.2%). Heterosis level was important ($P < 0.05$) for kidding rate, but not ($P > 0.2$) for weaning or stayability rates. Among purebreds, kidding rate was lower ($P < 0.02$) for B does (1.7 ± 22.0%) than for K (65.0 ± 19.2%), M (45.9 ± 18.8%) and S does (67.7 ± 19.2%); the later 3 did not differ. Weaning rate was lower ($P < 0.01$) for B (2.7 ± 17.7%) than K (62.9 ± 13.6%) and S does (55.3 ± 13.7%); M (30.5 ± 13.1%) only differed from K ($P < 0.05$). Stayability for B, K, M and S does was 54.6 ± 16%, 93.6 ± 6.9%, 82.5 ± 6.0% and 76.7 ± 7.0%, respectively. Only B and K differed ($P < 0.05$). In summary, BX performed better than B but did not differ from S and K. Heterosis was only evident for fertility. Among purebreds, M had relatively better stayability, but lower reproductive rates.

Key words: meat goats, crossbreeding, reproduction

662 Survival rates within a breeding population of Boer, Kiko, and Spanish does managed in the southeastern United States. A. Pellerin*[1], R. Browning Jr.[1], M. Leite-Browning[2], and M. Byars, Jr.[1], *[1]Tennessee State University, Nashville, [2]Alabama A&M University, Huntsville.*

Straightbred Boer (n = 132), Kiko (n = 92) and Spanish (n = 79) does were evaluated to determine if meat goat breed influences doe survival rates. The herd was semi-intensively managed on humid subtropical pasture in central Tennessee. Annual herd records across 6 production years (2003–04 to 2008–09) were used to assess survival rates and determine the reasons for doe exits. Does entered the herd in each year except Year 6. Regardless of entry year, records for all does remaining in the herd at the conclusion of Year 6 were considered censored (n = 106) and all does that exited the herd were considered failures (n = 197). All does that entered the herd had the opportunity to complete at least 2 yr of production. Does were bred to kid once each year. All culling from the breeding herd was involuntary. Does were culled if they failed to wean a kid for any 2 yr on study. Survival analysis to compare breeds within the herd was done by the product-limit method using the LIFETEST procedure of SAS (SAS Inst. Inc., Cary, NC). There were significant differences between the Boer and Kiko ($P < 0.001$) and between the Boer and Spanish ($P < 0.001$) for survival rate. No significant difference ($P = 0.285$) was found between the Kiko and Spanish. Overall survival rates and survival rates up to 2 yr in the herd were lower for Boer does (10.54 ± 0.03%, 58.33 ± 0.04%) than for Kiko (39.08 ± 0.06%, 85.87 ± 0.04%) and Spanish (31.99 ± 0.06%, 83.54 ± 0.04%) does. Individual doe exits were categorized into health, reproductive and accidental causes. Health-related failures constituted the largest proportion of whole-herd exits (78.68%) followed by reproductive failures (14.72%) and accidental losses (6.60%). These proportions were similar within each individual breed population. Breed of doe significantly influenced survival rates. Boer does demonstrated a lower level of fitness than the Kiko and Spanish does as evidenced by relatively higher exit rates under the management conditions of this study.

Key words: meat goats, breed, survival rate

663 The effect of increasing the nutrient and amino acid concentration of whole milk diets on dairy heifer individual feed intake, growth, development and lactation performance. J. K. Margerison*, *IFNHH Massey University, Palmerston North, New Zealand.*

Whole milk is known to less than an ideal feed for growing animals, while increasing the early (<3 mo.) growth rate of calves has been found to increase the milk production potential of dairy heifers. The aim of this research was to compare the effect of offering whole milk with added carbohydrate and amino acids on the growth, development and weaning age of Holstein Friesian dairy heifers. A total of 60 calves were selected at random and allocated (24 h of age) according to; birth date, breed, stature and live weight to one of 3 treatments; 0 to 18 d all were offered milk and probiotics and at 21 d of age calves were offered either; 4 l/h/d of whole milk (M), 4 l/h/d of whole milk, plus 200 g plant extracts (MP) 200 g plant extracts with amino acids (MPA). All calves weaned at set target weight of 90 kg, when calves were limited to 2 kg/h/d and pasture. Total milk used (l) was; M: 333, MP: 315.4, MPA: 302.1 and plant extract used (kgFM) was; M: 0, MP: 11.6, MPA: 10.9. Pelleted feed intake was significantly lower for calves offered MPA during the milk period (kgFM) (M: 68.3 a, MP: 60.9 a, b, MPA: 56.9 b, (sem 2.57) $P = 0.012$) as was total pellet intake (kgFM) (M: 82.3 a, MP: 74.9 a, b, MPA: 70.9 b, (2.57) $P = 0.012$), while straw intake (kgFM) did not differ (26.8, 24.5, 22.5 (1.4) $P = 0.098$). Calves offered MPA had significantly higher mean weight gain (g/d) (M: 765.5 b, MP: 814.9 a, b, MPA: 876.3 a (25.25) $P = 0.008$) and had a lower number of days to weaning from milk (M: 83.26 a, MP: 78.84 a, b, MPA: 75.53 b (1.88) $P = 0.012$)) and a higher mean hip width gain (mm) (M: 6.1 b, MP: 6.6 a, b, MPA: 7.4 a, (0.34), $P = 0.033$), while mean gain in hip height did not differ (M: 14.0, MP: 15.6, MPA: 15.9 (1.16) $P = 0.476$) compared with calves offered milk. Live weight, maturity levels and hip height and width was not significantly different at parturition, but milk yield and milk fat and protein yield were significantly higher in animals offered additional carbohydrates and AA with whole milk.

Key words: lactation, heifer nutrition, milk production

664 Integration of cyclic GMP-dependent protein kinase (PKG) and phosphatidylinositol 3-kinase (PI3K) on rumen protozoal chemotaxis to glucose and soluble peptides. H. L. Diaz* and J. L. Firkins, *The Ohio State University, Department of Animal Science, Columbus.*

Insulin (Ins) was hypothesized to activate PI3K, increase growth rate, deplete substrate, and increase protozoal chemotaxis. Wortmannin (WORT) is a specific inhibitor of PI3K, and sodium nitroprusside (SNP) activates PKG to polarize cells toward a chemoattractant gradient. We expected chemotaxis for both isotrichids (IS) and entodioniomorphids (EN) toward glucose and for peptides only by EN but hypothesized interactions with the following modifiers at higher dosages. Rumen fluid was collected 3 h after feeding and pre-incubated for 0 and 3 h with Control, 2.5 or 25 μM Ins, 50 or 500 μM SNP and 20 or 200 μM WORT. Two capillary tubes (75 mm) were not filled and uncapped (UN) (control for the protozoal count in beakers) or filled with either saline (Sal; control for random swimming), 1 M glucose (Glc), 1 g/L soluble peptides (Pep), or Glc+Pep and capped before insertion in beakers. In a randomized incomplete block design (blocked for 3 replicate runs), data were analyzed by protected LSD. For EN, the log10 counts in capillary tubes (20 minus 0 min) differed ($P < 0.05$) for UN by pre-incubation treatment, so data were covariate-adjusted to the mean UN (3.54 log10 counts). Main effects means were 2.31, 2.91, 2.81, and 3.22 for SAL, Glc, Pep, and Glc+Pep, respectively. Glc+Pep were additive at increasing chemotaxis, regardless of SNP or WORT. The interaction ($P < 0.05$) between pre-incubation beaker treatments and capillary chemoattractant treatments was from log10 counts being 2.41, 2.48, 2.28, 2.37, 2.05, 2.52, and 2.06 for Sal but 2.70, 2.86, 2.70, 2.92, 3.04, 2.92, and 3.22 for Glc for CONTROL, Ins2.5, Ins25, SNP50, SNP500, WORT20, and WORT200, respectively. For Sal, the SNP500 and WORT200 counts were decreased ($P < 0.05$) vs. CONTROL, but Glc increased ($P < 0.05$) chemotaxis for SNP500 and WORT200 vs. CONTROL. For IS, main effects means (log10, no pre-incubation treatment effect) were 1.56, 2.33, 1.11, 1.62, and 1.96 for Sal, Glc, Pep, Glc+Pep, and UN; Pep decreased ($P < 0.05$) chemotaxis. These data justify future experiments to integrate chemotaxis and growth rate.

Key words: rumen protozoa, chemotaxis, glucose

665 Evaluation of specificity of hydrolysis methods for separation of water-soluble carbohydrates. M. B. Hall*, *US Dairy Forage Research Center, USDA-ARS, Madison, WI.*

Various hydrolysis methods have been recommended to convert oligo- or polymeric water soluble carbohydrates to monomers for detection in reducing sugar assays, but responses and specificity for different carbohydrates have not been well characterized. The study objective was to evaluate reducing sugar responses of sucrose (SUC), maltose (MAL), lactose (LAC), raffinose (RAF), and inulin (INU) to hydrolysis (HYD) by invertase, 0.5 M HCl, or 0.037 M H_2SO_4 or a mixture of sucrase/maltase/pullulanase/β-amylase (Sucrase Mix). The p-hydroxybenzoic acid hydrazide reducing sugar method was used for detection. Hydrolyzed and unhydrolyzed samples were analyzed in 2 runs for each method. The statistical model included carbohydrate (WSC), HYD method, and the interaction (INT). Values presented are least squares means for reducing sugars as a percentage of sample DM. Unhydrolyzed carbohydrates differed in reducing sugar values ($P < 0.01$; SUC = 1.1%, MAL = 54%, LAC = 42%, RAF = 2.0%, and INU = 7.4%, SED = 1.5%). LAC and MAL values reflect reactivity of the reducing end hexose in both molecules, whereas RAF and SUC lack reactive reducing end hexoses. The value for INU may reflect presence of a small amount of damaged molecules. Hydrolyzed minus unhydrolyzed values describe the amount of reducing sugar released by hydrolysis. This difference differed by WSC ($P < 0.01$), HYD ($P < 0.01$), and INT ($P < 0.01$) (Table 1; SED = 3.5%). LAC was largely unaffected by HYD. Because of complete or partial hydrolysis of SUC, RAF, and INU by the same treatments, and responses of unhydrolyzed LAC and MAL, it is concluded that these hydrolyses do not allow separation of specific WSC.

Table 1. Hydrolyzed minus unhydrolyzed reducing sugar values by hydrolysis method, % of DM

	Hydrolysis Method			
Carbohydrate	Sucrase Mix	Invertase	HCl	H_2SO_4
Sucrose	84	103	101	102
Maltose	35	2.2	4.6	2.2
Lactose	0.6	3.1	2.8	1.4
Raffinose	0.4	91	89	92
Inulin	4.0	19	97	99

Key words: sugars, method

666 Effect of dietary protein level and rumen-protected amino acid supplementation on dietary amino acid apparent digestibility and recovery in milk in lactating dairy cows. C. Lee*[1], A. N. Hristov[1], T. Cassidy[1], K. Heyler[1], H. Lapierre[2], G. A. Varga[1], and C. Parys[3], *[1]Pennsylvania State University, University Park, [2]Agriculture and Agri–Food Canada, Sherbrooke, QC, Canada, [3]Evonik Degussa GmbH, Hanau, Germany.*

This study investigated the effect of dietary CP level and rumen-protected Lys and Met (RPLys and RPMet) supplementation on apparent total tract digestibility (ATTD) of amino acids (AA) and recovery in milk protein in dairy cows. The experiment was conducted with 8 Holstein cows (102 ± 28 DIM; 26.0 ± 0.79 kg/d DMI; 40.9 ± 1.46 kg/d milk yield) in a replicated 4 × 4 Latin square design trial with 21–d periods. Treatments were: 15.6% CP diet [HighCP; metabolizable protein (MP) balance: –24 g/d], 14.0% CP diet (LowCP, MP balance: –283 g/d), LowCP supplemented with RPLys (AminoShure–L, estimated 24 g/d digestible Lys supply; LowCPLys), and LowCP diet supplemented with RPLys plus RPMet (Mepron®, estimated 15 g/d digestible Met supply; LowCPLysMet). Data were analyzed using the mixed procedure of SAS with diet, square and period in the model and animal within group as a random effect. Plasma Met concentration was increased (30%; $P = 0.02$) by LowCPLysMet compared with LowCP. RPLys supplementation had no effect on plasma Lys. LowCPLys and LowCPLysMet increased ($P < 0.001$) Lys ATTD compared with HighCP and LowCP (51, 47, and 39%, respectively). Met ATTD was higher ($P < 0.001$) for LowCPLysMet compared with the other diets (54 vs. average of 44%). His, essential AA (EAA), and total AA ATTD were higher ($P = 0.001$ to 0.04) for HighCP compared with the LowCP diets. All AA secretion in milk was not affected by diet. RPLys and RPMet supplementation decreased ($P < 0.001$) milk Lys (by 25%) and Met (by 30%, respectively) recoveries (milk ÷ intake) compared with LowCP. Lys, His, EAA and total AA recoveries in milk were greater ($P < 0.001$ to 0.07) for the LowCP diets compared with HighCP. In conclusion, supplementation of LowCP with RPLys and RPMet increased ATTD of total intake Lys and Met, respectively. Supplementation, however, reduced the apparent efficiency of utilization of total intake Lys and Met for milk protein secretion. The apparent efficiency of utilization of all dietary AA for milk protein secretion was increased by decreasing dietary protein intake.

Key words: dietary protein, amino acid utilization, dairy cow

667 Microbiome analysis of the rumen, cecum, and feces of dairy cows with subacute ruminal acidosis. E. Khafipour[1], S. Li*[1], J. C. Plaizier[1], S. E. Dowd[2], and D. O. Krause[1], *[1]University of Manitoba, Winnipeg, MB, Canada, [2]Medical Biofilm Research Institute, Lubbock, TX.*

Subacute ruminal acidosis (SARA) is a metabolic disease common to high producing dairy cattle that is characterized by daily episodes of low rumen pH. It has been assumed that SARA primarily afflicts the rumen, but it may also affect the large intestine. The effects of SARA on the rumen, cecum and fecal microbiome were determined using next-generation sequencing. Six nonlactating Holstein cows with cannula in the rumen and the cecum were used in a replicated 3 × 3 Latin square. During the first 3 wk of each 4 wk experimental period, cows received a control diet containing 70% forage (DM basis). During wk 4 of each period, cows received one of the 3 diets; a control diet, a grain-based SARA challenge (GBSC) diet containing 64% concentrate including 34% wheat-barley pellets, or an alfalfa-pellet SARA challenge (APSC) diet containing 56% forage of which 37% was alfalfa pellets. Rumen, cecum and fecal samples (n = 54) were collected at 6h after feed delivery in wk 4. DNA was extracted from the samples and subjected to pyrosequencing of 16S rRNA. Sequence coverage was assessed with rarefaction and was 74.8%, 81.0%, and 77.7% for the rumen, cecum and fecal samples, respectively. In all compartments, the number of operational taxonomic units was highest in controls followed by APSC and GBSC ($P < 0.05$). Species richness and diversity was lowest in GBSC ($P < 0.05$). A total of 10 phyla were represented in all data sets. If a phylum was present in all animals at 1% or higher, it was considered a core-phylum. Bacteroidetes and Firmicutes were core phyla in all compartments. Proteobacteria and Spirochaetes only core to the rumen, and Fusobacteria only core in the cecum. The Bacteroidetes population was most abundant in the rumen (40% compared with 25% in the cecum and 17% in the feces) while Firmicutes were lowest (53% compare with 65% in the cecum and 80% in the feces). The increases in Rikenella, Butyrivibrio, and Treponema in the rumen were associated with APSC. The loss of Fusobacteria in the cecum and Lentisphaerae in the feces was associated with GPSC ($P < 0.05$). The cecum and fecal microbiome of GBSC was clearly distinct from other groups.

Key words: SARA, gastrointestinal tract, microbiome

668 The effect of diet on milk fatty-acid profiles in Holstein dairy cattle on commercial dairy farms. R. W. Swidan*[1], Y. Chouinard[2], R. Lacroix[1,3], D. Lefebvre[3], and K. M. Wade[1], *[1]McGill University, Montreal, QC, Canada, [2]Laval University, Quebec City, QC, Canada, [3]Valacta, Ste. Anne de Bellevue, QC, Canada.*

Milk samples were collected from 14 commercial dairy farms in Québec with a view to investigating the effects of diet on fatty-acid (FA) profiles. Data represented 284 individual cows covering the period 2006 to 2008. Feed information was obtained from the Québec DHIA (Valacta). The objective of the study was to determine the effects of main forage source (corn silage, grass silage, legume silage, and hay), main energy source (corn, barley, both corn and barley, mixed meal and "other concentrates"), and the presence or absence of both corn silage and corn grain, on the FA profile of Holstein milk. More specifically, the 3 groups investigated were omega-3 FA, conjugated linoleic acids (CLA), and trans FA. Samples were analyzed in a repeated-measure model using the PROC MIXED (SAS). Farms feeding grass silage and corn silage as a main source of forage were found to have lower concentrations ($P < 0.001$) of total omega-3 FA (0.59 and 0.63 g/100g FA, respectively) in the milk versus farms feeding legume silage or hay (0.85 and 1.11 g/100g FA, respectively), while farms feeding hay produced milk with more CLA (0.77 g/100 g FA) compared with those fed grass silage (0.44 g/100g FA). The presence of any corn silage in the diet versus no corn silage resulted in a significant decrease ($P < 0.005$) in total omega-3 FA (0.75 vs. 0.91 g/100g FA, respectively).

Corn silage also tended to decrease both CLA and trans FA concentration, but neither was significant ($P > 0.01$). Different sources of energy in the diet had no significant effect on total omega-3 FA in the milk fat. With regard to CLA, mixed-meal based diets led to a significant increase ($P < 0.001$) in the concentration, while the presence of any corn yielded significantly lower concentrations ($P < 0.001$) than all other energy sources. "Other concentrates" were intermediate in their effect on CLA. The results suggest that changing the diet of dairy cows on commercial farms may affect the fatty acid profile of milk fat, which may have an impact on its processing quality or nutritive value.

Key words: concentrates, forages, milk fatty acids

669 Effects of close-up dietary energy strategy and prepartal dietary monensin on production and metabolism in Holstein cows. J. A. Vasquez*[1], K. L. Perfield[2], H. B. Green[2], and J. K. Drackley[1], *[1]University of Illinois, Urbana, [2]Elanco Animal Health, Greenfield, IN.*

Effects of higher-energy close-up (CU) diets compared with single-group controlled energy (CE) diets remain controversial. Benefits of prepartal monensin (M) in each dietary strategy have not been determined. In a randomized design, multiparous (n = 70) and primiparous (n = 32) cows were assigned to 1 of 4 treatments in a 2 (dry period diet) x 2 (monensin supplementation) factorial arrangement. Dry period diets were either a single CE diet (1.30 Mcal NEL/kg DM) or CE in the far-off period followed by 21 d of CU (1.49 Mcal NEL/kg DM). Diets were either unsupplemented or supplemented with M (22 g/T). Cows received diets for a target of 50 d prepartum. After parturition all cows received a common lactation diet (1.70 Mcal NEL/kg DM) that contained M (14 g/T); data were collected for 84 d. Dry period diet did not affect DMI during the far-off period ($P = 0.21$), but DMI was greater ($P < 0.001$) during the close-up period for cows fed CU; DMI was unaffected by M in either period. Neither diet nor M affected DMI, BW, or BCS postpartum. Prepartum diet did not affect milk yield, milk protein percent, yields of milk components, or FCM but milk fat percent was lower ($P = 0.03$) for CE than for CU. Prepartal M tended ($P = 0.06$) to increase milk yield and increased ($P < 0.01$) lactose content in milk. Contents of fat, protein, and total solids were not affected by M, but yields of fat ($P = 0.01$), lactose ($P = 0.03$), and total solids ($P = 0.03$) as well as FCM ($P = 0.01$) were greater for cows fed M prepartum. Prepartal NEFA were greater ($P < 0.01$) but postpartum NEFA were lower ($P = 0.05$) for cows fed CE. Concentrations of NEFA and BHBA were not affected pre- or postpartum by prepartal M. Concentrations of total lipid, triacylglycerol, and glycogen in a subset of mature cows at d −10 and d 7 were unaffected by diet or M. Other than increasing milk fat content, probably due to greater NEFA, feeding a higher-energy CU diet did not benefit production or metabolism. Prepartum supplementation of M increased yields of milk fat, lactose, total solids, and FCM.

Key words: monensin, prepartum dietary energy, metabolism

670 Effects of close-up dietary energy strategy and prepartal dietary monensin on rumen dynamics and fermentation in Holstein cows. B. F. Richards*[1], J. A. Vasquez[1], K. L. Perfield[2], H. B. Green[2], M. R. Murphy[1], and J. K. Drackley[1], *[1]University of Illinois, Urbana, [2]Elanco Animal Health, Greenfield, IN.*

Concern exists about postpartal rumen adaptation in cows fed single-group controlled energy (CE) diets prepartum rather than traditional close-up (CU) diets. Effects of prepartal monensin (M) on rumen adaptation with these diets are unknown. Multiparous cows (n = 16) with ruminal cannulas were assigned to treatments in a 2 (diet) x 2 (M supplementation) factorial arrangement. Prepartum diets fed for 50 d were either a single CE diet (1.30 Mcal NEL/kg DM) or CE in the far-off period followed by 21 d of CU (1.49 Mcal NEL/kg DM). Each diet was fed without and with M (24.2 g/tonne). Postpartum all cows received a common lactation diet (1.70 Mcal NEL/kg DM) containing M (15.4 g/tonne) for 84 d. Rumen measurements were made at d −14, 2, 14, and 28 relative to parturition. Neither diet nor M affected DMI or BW pre- or postpartum. Supplemental M increased ($P < 0.01$) milk yield. Mass of rumen contents decreased ($P < 0.05$) from d −14 (59.4 kg) to d 2 (45.9 kg) but did not differ among treatments. Rumen fluid dilution rate decreased when M was added to CE but increased when M was added to CU (diet x M interaction, $P < 0.01$). Rumen particulate passage rate did not differ among diets or days. Ruminal pH was higher ($P < 0.01$) at d −14 (6.58) than postpartum (6.23, 6.30, 6.23 for d 2, 14, 28) but did not differ by diet or M. Total VFA concentration tended to increase when M was fed with CE but decreased slightly when M was fed with CU (diet x M, $P = 0.09$). Total VFA decreased at d 2 for cows not fed M (96.9 mM) but increased at d 2 (132.1 mM) when M was fed (M x day, $P < 0.01$). Acetate (% of total VFA) tended to decrease when M was fed with CE but increased when M was added to CU (diet x M, $P = 0.10$); propionate followed the opposite trend ($P = 0.10$). Butyrate tended ($P = 0.09$) to be greater for CE. Mean papillae length was decreased by M at d 2 mainly in cows fed CE (diet x M x day, $P = 0.02$). Feeding a CU diet had few effects on rumen characteristics compared with the single CE diet. Supplemental M shifted rumen fermentation differently between diets and modulated changes in rumen environment across the transition.

Key words: monensin, prepartum dietary energy, rumen

Ruminant Nutrition Symposium: Modulation of Metabolism Through Nutrition and Management

671 Optimizing production of the offspring: Nourishing and managing the dam and the calf early in life. A. Bach*[1,2], [1]*Department of Ruminant Production, IRTA, Barcelona, Spain,* [2]*ICREA, Barcelona, Spain.*

On several mammalian species, it has been shown that fetal and early life nutrition has a role in long-term lipid and glucose metabolism of the offspring, and thus it may also have consequences on milk yield in the dairy cow. For instance, high-energy diets during the last weeks of pregnancy may result in elevated glycemia, which in turn, may alter fetal adipose tissue development. However, most research efforts on management and nutrition of dry cows have focused on minimizing metabolic disorders of the postpartum cow without devoting any attention to potential consequences for the offspring. Similarly, nutritional needs for proper placental development and early fetal growth have received little attention, despite the fact that alterations in placental and fetal development may alter expression of genes participating in homeorhesis of the offspring. Similarly, newborn calves and young heifers are fed to ensure a particular growth target without compromising mammary development, however, data linking growth targets with future milk yield are scarce, and the impact of plane of nutrition on mammary development during prepubertal periods has been shown to be less important than initially thought. However, milk yield not only depends on mammary development, but also on nutrient partitioning, which is regulated by the endocrine milieu. There are some periods of time during development where nutrition may have long-lasting effects on milk production. For instance, the first months of life seem to be critical as recent data from both retrospective and controlled studies indicate that elevated growth rate (or plane of nutrition) during this phase is positively associated with future milk production. Growth rate during early life depends on nutrition (a necessary but not sufficient condition) and management (i.e., grouping strategies and housing systems), and thus optimal rearing programs should be designed considering long-term consequences on milk yield. Likewise, nutrition of the pregnant cow, both while lactating and dry, should also consider aspects of placental and fetal development that may affect milk performance of the progeny.

Key words: epigenetics, metabolism, imprinting

672 Optimizing production of the dairy cow: Nutrition and management during late pregnancy. J. K. Drackley*, *University of Illinois, Urbana.*

Nutrition and management during late gestation impact occurrence of peripartal health problems and influence subsequent milk production. Obesity at calving is a serious risk factor for health problems and suboptimal production. Likewise, extreme under-nutrition may adversely affect postpartum outcomes. The accumulated evidence is that higher energy-density close-up diets do not increase subsequent milk production or energy balance. Evidence from our laboratory indicates that even modest overfeeding results in changes analogous to obesity, with elevated insulin and NEFA before calving, poor DMI before calving, substantial body fat mobilization, increased fat deposition in the liver, prolonged increases in ketone bodies in blood after calving, and, if severe, impairment of liver function. The liver of modestly overfed cows displays a greater specific metabolic capacity for NEFA esterification and a decreased capacity to oxidize NEFA during the periparturient period. A modest energy excess during the dry period can lead to substantial internal fat deposition even in the absence of detectable changes in body condition. Adipose tissue of overfed cows undergoes marked changes in expression of enzymes and other gene products, including inflammatory responses. On the basis of available data, we conclude that requirements for energy (and other nutrients) should be met but not greatly exceeded during the dry period. This concept may be applied via several approaches, ranging from limit-feeding of moderate-energy diets to ad libitum feeding of high-roughage low-energy diets. Requirements for energy for dry cows and first-gestation heifers are modest (ca. 100 MJ ME or 14 Mcal NE per cow daily) and can be met with relatively low-energy diets. Conversely, diets high in starch from corn silage or whole-crop cereals and supplemented with additional concentrates result in excess energy intake relative to requirements, as cows do not regulate intake to meet energy needs over the short-term. Careful feeding management is critical to ensure that formulated nutrient intakes are actually achieved in practice.

Key words: periparturient period, transition period, management

673 Optimizing production of the dairy cow: Nutrition and management during early lactation. J. P. McNamara*, *Washington State University, Pullman.*

Optimal production of the dairy cow entails selecting top overall genetic attributes, not only of milk and component production but for fertility and longevity. Management of these animals from birth and through multiple cycles of pregnancy and lactation will help bring genetic efficiency to full fruition. We must take into account not only feed intake and milk production, but also metabolic flux in body tissues, primarily in visceral, muscle, and adipose tissues. Metabolic processes are affected by genotype, phenotype, and intake, processes that are usually under control of hormonal and neural systems. Reproductive processes leading to additional timely pregnancies must also be understood; as well as the interactions of the genome and transcriptome with the environment in terms of immune function and resistance to disease. A systems approach must be taken to lead to better genetic selection and management. We have continued our work with the objective of identifying the patterns of metabolic flux in the most efficient dairy cattle, using an existing mechanistic metabolic model (Molly, UC Davis) and have expanded that to integrate transcriptional control aspects and reproductive functions to identify the patterns of the most efficient animals. The combination of the transcriptomic and modeling analyses identified key differences in control of nutrient metabolism in the most efficient dairy cattle, rates of adipose tissue metabolism were directly related to overall efficiency. Feed intake was a major component of overall feed efficiency, while the ability of body tissue to support milk production and recover after peak production was another major contributor. We have created the first mechanistic model of control of estrogen and progesterone dynamics, early embryonic development and control of these processes by metabolic rate and genetic selection in the dairy cow. This systems approach can focus our research to make faster and large advances in efficiency, and show directly how this can be applied on the farms.

Key words: dairy cattle, systems biology, metabolic control

674 Optimizing production during heat stress: Nutrition and Management. L. H. Baumgard*[1] and R. P. Rhoads[2], [1]*Iowa State University, Ames,* [2]*University of Arizona, Tucson.*

Heat stress (HS) compromises efficient animal production by marginalizing efforts to reduce food production inputs while negating genetic selection for performance endpoints. Modifying farm infrastructure has yielded modest success in mitigating HS-related losses yet HS remains arguably the costliest issue facing livestock producers. Reduced output (milk yield, muscle growth, egg production, etc.) during HS was traditionally thought to result from decreased nutrient intake (a classic biological response shared by all animals during environmental-induced hyperthermia). Our recent observations have begun to challenge this belief and indicate heat-stressed animals employ novel homeorhetic strategies to direct metabolic and fuel selection priorities independently of nutrient intake or energy balance. Alterations in systemic physiology support a shift in carbohydrate metabolism, evident by increased basal and stimulated circulating insulin levels. Cellular metabolism of the hepatocyte and myocyte also show clear differences in glucose production and use, respectively due to HS. The apparent dichotomy in intermediary metabolism between the 2 tissue types may stem from factors such as mitochondrial function and antioxidant capacity. Perhaps most intriguing given the energetic shortfall of the heat-stressed animal is the apparent lack of basal adipose tissue mobilization coupled with a reduced responsiveness to lipolytic stimuli. Thus, the HS response markedly alters post-absorptive carbohydrate, lipid and protein metabolism independently of reduced feed intake through coordinated changes in fuel supply and utilization by multiple tissues. Interestingly, the systemic, cellular and molecular changes appear conserved among different species and physiological states as we have characterized similar events in growing and lactating ruminants, pigs, poultry and adult rodents. Ultimately, these changes result in the reprioritization of fuel selection during HS which appears to be primarily responsible for reduced animal productivity during the warm summer months.

Key words: heat stress, homeorhesis, metabolism

675 Toxicokinetic and carry-over of ochratoxin A in lactating goats. R. Blank*[1], M. Looff[2], M. Mobashar[2], A. Westphal[1], and K.-H. Südekum[2], *[1]University of Kiel, Germany, [2]University of Bonn, Germany.*

The aim of the present study was to investigate the effects of chronic feeding of 2 different doses of ochratoxin A (OTA) on feed intake, milk yield as well as systemic availability, urinary excretion and carry-over of OTA into milk in lactating goats fed high concentrate diets. Additionally, the effect of sodium bicarbonate (NaHCO3) supplementation was evaluated. For the experiment, 10 mid-lactating goats, divided into 2 groups of 5 animals each, received a diet consisting of 70% concentrate (1.5 kg/d) and 30% hay (0.65 kg/d). After feeding the OTA free diet for 2 weeks, the animals received a concentrate containing 1.5 or 2.8 mg/kg of OTA. After 3 weeks of feeding the OTA-concentrate, animals were switched for a period of 2 weeks to the same compound feed, except that it was supplemented with 15 g/kg NaHCO3. During the entire experiment, feed intake, milk yield, and urinary output was measured. Additionally blood samples from the jugular vein were drawn. Blood, urine, milk, and casein samples were analyzed for OTA and ochratoxin α (OTα). No toxic effects due to OTA could be detected. Feed intake of goats fed the high OTA concentrate was marginally lower ($P < 0.05$) compared with the low dosage group. Milk yield decreased slightly ($P < 0.05$) during the entire experiment but was unaffected by OTA feeding. Concentration of OTA in blood was lower ($P < 0.05$) in the low compared with the high dose group. Renal excretion of OTA (1.2–1.6% of OTA intake) was not affected by dose or NaHCO3 supplementation. Carry over of OTA into milk was unaffected by the dose (0.016 and 0.017% of intake) fed, while NaHCO3 supplementation reduced carry over of OTA (0.006 and 0.009% of intake). In the casein fraction, being the most relevant for cheese making, only OTα and no OTA could be detected. In conclusion, daily intake of 2–4 mg OTA in lactating goats fed high concentrate diets has no impact on milk performance, but may lead to marginally carry-over of OTA into milk. Supplementation of NaHCO3 has some potential to reduce carry-over of OTA in ruminants.

Key words: lactating goats, carry over, ochratoxin A

676 Effects of replacing rolled barley grain with wheat dried distillers' grains with solubles in Merino sheep rations. A. S. O'Hara*[1], A. V. Chaves[1], E. Jonas[1], A. Tanner[2], D. Palmer[1], and R. D. Bush[1], *[1]Faculty of Veterinary Science, The University of Sydney, Sydney, NSW, Australia, [2]Faculty of Agriculture, Food and Natural Resources, The University of Sydney, Sydney, NSW, Australia.*

Three experimental trials were conducted to determine the effects of replacing rolled barley grain with either 20% or 40% diet DM of wheat dried distillers' grains with solubles (DDGS) in Merino wether diets. Effect on ruminal fermentation from the experimental diets was measured using by a batch culture in vitro incubation trial. Nutrient degradability of dry matter (DM), neutral and acid detergent fiber (NDF and ADF) and crude protein (CP) in the diets was measured with an in situ study using 2 cannulated Holstein dairy cows. Finally, an in vivo experiment was conducted using 36 Merino wethers in a complete randomized design over a period of 50 d to determine the effect of feeding pelleted diets containing either 0%, 20% or 40% diet DM of wheat DDGS on wool production and growth performance. Diets were provided ab libitum to the Merino wethers by 9 automatic feeders. The data were analyzed using the mixed model procedure of SAS. In the in vitro study, gas and ammonia production were not affected by dietary treatment ($P = 0.34$). The addition of wheat DDGS in the diet increased total volatile fatty acids (VFA), in vitro dry matter digestibility, propionate production and slightly lowered culture pH ($P < 0.01$). In the in situ study, the wheat DDGS diets demonstrated faster ($P = 0.04$) rate of NDF degradation (k, h^{-1}) compared with control diet. All diets had high proportions of soluble CP (above 90% of total CP). In addition, replacing rolled barley grain with wheat DDGS increased ($P < 0.01$) the ruminal degradability of crude protein. The inclusion of wheat DDGS in the diets did not effect wool yield, fiber diameter or wool softness traits, however wool growth, staple length and the coefficient of variation were improved by feeding wheat DDGS to the Merino wethers ($P \leq 0.03$). This study showed up to 40% dietary DM of wheat DDGS can be used to replace rolled barley grain in Merino sheep rations to improve wool production, maintain growth performance and promote efficient rumen fermentation.

Key words: by-products, ruminal fermentation, wool

677 Effects of dried distillers grains with solubles on feedlot lamb performance and carcass characteristics. T. L. Felix*, H. N. Zerby, S. J. Moeller, and S. C. Loerch, *The Ohio State University, Wooster.*

Dried distillers grains with solubles (DDGS) may be a cost effective source of energy and protein for feedlot lambs. However, the S content of DDGS may affect animal health, performance, and mineral metabolism. Information is lacking on the negative effects of elevated DDGS inclusion in lamb diets. The objectives of this study were to determine the effects 0, 20, 40 or 60% dietary DDGS on growing lamb performance, carcass characteristics, and tissue minerals. Ninety-six lambs were blocked by gender (ewes, n = 48; wethers, n = 48) and weight, housed in 24 pens (4 lambs per pen), and used in a 92 d feedlot trial (initial BW = 26.4 ± 16.7 kg). Lambs were fed 1 of 4 dietary treatments: 1) 0% DDGS, 2) 20% DDGS, 3) 40% DDGS, and 4) 60% DDGS. Dietary S was 0.12, 0.22, 0.36, and 0.47%, respectively. The DDGS replaced primarily corn and diets were fed as a complete pellet. There was a quadratic effect of DDGS inclusion on ADG; lambs fed the 20% DDGS diet had the greatest ($P = 0.04$) gains at 0.358 kg/d. This effect on ADG led to a quadratic ($P = 0.03$) effect of DDGS on final BW. There was no effect ($P > 0.05$) of treatment on DM intake. There was a linear ($P = 0.02$) effect of treatment on G:F (means: 0.216, 0.232, 0.206, and 0.209 for 0, 20, 40, and 60% DDGS, respectively). In the liver, S increased linearly ($P = 0.05$) while Cu decreased linearly ($P < 0.01$) with increasing dietary DDGS. No other liver minerals were affected ($P > 0.05$). In the kidney, increasing dietary DDGS increased ($P < 0.04$) P, Mg, and S concentrations linearly but did not affect ($P > 0.05$) other minerals. There was no effect ($P > 0.05$) of dietary DDGS on muscle mineral concentrations. Lamb HCW were 65.9, 71.6, 64.1 and 63.3 kg for 0, 20, 40, and 60% DDGS, respectively (quadratic; $P = 0.03$). Yield grade was not affected ($P > 0.05$) by dietary DDGS. Yield grade means were 3.10, 3.58, 2.97, and 2.86 for 0, 20, 40, and 60% DDGS, respectively. Lambs fed 20% DDGS had optimum performance in this study. Lambs fed 40 or 60% DDGS had similar performance as those fed 0% DDGS. Sulfur increased in the liver and kidneys of lambs fed DDGS reflecting the increase in S intake.

Key words: dried distillers grains, lambs, sulfur

678 Estimation of milk yield of West African Dwarf (WAD) ewe fed Mexican sunflower leaf meal (MSLM) based diets. A. H. Ekeocha*, K. D. Afolabi, and A. O. Akinsoyinu, *University of Ibadan.*

A study was carried out to estimate the milk yield of West African Dwarf (WAD) ewe fed Mexican Sunflower Leaf Meal (MSLM) on a basal diet of Panicum maximum(Pm). Sixteen WAD ewe weighing 19.50 to 22.46kg on a basal diet of Pm were allotted into four treatment groups such that each treatment had four replicates of four ewes. The MSL replaced wheat bran (WB) gravimetrically at 0, 15, 30 and 45%. Diets were formulated on a DM basis. Animals on treatment A served as control while animals in treatments B, C and D received Mexican Sunflower Leaf Meal (MSLM) at 15, 30 and 45% respectively. The experiment lasted for thirteen weeks (91 days). Assessment of milk yield started in day 2 after lambing to enable lambs suckle colostrum. Lambs were kept separately from ewes and were only allowed together at periods of suckling. Milk production of the ewes were estimated by the indirect method of weighing lambs before and after suckling using a sensitive weighing balance thrice daily. Animals were weighed from day 2 to day 91 of lactation. Data were analyzed using descriptive statistics and ANOVA. From parturition there was an increase in milk production from 422.75g/day at first week to a peak of 570 g/day at third week and thereafter a gradual decline to 281.25 g/day at 13th week of lactation. Treatment effects on the variations in obtained yield (g/day) at week 2 and then from 6th week to 13th week of lactation were not significantly ($P > 0.05$) different. Overall total milk yield (kg) for the entire lactation period of 13 weeks were 36.7, 37.9, 37.3 and 35.6 kg for treatments A, B, C and D respectively. Variations observed were not significant ($P > 0.05$). Maximum daily milk production of 0.57 to 0.50 kg was obtained for WAD ewe. The total milk yield of 35.6 to 37.9 kg/ewe was obtained during the entire lactation period of 91 days. Feeding up to 30% Mexican sunflower leaf meal to West African dwarf ewe enhanced milk yield without deleterious effect.

Key words: milk yield, West African dwarf ewe, Mexican sunflower leaf meal

679 Iron carbonate supplementation of lambs administered high-sulfur water. A. M. Jons*[1], K. L. Kessler[1], K. J. Austin[1], C. Wright[2], and K. M. Cammack[1], *[1]University of Wyoming, Laramie, [2]South Dakota State University, Brookings.*

Drinking water with high sulfur (S) concentrations can reduce the performance and cause health problems such as polioencephalomalacia in livestock raised in the western US Monitoring and treating water for high levels of S are both expensive and often impractical; therefore, an alternative method of controlling this problem is needed. Our objective was to determine if supplemental Fe, commonly used in water treatment plants to bind S, prevents reduced performance and poor health caused by administration of high-S water. We hypothesized that dietary supplementation with an Fe compound would bind excess S in ruminant animals, preventing the negative effects associated with high-S drinking water. Wether lambs (n = 80) were assigned to one of 4 treatments in a randomized complete block design with 20 lambs per treatment replicated over 2 pens per treatment. Treatments included: 1) control feed and low-S well water; 2) control feed and high-S water (2,500 mg SO_4^{2-}/L); 3) low-Fe (250 ppm Fe as $FeCO_3$) feed and high-S water (2,500 mg SO_4^{2-}/L); and 4) high-Fe (500 ppm Fe as $FeCO_3$) feed and high-S water (2,500 mg SO_4^{2-}/L). All lambs received ad libitum access to feed and water. Body weights and blood samples were taken on d −1, 25, and 50, and H_2S gas in the rumen was measured on d −1 and 50. Effects of dietary treatment were estimated using the MIXED procedure of SAS. There were no differences in ADG ($P = 0.668$), daily water intake ($P = 0.795$), or daily feed intake ($P = 0.659$) between treatments. Trace mineral analysis showed no treatment differences in serum concentrations of Cu ($P = 0.199$), Fe ($P = 0.590$), Mo ($P = 0.119$), Mn ($P = 0.549$), or Zn ($P = 0.422$). Production of H_2S gas was less ($P \leq 0.001$) in low-S control lambs compared with lambs in the high-S treatment groups; no differences in H_2S gas production were detected between high-S treatment groups. These results indicate that supplementation of an Fe compound to lambs exposed to high-S water was not effective at preventing the reduced performance associated with elevated dietary S.

Key words: lambs, sulfur, water

680 Effect of supplementing ewes during late gestation with metabolizable protein on wether lamb feedlot performance, carcass characteristics, and nitrogen balance. M. L. Van Emon*[1,2], K. A. Vonnahme[1], S. E. Eckerman[1], L. A. Lekatz[1], K. R. Maddock Carlin[1], M. M. Thompson[2], 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.*

The objective was to determine the effect of metabolizable protein (MP) supplementation to ewes during the last 50 d of gestation on wether offspring nitrogen (N) balance, feedlot performance, and carcass characteristics. Maternal dietary treatments were isocaloric and contained 100% (CON), 80% (MED), and 60% (LOW) of MP requirements for ewes bearing twins during the last 50 d of gestation. Feedlot (29 ± 2 kg) and N balance wethers (32 ± 0.4 kg) were fed a common feedlot ration (84.4% whole corn, 15.6% commercial market lamb pellet). Initial and final feedlot BW, ADG, and G:F were not affected ($P \geq 0.17$) by maternal dietary treatment. Wethers born to ewes fed the LOW diet had increased ($P = 0.01$) DMI compared with the wethers born to ewes fed the MED diet during the feedlot phase. Wethers born to CON had reduced ($P = 0.10$) days on feed compared with wethers born to MED ewes. Wethers born to CON ewes had increased ($P = 0.04$) percent boneless, closely trimmed, retail cuts compared with wethers born to the LOW and MED ewes, with all other carcass characteristics not affected ($P \geq 0.13$). Nitrogen balance trial DMI, NDF intake, total tract digestibility of DM, NDF, and N, fecal N excretion, and N balance were not affected ($P \geq 0.12$) by maternal dietary treatment. Wethers born to LOW ewes had increased ($P = 0.08$) daily N intake and reduced ($P = 0.08$) daily digested N retained compared with wethers born to CON and MED ewes. Wethers born to LOW ewes had increased ($P = 0.03$) daily urinary N excretion compared with wethers born to the MED and CON ewes. A treatment × day interaction was observed ($P = 0.004$) for serum urea N concentrations. On collection d 2, 4, 5, and 6 of a 7 d collection period, the wethers born to LOW ewes had increased ($P \leq 0.001$) serum urea N concentrations compared with the wethers born to MED and CON ewes. These results suggest that wethers born to ewes fed below MP requirements are less efficient in N retention, require more feed to finish in the feedlot, and have decreased retail product.

Key words: feedlot, metabolizable protein, nitrogen balance

681 Effect of increasing dietary inclusion of dried distillers grains with solubles on nutrient digestion and retention in growing lambs. T. L. Felix* and S. C. Loerch, *The Ohio State University, Wooster.*

Dietary inclusions of dried distillers grains with solubles (DDGS) greater than 40% have been shown to decrease lamb performance. This may be due in part to dietary S in excess of the maximum tolerable limit. Recent data suggest that feeding 60% DDGS to growing cattle decreases digestibility of DM, NDF, and fat. The effects of DDGS on nutrient digestibility and retention in lambs are not known. Therefore, the objectives of this study were to determine the effects of increasing dietary inclusion of DDGS on nutrient and mineral digestibility and retention in growing lambs. Twenty-four Dorset × Suffolk lambs (initial BW = 43.0 ± 4.4 kg) were used in a metabolism study. Lambs were adapted to experimental diets for 17 d before a 5 d sampling period during which total feces and urine were collected. The treatment diets were fed for ad libitum intake and were: 1) 0% DDGS, 2) 20% DDGS, 3) 40% DDGS, and 4) 60% DDGS. The DDGS replaced primarily corn and diets were fed as a complete pellet. Dietary S concentrations were 0.12, 0.21, 0.35, and 0.45%, respectively. The apparent digestibility of dietary DM decreased linearly ($P < 0.01$) with increasing dietary inclusion of DDGS (79.6, 78.4, 75.2, and 72.7% for treatments 1 through 4, respectively). Digestibility of fat, followed a similar pattern, whereas, N, S, and P digestibility increased linearly ($P < 0.03$) with increasing dietary DDGS. The digestibility of NDF was not affected ($P > 0.05$) by dietary treatment. Apparent retentions (as a percentage of intake) of N, K, Mg, Cu, Fe, and Zn, were not affected ($P > 0.05$) by dietary DDGS inclusion. The retention of S and P was decreased ($P < 0.04$) with increasing dietary DDGS. Daily urine output increased linearly ($P < 0.01$) with increasing dietary inclusion of DDGS. Urine pH decreased linearly ($P < 0.01$) with increasing DDGS (7.46, 5.86, 5.52 and 5.32 for treatments 1 to 4, respectively). These data suggest urine is a major route for excretion of acid when high S diets containing DDGS are fed. Increases in dietary DDGS resulted in decreased digestion of DM and fat which may affect lamb feedlot performance.

Key words: dried distillers grains, lambs, metabolism

682 Performance of growing West African Dwarf ewe fed Mexican sunflower leaf meal based diets. A. H. Ekeocha*, *University of Ibadan, Ibadan, Oyo, Nigeria.*

Studies were conducted using 16 lambs weighing 13–15kg on based diet of *Panicum maximum* were allotted into 4 treatments. The experiment was conducted using completely randomized design with 4 replicates. The Mexican sunflower leaf meal (MSLM) replaced wheat Bran (WB) gravimetrically at 0, 15, 30, 45%. Animals on diet A served as control while animals in diets B, C and D received Mexican sunflower leaf meal (MSLM) at 15, 30 and 45% respectively. The experiment lasted 84 d. Parameters measured included voluntary dry matter intake (VDMI) which comprised concentrate DMI (CDMI) and grass DMI (CDMI), changes in body weight (BW) and feed conversion ratio (FCR). Data were analyzed using descriptive statistics and ANOVA. The VDMI (g/d) varied from 351.0 to 621.9 for ewe-lambs. CDMI (g/d) varied from 162.70 to 480.30 and GDMI (g/d) varied from 116.90 to 193.22 for ewe-lambs. Approximately 75.5 ± 1.1 of the VDMI came from the supplement. Diets containing 30% MSLM was superior to others for GDMI (116.9–193.2 g/day) and CDMI (162.7- 480.3g/day) during the growth phase ($P < 0.05$). BW gain (Kg) varied from 3.50 to 3.58 and FCR varied from 8.42 to 14.92 and these were similar. Inclusion of up to 45% MSLM based-diets enhanced the performance of ewe-lambs in terms of BW gain, growth and feed conversion ratio.

Key words: Mexican sunflower leaf, West African Dwarf ewe

683 Use of *Megasphaera elsdenii* NCIMB 41125 during introduction of sheep on corn crop residues and un-harvested corn lands. P. H. Henning* and F. M. Hagg, *MS Biotech, Centurion, South Africa.*

Ruminants are often grazed on corn crop residues to utilize grain wasted during harvesting. They may also be grazed on un-harvested corn lands. In both cases rumen acidosis is a problem due to the sudden high intake of starch-rich grain. *Megasphaera elsdenii* is a rumen bacteria which utilizes lactic acid, thus preventing rumen acidosis. Its numbers are low on grass diets and only increase slowly when animals change to high starch diets. It is hypothesized that supplying *Megasphaera elsdenii* as a DFM when placing animals thus may benefit adaptation and production. The objective of this study was to determine the benefit of drenching sheep with *Megasphaera elsdenii* NCIMB 41125 (Me) just before introduction onto intact or harvested corn lands. In Trial 1 300 recently weaned male and female lambs (average live-weight 25 kg), on grass pasture, were randomly divided into 2 equal groups. Both groups were subsequently placed on the same newly harvested corn land for 50 d. One group (Me-treated) received a single 70 mL oral dose of Me (10^8 cfu ml^{-1}) 60 min before this placing, while the other group (control) received none. In Trial 2 184 castrated male lambs (average live-weight 47 kg), on grass pasture, were randomly divided into 2 equal groups. Both groups were subsequently placed on the same un-harvested corn land for 50 d. One group (Me-treated) received a single 70 mL oral dose of Me (10^8 cfu ml^{-1}) 60 min before this placing, while the other group (control) received none. In Trial 1 Me-treated male and female sheep gained 16.2 and 9.3 kg live-weight, respectively, which was significantly ($P < 0.01$) more than the corresponding 15.9 and 8.3 kg for the control group. In Trial 2 Me-treated lambs gained 6.64 kg, which was significantly ($P < 0.05$) greater than the 5.92 kg gain for the control group. It is concluded that a single oral dose of *Megasphaera elsdenii* NCIMB 41125 given to sheep just before placing them on harvested or un-harvested corn land can benefit production, probably by controlling rumen acidosis.

Key words: corn crop residues, *Megasphaera elsdenii*, rumen acidosis

684 White blood cell populations in goat kids and lambs during the first four days of life, with special reference to CD4 and CD8. A. Arguello*[1], L. E. Hernandez-Castellano[1], A. Morales-delaNuez[1], I. Moreno-Indias[1], J. Capote[2], and N. Castro[1], *[1]Universidad de Las Palmas de Gran Canaria, Arucas, Las Palmas, Spain, [2]Instituto Canario de Investigaciones Agrarias, La Laguna, Tenerife, Spain.*

To investigate the white blood cell populations (including CD4 and CD8) in goat kids and lambs, 10 goat kids (Majorera dairy breed) and 10 lambs (Canaria dairy breed) were used. Blood samples were obtained at birth, and at 2 and 4 d of life in Lithium heparin containers. Immediately after collection, 50 μL of unclothed blood were added with 5 μL of CD4 (FITC) and 5 μL of CD8 (RPE) monoclonal antibodies (Serotec, Dusseldorf, Germany) and the reaction ran for 15 min at room temperature. After that, 50 μL of Optilyse (Beckman Coulter, Brea, CA) were added and the reaction ran for 15 min at room temperature to lyses red blood cells. Subsequently, 150 μL of saline serum were added to clarify the solution. Fifteen minutes later, the samples were redden using an FC500 flow cytometry device (Beckman Coulter, Brea, CA). An ANOVA (with repeated measures) procedure from SAS was used. Two white blood cell populations were observed clearly, lymphocytes plus macrophages (L+M) and polymorphonuclear (PMN), in both species at all tested times. L+M population was higher ($P \leq 0.05$) in goat kids than in lambs at all tested times (75.5, 63.5 and 74.0% in goat kids and 53.2, 45.7 and 59.5%, at birth, 2 and 4 d of life respectively). Concomitantly, the PMN population was greater ($P \leq 0.05$) in lambs than in goat kids. Goat kids CD4 population (expressed as a L+M percentage) was lower ($P \leq 0.05$) than in lambs at all tested times (29.3, 30.4 and 22.6 for goat kids and 53.7, 41.4 and 40.2 for lambs at birth, 2 and 4 d of life, respectively). No significant differences were observed for CD8 between species (ranged from 9.8 to 18.1% of L+M). There was no breed effect on CD4/CD8 ratio but a trend was observed, being goat kid CD4/CD8 ratio lower than lamb ratio (2.7, 2.1 and 2.4 for goat kids and 3.7, 3.0 and 2.8 for lambs at birth, 2 and 4 d of life, respectively). In conclusion, goat kids and lambs are different in the innate immune system during the first days of life.

Key words: goat kid, lamb, CD4 CD8

685 Immune status of goat kids fed cow′s milk with an exogenous source of DHA. I. Moreno-Indias*[1], L. E. Hernández-Castellano[1], A. Morales-delaNuez[1], A. Torres[2], D. Sánchez-Macías[1], N. Castro[1], and A. Argüello[1], *[1]Universidad de las Palmas de Gran Canaria, Arucas, Las Palmas, Spain, [2]Instituto Canario de Ciencias Agrarias, La Laguna, Santa Cruz de Tenerife, Spain.*

As the main role of dairy goat farming is to yield marketable milk, artificial rearing is closely linked to the intensification of these farms. Therefore, the use of milk replacers has been suggested. Classic works did not recommend the use of cow′s milk to feed goat kids, due mainly to problems with diarrhea. Recently, the benefits of the use of omega-3 fatty acids in nutrition such as the docosahexaenoic acid (DHA) have been presented. In this study different diets were supplied to 3 groups of goat kids: goat milk (GM), cow milk (CM) and cow milk with a supplemented source of DHA (DHA-gold) (CM-DHA). Animals were fed ad libitum twice a day. Blood samples were collected from the jugular vein until d 10 of life, and after that, each 5 d until animals weighed 8 kg (animals were weighed twice a week). IgG, IgM, total and alternative pathway complement system activity and chitotriosidase activity were measured to establish the immune status of goat kids. The MIXED procedure of SAS (version 9, SAS Institute Inc., Cary, NC) was used to evaluate the effects of the treatments on immune status of goat kids. When goat kids reached 8 kg, concentrations of IgG were 3.855, 4.002 and 3.662 mg/mL and concentrations of IgM were 0.802, 0.736 and 0.730 mg/mL for GM, CM and CM-DHA, respectively. Differences did not reach significance among treatments. When dairy kids weighed 8 kg, complement system activity did not show significant differences among treatments neither in total (GM: 58.54%, CM: 56.69% and CM-DHA: 55.09%) nor in the alternative pathway (GM: 37.94%, CM: 37.47% and CM-DHA: 34.91%). However, significant differences were found ($P = 0.03$) in the alternative pathway between GM (39.76%) and CM-DHA (23.30%) treatments when goat kids weighed 7 kg, although without continuity in the time. Finally, the chitotriosidase activity in goat kids at 8 kg did not differ significantly among treatments (GM: 1867.67 nmol/mL/h, CM: 1895.83 nmol/mL/h and CM-DHA: 1893.10 nmol/mL/h). In conclusion, CM is a good option to feed goat kids instead GM. However, DHA at this concentration did not show any effect on goat kid immune status.

Key words: DHA, milk replacer, cow milk

686 Effects of feeding sericea lespedeza as a natural anthelmintic for *Haemonchus contortus* in lactating does. J. L. Vest*[1], M. A. Brown[4], J. D. Kohler[1], M. D. Hudson[1], S. R. Nusz[5], J. M. Burke[3], J. E. Miller[2], C. T. Mackown[4], and E. L. Walker[1], *[1]Missouri State University, Springfield, [2]Louisiana State University, Baton Rouge, [3]Dale Bumpers Small Farms Research Center, USDA-ARS, Booneville, AR, [4]Grazinglands Research Laboratory, USDA-ARS, El Reno, OK, [5]Redlands Community College, El Reno, OK.*

In the United States, infection with the gastrointestinal nematode *Haemonchus contortus* is the leading cause of goat mortality. Use of alternative parasite control methods, including forages containing condensed tannins (CT), has been found to reduce the effect of gastrointestinal nematode parasites. During the last 30 d of gestation, 37 Boer-cross does kidding from April to June were randomly assigned to diets of alfalfa (*Medicago sativa*; 21% CP; n = 16) pellets (Alf) or sericea lespedeza (*Lespedeza cuneata*; 16% CP; n = 21) pellets (SL) and allowed to graze on 0.61 ha bermudagrass pasture. Does were fed pellets at a maximum of 3% of BW throughout the study. At parturition, BW and gender of kids was recorded. On d 7, 21, 35, 49, and 63 postkidding, doe fecal samples, BCS, blood samples, and measurements of milk yield and composition were obtained. To account for environmental changes during the 62 d kidding period, does were grouped in 2 kidding periods, early (those kidding from d 1 to d 31) and late (d 32 to d 62 of the trial). The climate during the later kidding period included increased rainfall and high humidity compared with the early period. The later kidding does had greater fecal egg counts (FEC) on d 7, 21, 35 and 49 ($P < 0.003$) and greater packed cell volume (PCV) on d 21, 49, and 63 ($P < 0.05$) compared with early kidding does. SL-fed does had lower FEC ($P < 0.05$) than the Alf does on d 35. On d 63, does with singles had lower FEC ($P \geq 0.03$) and greater PCV levels ($P \geq 0.006$) than does with twins. Doe FAMACHA scores gradually increased from d 7 to d 49 with an improvement by d 63 ($P < 0.0001$). Does with singles tended to have lower FAMACHA scores ($P = 0.08$) and greater BCS ($P = 0.0002$) than does with twins. Does raising twins produced more milk on d 7 and 21 becoming similar to single parity does by d 35 ($P = 0.0001$). Alf-fed, later kidding does had the lowest milk production ($P = 0.0089$). In conclusion, SL decreased FEC at d 35

but not at other times. It is possible the minimal differences in FEC and PCV between alfalfa and SL may have been influenced by treatment differences in crude protein.

Key words: goats, sericea lespedeza, parasite

687 Polymorphisms in the melanocortin-1 receptor (MC1R) gene in Nigerian indigenous goats. M. A. Adefenwa[1], B. Oboh[1], G. O. Williams[1], M. Wheto[2], C. O. N. Ikeobi[2], K. Adekoya[1], M. Okpeku[3], M. De Donato*[4], and I. G. Imumorin[4], *[1]Dept of Cell Biology and Genetics, University of Lagos, Lagos, Nigeria, [2]Dept of Animal Breeding and Genetics, University of Agriculture, Abeokuta, Nigeria, [3]Dept of Livestock Production, Niger Delta University, Amassoma, Nigeria, [4]Dept of Animal Science, Cornell University, Ithaca, NY.*

Coat color is an adaptive trait in mammals with implications for physiological efficiency. The extension locus, which encodes the melanocortin-1 receptor (MC1R), is known to control the synthesis of the pigment granules, eumelanin and pheomelanin, which in turn affects coat color. Functional mutations is said to cause black coat color while inactivating mutations is said to cause red coat color. There is paucity of information regarding the genetics of coat color in indigenous livestock species in Nigeria and Sub-Saharan Africa. In this study, we examined polymorphisms in the caprine MC1R gene in the 3 major Nigerian goat breeds which exhibit different coat colors: (West African Dwarf, black; Red Sokoto, brown/red; and Sahel, white). We amplified and sequenced a 716 bp fragment spanning part of the coding region of the MC1R gene (716 bp) in 69 Nigerian goats (17 West African Dwarf, 23 Red Sokoto, and 29 Sahel), sampled from across the country, using genomic DNA obtained from whole blood samples. Sequences were aligned using CLUSTALX and DnaSP version 5.10.01 was used for identifying single nucleotide polymorphisms (SNPs). Four single nucleotide polymorphisms were identified: 2 silent mutations (g.T125C and g.G128A) and 2 missense mutations (g.C126G, p.R30G and g.A729C, p.I231L). Our results in this pilot experiment showed no association between coat color and the identified SNPs as none of the variants seem to be fixed in any of the breeds. The SNPs g.T125C, g.G128A and g.C126G were identified in the same set of animals, 7 out of 69, which were cut across the 3 breeds (3 West African Dwarf, 3 Red Sokoto and 1 Sahel). The allele C for the g.A729C polymorphism occurred with a frequency of 0.029. Additional work to genotype these polymorphisms in a larger number of animals for population genetic analysis are in progress.

Key words: MC1R gene, goat, coat color

688 Molecular identification of *Trypanosoma vivax* Infection and physiological indices in Nigerian sheep. G. O. Onasanya[1], M. A. Adefenwa[2], B. O. Agaviezor[3], C. O. N. Ikeobi[1], M. Wheto[1], M. Okpeku[4], A. Yakubu*[5], M. I. Takeet[6], M. De Donato[7], and I. G. Imumorin[7], *[1]Dept of Animal Breeding and Genetics, University of Agriculture, Abeokuta, Nigeria, [2]Dept of Cell Biology and Genetics, University of Lagos, Lagos, Nigeria, [3]Dept of Animal Science and Fisheries, University of Port Harcourt, Port Harcourt, Nigeria, [4]Dept of Livestock Production, Niger Delta University, Amassoma, Nigeria, [5]Department of Animal Science, Nasarawa State University, Lafia, Nigeria, [6]Dept of Veterinary Microbiology and Parasitology, University of Agriculture, Abeokuta, Nigeria, [7]Dept of Animal Science, Cornell University, Ithaca, NY.*

Trypanosomiasis remains a major challenge to livestock production in endemic areas of Sub-Saharan Africa. Nationwide prevalence of *Trypanosoma vivax* (*T. vivax*) infection was estimated in 4 extant sheep breeds using 161 samples collected from across Nigeria and to ascertain associations of parasite presence with physiological indices. The presence of *T. vivax* was determined by polymerase chain reaction to amplify a 400 bp DNA fragment of the parasite genome. Results showed that 73.9% of sheep sampled were infected with *T. vivax* with geographical locations showing prevalence rates of 73.5% (Southwest), 71.7% (Northwest) 73.5% (Northeast) and 88.0% (Northcentral). Breed prevalence were Balami (85.4%), West African Dwarf (75%), Uda (62.5%) and Yankasa (72.5%). There was a significant ($P < 0.05$) interaction of *T. vivax* and sex status on pulse rate with non-infected females showing higher pulse rates of 129.138 ± 5.57 beats per minute (bpm) compared with infected rams (111.8 ± 5.96 bpm) and infected females (122.6 ± 3.00). Also, non-infected females had higher respiratory rate with 64.4 ± 4.04 bpm compared with infected rams with respiratory rate of 51.217 ± 3.25 bpm. The interaction of *T. vivax* infection and breed on pulse rate was significantly different ($P < 0.5$) between non-infected Balami (159.3 ± 9.98 bpm) compared with infected West African Dwarf (106.7 ± 6.18 bpm) goats. Similarly, respiratory rates differed significantly ($P < 0.05$) between non-infected West African Dwarf (71.6 ± 11.31 bpm), while infected Uda had the lowest respiratory rate (53.560 ± 3.33 bpm). The interaction effect of *T. vivax* infection and sex was also significant on body weight with non-infected males weighing more (39.962 ± 4.43 kg) than infected females. Molecular diagnosis using PCR seem effective and the presence of trypanosome appears to have important implications for physiological efficiency of sheep in Nigeria.

Key words: *Trypanosoma vivax*, Nigeria, sheep

689 Polymorphism in the ovine TNXB gene and association with morphological traits and physiological status in Nigerian indigenous sheep. O. Ajayi[1], M. A. Adefenwa[2,6], B. O. Agaviezor[3,6], C. O. N. Ikeobi[1], M. Wheto[1], M. Okpeku[4], A. Yakubu[5,6], M. De Donato[6], and I. G. Imumorin*[6], *[1]Dept of Animal Breeding and Genetics, University of Agriculture, Abeokuta, Nigeria, [2]Dept of Cell Biology and Genetics, University of Lagos, Lagos, Nigeria, [3]Dept of Animal Science and Fisheries, University of Port Harcourt, Port Harcourt, Nigeria, [4]Dept of Livestock Production, Niger Delta University, Amassoma, Nigeria, [5]Dept of Animal Science, Nasarawa State University, Lafia, Nigeria, [6]Dept of Animal Science, Cornell University, Ithaca, NY.*

The major histocompatibility complex (MHC) plays an important role in the adaptive immune response of vertebrates and tenascin XB (TNXB) localizes to the MHC class III region and encodes a member of the tenascin family of extracellular matrix glycoproteins. The tenascins have anti-adhesive effects and are thought to function in matrix maturation in connective tissues such as blood vessels. Given the role of blood vessel function in adaptive physiological response, we aimed to determine the influence of variation in the ovine TNXB gene on physiological variables in Nigerian indigenous sheep in the hot humid tropics. We sequenced a 450 bp fragment of the ovine TNXB gene in 150 randomly sampled indigenous sheep, comprising 30 West African Dwarf and 40 each of Yankasa, Uda and Balami from 4 geographical zones of Nigeria, and genotyped the identified SNP using PCR-RFLP. The frequencies of genotypes TT, Tt and tt were 40.0%, 48.0% and 12.0%, respectively. While morphological traits did not significantly differ among TNXB genotypes, there were significant ($P < 0.05$) differences for pulse rates in beat per minute (bpm) [129.28 ± 6.64 (tt) versus 111.93 ± 4.05 (TT) versus 110.38 ± 3.82 bpm (Tt), respectively] and in body temperature (35.82 ± 0.65 (tt) versus 37.94 ± 0.40 (TT) versus 38.81 ± 0.370C (Tt); $P < 0.05$, respectively]. Breed x TNXB

genotype and zone x TNXB genotype interaction effects were significant ($P < 0.05$) for heart girth and body temperature, while the interaction effect of breed x sex x TNXB genotype was significant ($P < 0.05$) for body weight, rump height, heart girth and rump width, respectively. Variation in TNXB may be mediated through a possible role in connective tissue biology such as blood vessels which may in turn be a potential genetic marker for heat tolerance traits, as well as for disease resistance when validated in a larger population supported by functional studies.

Key words: Tenascin XB gene, sheep, Nigeria

690 Lean lamb production during the process of grading up to hair sheep genetics. D. K. Aaron*, D. G. Ely, E. Fink, B. T. Burden, M. E. Hoar, M. M. Simpson, and A. K. Lunsford, *University of Kentucky, Lexington.*

The overall objective of a long-term grading-up project was to track changes in production as breed composition of the flock changed from Polypay (PP) to White Dorper (WD). This portion of the project evaluated carcass characteristics of a sample of wether lambs selected for harvest from lamb crops produced from 2003 through 2010. Percentages of WD breeding in harvested lambs were 0 (PP; n = 50), 50 (1/2 WD; n = 50), 75 (3/4 WD; n = 50), 87.5 (7/8 WD; n = 35) and 93.75% or higher (WD; n = 48). Each year lambs were born in April, creep fed on pasture, and weaned at 70 d of age. Lambs were managed postweaning on pasture and supplemented with grain at 2 to 3% BW. Lambs were harvested at a live target weight of 54 kg. Data were analyzed using mixed model procedures. Orthogonal polynomials were used to partition differences among lamb genetic types (0, 50, 75, 87.5 and 93.75% or higher WD). Polypay lambs were youngest at harvest (197 d) and age increased (Linear, $P < 0.01$) as percent WD increased with 93.75% or higher WD lambs being oldest (220 d). Harvest weights decreased as percent WD increased (54.2, 54.3, 53.2, 51.3 and 52.3 kg; Linear, $P < 0.01$). Carcass weights responded quadratically (26.5, 27.4, 27.1, 26.4 and 26.3 kg; $P < 0.01$). Rack weights (1.98, 2.09, 2.25, 2.23 and 2.13 kg) and loin weights (2.38, 2.65, 2.79, 2.84 and 2.72 kg) increased linearly ($P < 0.01$) as percent WD increased. There were no differences in leg weights. Carcasses from 7/8 WD were fattest while carcasses from PP lambs were leanest (Quadratic, $P < 0.01$). Longissimus muscle area was largest for WD and smallest for PP lambs (Linear, $P < 0.01$). Yield grades were lowest for PP and WD lambs (1.8, 2.3, 2.6, 2.9 and 1.8; Cubic, $P < 0.01$). Percent closely trimmed boneless retail cuts increased as percent WD increased (48.3, 48.1, 47.9, 48 and 49.1%; Linear, $P < 0.01$). Results from this project indicate carcasses of percentage WD lambs compare favorably to those of PP lambs for most traits.

Key words: White Dorper, Polypay, carcass characteristics

Alpharma Beef Cattle Nutrition Symposium: Enhancing Beef Production Efficiency with New Knowledge and Technologies: Building the Bridges for Future Collaboration

691 Implications of nutritional management for beef cow/calf systems. R. N. Funston*, *University of Nebraska, West Central Research and Extension Center, North Platte.*

The beef cattle industry relies on the utilization of high forage diets to maintain the cow herd, develop replacement females, and stocker operations. Forage quantity and quality fluctuate with season and environmental conditions. Depending on the class and physiological state of the animal, a grazed forage diet may not always meet nutritional requirements resulting in low ADG or weight loss if supplemental nutrients are not provided. It is important to understand the consequences of such weight loss and the economics of providing supplementation to the beef production system. Periods of nutrient restriction can actually result in compensatory gain once dietary conditions improve and may be of less impact in breeding animals where actual weight is not as important as animals destined for the feedlot provided reproductive efficiency is not compromised. A rapidly evolving body of literature is also demonstrating effects on subsequent offspring developing in a restricted environment in utero. Maternal stimuli or an insult during a critical period of fetal development having long-term implications for the offspring is the concept of fetal programming. In recent studies at the University of Nebraska, calf birth weights were unaffected while calf weaning weights were greater from cows gestated on dormant winter range receiving protein supplementation during late gestation compared with non-supplemented cows. Subsequent steer carcass weights and quality grades were also improved in calves born to supplemented dams and more heifers from supplemented dams were pubertal before breeding and had greater pregnancy rates. This body of research provides compelling evidence of a fetal programming response to maternal nutrition in beef cattle. Future competitiveness of the beef industry will continue to be dependent on the utilization of high forage diets to meet the majority of nutrient requirements. Consequences of nutrient restriction must be considered not only on individual animal performance but also the developing fetus.

Key words: beef cattle, fetal programming, nutrition

692 Altering the ruminal microbiome and its potential impact on animal nutrition and performance. S. L. Lodge-Ivey*, *New Mexico State University, Las Cruces.*

This presentation will address current advancements in rumen biochemistry and how these advancements may need to be dealt with in current paradigms. How these interactions within rumen microbiology, nutrition or metabolism may be understood and how future research may account for this additional source of variation. Characterization of the rumen microbial communities may eventually lead to enhanced production efficiency of grazing animals. Conventional culture-base methods of enumerating rumen microorganism are being replaced by culture independent methods that rely on analysis of nucleic acids extracted from ruminal samples. For example, sampling location within the rumen, liquid versus particulate faction and handling techniques are all areas of consideration when collecting ruminal samples for analysis with DNA- and RNA-based techniques. Application of modern tools has modified and altered how rumen microbial diversity is measured. The rumen microbiome represents a huge resource with great potential. The future of rumen microbiology research is dependent upon the application of molecular research technologies. There is a need to apply modern technologies to improve production efficiency of ruminants. The goal of this presentation is to identify areas of current research within the field of rumen microbiology and how research nutritionists, consultants and other disciplines can develop partnerships for interactions of multidisciplinary, integrated research approaches to address large novel projects being requested currently by granting agencies.

Key words: rumen microbiology, modern techniques, multidisciplinary interactions

693 Nutrition and the genome. H. L. Neibergs*, *Washington State University, Pullman.*

It has long been appreciated that animals fed the same diet may perform differently. This is due to the ability of nutrients to interact with and affect molecular pathways that result in differences in weight gain, production performance or disease resistance. To understand these effects, studies are being undertaken to discover how the differential expression and function of genes occurs with different diets. These studies are exploiting new technologies, genomic resources and analyses that have recently become available for domestic animals. Nutrigenomics and nutrigenetics incorporate these research approaches to optimize health by looking beyond the diet to understand the effects of food at the genetic and epigenetic levels. Nutrigenomics is focused on the effects of diet on health through an understanding of how bioactive chemicals in foods and supplements alter gene expression or the structure of an animal's genome. Nutrigenetics focuses on how the genetic composition (genetic variation) of an animal influences their response to a given diet. Results from these studies will aid in formulating nutritious efficient diets that may be optimized for animals based on their genomic underpinnings. Nutrigenomics and nutrigenetics unite many fields: nutrition, bioinformatics, molecular biology, genomics, functional genomics, epidemiology and epigenomics. The use of multi-disciplinary tools from these fields promises new opportunities to investigate the complex interactions of the genome and an animals diet. Through these new approaches, the partnerships of the genome and nutrition will be revealed resulting in improved efficiency of diets, enhanced sustainability of animals as a protein source and improved methods for preventing illnesses.

Key words: nutrigenomics, nutrigenetics

694 Impacts of health status and disease prevention with nutrition and performance of beef cattle. B. P. Holland*[1] and L. O. Burciaga-Robles[2], [1]*Department of Animal and Range Sciences, South Dakota State University, Brookings,* [2]*Feedlot Health Management Services Ltd., Okotoks, Alberta, Canada.*

Research in the health of growing and finishing cattle by nutritionists has focused primarily on the interaction of diet, management, and incidence of BRD, and the effects of clinical BRD on subsequent animal performance. Veterinary research has provided a wide array of vaccines, combined with antimicrobials and health management protocols for disease prevention and intervention. While some strategies have

been shown to reduce morbidity and improve performance on an individual lot basis, overall incidence of BRD has increased over time. Management strategies can be employed to minimize the effects of disease on carcass characteristics and profitability. However, diagnosis of disease is subjective and inconsistent, requiring that these strategies be applied to diverse populations with limited discrimination. Recent advances in technology can help researchers understand the metabolic status of animals in healthy and diseased states and the impact of disease and the immune response on nutrient requirements. Results from proteomic methods have cast doubts on traditional experimental models of stress-induced immunosuppression. Data such as these can be used to more accurately create experimental models for studying animal health. In addition, definitions of illness based on biochemical measures can be created so that health responses to treatment can be assessed more accurately and more targeted management can be imposed. Ongoing research is being conducted to determine impacts of prenatal nutrition and lifetime management strategies on animal reproduction, growth, and carcass traits. Measures of health and immune responses should be included in such research to better understand nutrition and epigenetic effects on disease susceptibility and create more inclusive lifetime management systems. Discoveries made using biochemical methods should be incorporated into practical tools so that illness can be prevented, reducing the use of antimicrobials and the subsequent impacts of the immune response on beef production. This paper will review interactions of health and nutrition in beef cattle and propose considerations for future research.

Key words: beef cattle, health, growth

695 Interactions with beef cattle nutrition and metabolism: Developing an integrated across discipline approach to research; building the bridges for future collaboration, summary. D. L. Boss*, *Montana State University, Bozeman.*

As animal science disciplines embark on future research, each discipline is finding and understanding interactions that affect more than one traditional area of training and research. Alpharma Beef Cattle Nutrition symposium proposes to address reviews of current and potentially new interactions between beef cattle nutrition and other major animal science disciplines. Grant opportunities are becoming larger and need to include multidisciplinary approaches to solve intricate systems biology research questions. Granting agencies are requesting applications that address an integrated approach. Synergistic collaboration of interdisciplinary team approach to research and outreach allows new collaborative teams to address issues or questions that are vital to stakeholder interests. As research and industry beef cattle nutritionists develop programs for the next 10 to 20 years, these interactions will need to be addressed in design and implementation of new novel nutrition research. In this symposium, experts in several areas discuss and identify future areas for multidisciplinary interaction and development of integrated research programs to address complex and novel areas of investigation to help in the process of building the bridges for future collaboration. By crossing disciplines to integrate research programs, an increased allocation of resources can be achieved and integrated approaches can assist with large scale biological questions. Current advancements in ruminal biochemistry need to be placed in context within existing paradigms of conventional nutritional research. Genomics and endocrinology as influenced by nutrition will address interactions as well as emerging technologies and techniques to beef cattle nutrition. Past, present and future management decisions and their impacts upon beef cattle nutrition such as fetal programming and disease prevention and intervention will be investigated through across discipline research discussions.

Key words: beef cattle nutrition, integrated across discipline

696 Effect of a micronutrient supplement on the functional capacity of neutrophils harvested from the blood of dairy cows during the periparturient period. X. S. Revelo*, A. L. Kenny, N. M. Barkley, and M. R. Waldron, *University of Missouri, Columbia.*

The objective of this study was to investigate the effect of a micronutrient supplement on the functional capacity of neutrophils (PMNL) isolated from the blood of dairy cows during the periparturient period. Cows received 56 g/day of either OmniGen-AF (n = 8) or sham control (soybean hulls; n = 12) mixed into total-mixed rations from d 46 ± 1 before calving until d 31 after parturition. PMNL were collected from cows on d 49 ± 2, 28 ± 1, 19 ± 1, and 9 ± 1 prepartum and 1, 7, 14, and 30 postpartum to determine their luminol-dependent generation of reactive oxygen species (ROS), formation of extracellular traps (NETs), chemotaxis toward interleukin-8 (IL-8) and antimicrobial capacity against Staphylococcus aureus. There was no effect of dietary OmniGen-AF on any of the parameters used to assess PMNL function ($P \geq 0.20$). In contrast, ROS production and NET release by phorbol 12-myristate 13-acetate (PMA)-activated PMNL changed between days relative to parturition (time effect, $P \leq 0.01$). ROS production increased by 40% between 49 and 19 d prepartum ($P \leq 0.05$) and then declined 63% to reach a lowest level on d 1 postpartum ($P \leq 0.05$). ROS generation by PMA-activated PMNL did not differ and persisted low on d 1, 7 and 14 ($P \geq 0.20$), however, it recovered to a level similar to that found prepartum by d 30 postpartum. NET release by PMA-stimulated PMNL collected from all cows was highest on d 49 prepartum but decreased 26% and 40% by d 28 and 19 prepartum, respectively ($P \leq 0.05$). The expression of NETs by PMNL remained low until d 14 relative to parturition, but slightly increased on d 30 postpartum (25% higher compared with d 19 prepartum, $P \leq 0.05$). There was no effect of day relative to parturition on PMNL chemotaxis toward IL-8 or killing ability against S. aureus ($P \geq 0.05$). These results suggest that impairment of ROS production and release of NETs contribute to the altered PMNL function in periparturient dairy cows.

Key words: neutrophil, immunosuppression, micronutrient supplement

697 Multiple *Mycoplasma* spp. detected in bulk tank milk samples using real-time PCR and conventional culture, and agreement between test methods. D. J. Wilson*[1], A. Justice-Allen[2], J. D. Trujillo[3], and G. Goodell[4], *[1]Utah State University, Logan, [2]Arizona Game and Fish Department, Phoenix, [3]Iowa State University, Ames, [4]The Dairy Authority, Greeley, CO.*

A PCR method and standard culture were both used to test for Mycoplasma spp. in bulk tank milk samples, and results were compared. Bulk tank milk samples (n = 165) from 16 dairy farms that had been found mycoplasma-positive were tested as were 15 samples from a farm previously negative. All samples were cultured on modified Hayflick medium and incubated at 37°C in 10% CO_2. DNA extraction, PCR reaction using SYBR green, and dissociation curve analysis to determine the melt curve and Tm were also performed in triplicate. For selected samples, and samples with Tm different than the M. bovis positive control, bp length was determined by capillary electrophoresis, and DNA sequence of amplicons was compared to known sequences using BLAST to detect multiple *Mycoplasma* spp. A true mycoplasma-positive sample was defined as having at least 1 positive test, whether culture or at least 1 SYBR PCR; specificity was 100% by definition. Test sensitivity was calculated as the number of positive cultures or PCR tests divided by the number of tests performed on true positive samples. The confidence interval for sensitivity of the 2 tests was calculated and evaluated for overlap, and test method agreement was also assessed with a kappa statistic. Results are in the table. Ninety samples were mycoplasma-negative and 90 were positive. Forty-eight samples were positive on all 4 tests (1 culture, 3 PCR). Culture sensitivity = 62/90 = 68.9%; PCR sensitivity (3 tests/sample) = 207/270 = 76.7%; Agreement = 141/180 = 78.3% ($\kappa = 0.54$, moderate agreement); 95% CI overlap indicated comparable sensitivity. Of 52 speciated samples there were 39 *M. bovis* (75%) isolates, 13 *M. alkalescens* (25%), 4 *M. arginini* (8%), 2 *M. gateae* (4%), 1 *M. bovigenitalium* (2%). All 7 double-positive samples included *M. bovis*. The *M. bovigenitalium* was found in 1 tank sample from the herd previously mycoplasma-negative. Both test methods demonstrated useful and comparable sensitivity for detection of mycoplasma in bulk milk.

Table 1. Comparison of mycoplasma culture and PCR results on bulk tank milk

	PCR positive	PCR negative	Total
Culture positive	51	11	62
Culture negative	28	90	118
Total	79	101	180

Key words: mastitis, mycoplasma, PCR

698 Multiple tests based estimates of *Mycobacterium avium* ssp. *paratuberculosis* prevalence in domestic ruminant population suspected for Johne's disease. S. V. Singh*[1], P. K. Singh[1], A.V. Singh[1], B. Singh[1], A. Kumar[1], A. Srivastav[2], S. Gupta[1], H. Singh[1], A. Mittal[1], S. Yadav[2], and J. S. Sohal[1], *[1]Central Institute for Research on Goats, Mathura, Uttar Pradesh, India, [2]College of Veterinary Sciences, Mathura, Uttar Pradesh, India.*

Mycobacterium avium subspecies *paratuberculosis* (MAP), the cause of Johne's disease (JD) is a major animal pathogen worldwide and is endemic in the animal population wherever investigated. Despite low per animal productivity, JD received low priority outside developed countries. JD is endemic in the domestic ruminant population of the country. Planning major initiative on the control knowledge of epidemiology of MAP is essential. Due to lack of "true estimates" on the prevalence of MAP, disease is not a priority for the control in the domestic livestock in the country. In 2010, 3007 samples were submitted to Animal Health Division (Central Institute of Research on Goats, Mathura) for screening against MAP. Samples originated from cattle, buffaloes, sheep and goats suspected for JD from 9 states (Uttar Pradesh, Tamil Nadu, Himanchal Pradesh, Gujarat, Assam, Kerala, Madhya Pradesh, Rajasthan and Punjab). Samples (3007) were screened by microscopy (716 feces), IS900 PCR (183 feces and 510 blood) and "indigenous ELISA kit" (1598 serum). Using microscopy, fecal PCR, blood PCR and indigenous ELISA kit, 51.0, 27.3, 19.6 and 68.4% samples were positive, respectively. With respect to the 4 tests, study showed moderate to high levels of prevalence in the suspected livestock population. Study revealed value of microscopy and indigenous ELISA kit as screening tests, whereas IS900 PCR (blood and feces) was at best confirmatory. Higher presence of MAP in the test samples showed the need for wider study to estimate sero and molecular prevalence of MAP in domestic ruminants population of the country.

Key words: paratuberculosis, epidemiology

699 Evaluation of a BVD milk ELISA test detecting anti-p80 antibody and comparison with ear notch testing for PI cattle. D. J. Wilson*[1], K. A. Rood[1], and G. Goodell[2], [1]*Utah State University, Logan,* [2]*The Dairy Authority, Greeley, CO.*

A milk ELISA test for antibody (Ab) against Bovine Viral Diarrhea (BVD) was studied and compared with standard ear notch testing for Persistently Infected (PI) cows. Milk metered samples were tested from a dairy herd with past diagnoses of BVD abortions and PI cows. BVD MLV vaccine was given to calves 3 mo and 4 mo old, to all cows at dryoff and 15-21 DIM post calving. 247 and 258 cows were tested 1 mo apart using a competitive ELISA for milk antibody (Ab) binding to p80 BVD protein. Results are reported as % binding by a second test kit Ab; higher second Ab binding means the milk had less anti-BVD p80 Ab. Interpretation: 90-100%, little Ab - PI or vaccine failure if consistent; 60-89%, moderately low Ab; 30-59%, moderate Ab; 10-29%, high Ab; 0-9%, very high anti-BVD Ab. Four samples from each cow were handled differently: fresh milk, fresh with preservative pill, frozen 7 days, room temp 7 days with preservative. Ear notches were sampled concurrently from all cows for BVD antigen (Ag) testing. No PI cows were found from ear notch Ag tests of 345 cows. Milk handling method was significant; fresh milk mean 49% second Ab binding was higher than other methods, 7 days preserved was especially lower at 42% ($P \leq 0.01$, ANOVA, Tukey's). All further results here are from fresh milk. Binding ranged from 3%-98%, quartiles 29%, 47%, 62% 1st mo, 35%, 56%, 71% 2nd mo. 15 cows had 90-98% binding on one test, but 14 were milking each mo and were below 90% on the other test; 60% mean binding the other mo. For cows >90%, DIM was 41-188, 305ME mean 12,935 kg, daily milk mean 44 kg. No PI or vaccine failures (consistently >90%) were found by milk ELISA. DIM significantly affected Ab binding: 1-9 DIM, 16%*; 10-30 DIM, 34%*; 31-60 DIM, 46%; 61-150 DIM, 60%*; 151-300 DIM, 47%; 301-360 DIM, 40%; >360 DIM, 46%. * = $P \leq 0.025$, ANOVA, Tukey's. Lactation number did not affect binding. The milk ELISA agreed with ear notch testing in finding no PI cows. Anti-BVD Ab was high in early lactation and then decreased. The ELISA warrants further study.

Key words: BVD, antibody, ELISA

700 Biophotonic imaging as a method to evaluate efficacy of intramammary antibiotics against *Staphylococcus aureus* in vitro. J. Curbelo*, J. Brett, C. Steadman, H. L. Sanchez, T. Rowlison, K. S. Seo, P. L. Ryan, and S. T. Willard, *Mississippi State University, Mississippi State.*

In this study we evaluated whether biophotonic imaging (BI) could be adapted to evaluate antimicrobial efficacies of intramammary antibiotic preparations (IAP) against bioluminescent *Staphylococcus aureus* (S. aureus-Xen8.1) in bovine milk in vitro. Whole bovine milk (500 mL; n = 4) were inoculated with S. aureus-Xen8.1 and treated with commercial IAP (cephapirin sodium (CEP), hetacillin potassium (HET) and/or pirlimycin hydrochloride (PIR)), and a control (CON) containing no antibiotics. Aliquots were collected from each inoculated sample (100µL; n = 5) over a 9 h period, placed in a 96-well plate, imaged and plated to correlate the number of cfu with photonic emissions (PE). An ANOVA and Fisher LSD test were performed to determine significant differences in PE and cfu between treatments. Photonic emissions from S. aureus-Xen8.1 increased in CON, HET and CEP treatments in a parallel manner with no differences in PE and cfu ($P > 0.05$) from 0 to 2 h post antibiotic addition. PE in the PIR treatment decreased during the same period ($P < 0.05$), but remained stable for the remaining 7 h. However cfu did not correspond with these results, remaining unchanged during the first 4 h. Differences in PE between HET and CEP were first observed at 2 h post antibiotic addition (243.3 ± 4.5 and 236.9 ± 1.4, respectively; $P < 0.0001$), which corresponded to the differences first observed in cfu between these 2 treatments after 2 h ($3.4 \times 10^7 \pm 4.4 \times 10^6$ and $2.2 \times 10^7 \pm 1.1 \times 10^6$, respectively; $P < 0.0001$). In summary, the discrepancies found between PE and cfu in the PIR treatment could be attributable to its mode of action. Pirlimycin is a bacteriostatic antibiotic and interferes with protein synthesis, therefore suppressing the production of light at the ribosomal level. In contrast, CEP and HET are bactericides and target cell wall synthesis. Therefore, the degree of impairment caused by these 2 antibiotics against S. aureus-Xen8.1 corresponded to the changes in PE detected, which allows for the quantification in real time of bacterial progress during in vitro and/or in vivo antimicrobial studies.

Key words: biophotonic, *Staphylococcus aureus*, mastitis

701 Experimental induction of *Streptococcus uberis* mastitis in bred dairy heifers: A challenge model. K. A. Jackson*, D. J. Hurley, F. M. Kautz, L. O. Ely, and S. C. Nickerson, *University of Georgia, Athens.*

A challenge model for experimentally inducing *Streptococcus uberis* mastitis in 7 bred dairy heifers from a university herd was developed. Heifers were randomly assigned 2 contralateral quarters to receive an infusion of the *S. uberis* challenge strain NIRD-0140J. To challenge the heifers, a bacterial suspension was created to achieve a concentration of 1000–2000 cfu/mL in 1 mL of physiological saline. For a successful challenge, 3 of 4 consecutive microbiological cultures had to be positive for *S. uberis* based on the API 20 Strep miniaturized identification kit. Once infection was confirmed, the challenged quarter was treated with SPECTRAMAST DC. Preliminary analysis showed that 6 of the 7 heifers (85%) were challenged successfully with the dose used. The average concentration used to challenge the 7 heifers was 1,080 cfu/mL, which fell within the goal range of 1000–2000 cfu/mL. Data showed that before challenge, SCC averaged 11.5×10^6/ml across control and challenge quarters. At 24 h post challenge, SCC increased to 23.8×10^6/ml in challenged quarters and remained elevated. In contrast, unchallenged quarters resulted in no change in SCC and the concentration remained at or below 10.1×10^6/mL. Differential leukocyte data showed that before challenge, macrophages predominated in secretions followed by lymphocytes and neutrophils. By 24 h after challenge, there was a marked spike in neutrophils, which lasted for the duration of the trial. Results suggest that the challenge model developed was successful in routinely establishing experimental S. uberis mastitis in dairy heifers, which was controlled (100% cure) by the administration of nonlactating cow therapy.

Key words: experimental challenge, mastitis, *Streptococcus uberis*

702 Effects of OmniGen-AF on enhancing immunity in dairy heifers vaccinated with a *Staphylococcus aureus* bacterin. V. J. Eubanks*[1], N. E. Forsberg[2], Y. Q. Wang[2], K. Zanzalari[3], J. Chapman[3], D. J. Hurley[1], F. M. Kautz[1], L. O. Ely[1], and S. C. Nickerson[1], [1]*University of Georgia, Athens,* [2]*Oregon State University, Corvallis,* [3]*Prince Agri Products Inc., Quincy, IL.*

The purpose of this study was to evaluate the effect of a commercial feed additive on amplifying heifers' immune response to *Staphylococcus aureus* vaccination, with the goal of calving heifers free of infection with low somatic cell counts (SCC) to meet the proposed

legal limit of 400,000/mL. Overall animal health was monitored by measuring blood immune parameters, body growth, health incidents, and prevalence of mastitis. Bacterial culture of teat canal swabs and mammary secretions to determine presence of mastitis revealed that 40% and 55.1%, respectively, were infected with *S. aureus* and other *Staphylococcus* and *Streptococcus* spp. along with elevated SCC $\geq 1 \times 10^6$/ml. S. aureus was found to be the most prevalent pathogen in both the teat canal swabs (11.4%) and mammary secretions (20.5%). Heifers fed the commercial feed additive did not show a significant advantage or disadvantage in growth based on weight and height measurements. However, L-selectin and IL-8 receptor mRNA analyses on blood leukocytes showed that post-treatment L-selectin (3.6) and Il-8 (2.38) receptor mRNA levels were higher for heifers fed the commercial feed additive than control heifers (1.53 and 1.19, respectively), suggesting greater antibacterial leukocyte activity and elevated immune status in treated animals. S. aureus antibody titers across both treatment groups before vaccination averaged 1:400. By 1 mo post-vaccination, titers increased 2–10 fold, and the titers of several heifers continued to increase through the 3rd mo post-vaccination; however, no differences have been detected between treatments.

Key words: mammary immunity, mastitis, *Staphylococcus aureus*

703 Genetic parameters of adaptive immune response traits in Canadian Holsteins and implications for health. K. Thompson-Crispi*[1], A. Sewalem[2,3], F. Miglior[2,3], and B. Mallard[1], *[1]Dept. Pathobiology, Ontario Veterinary College, University of Guelph, Guelph, Ontario, Canada, [2]Guelph Food Research Center, Agriculture and Agri-Food Canada, Guelph, Ontario, Canada, [3]Canadian Dairy Network, Guelph, Ontario, Canada.*

Infectious diseases contribute to substantial economic loss in the dairy industry with human and animal health implications. The immune system is a tightly genetically regulated system that largely controls response to infectious disease. Including estimated breeding values (EBV) of immune response (IR) traits in a selection index has the potential to improve inherent animal health. Previously, cows classified as High Immune Responders in dairy herds in Ontario and the US were found to have improved response to vaccine, increased milk and colostrum quality and decreased incidence of diseases like mastitis, metritis, ketosis and retained placenta. The objectives of this study were to evaluate antibody-mediated (AMIR) and cell-mediated IR (CMIR) traits in Holstein cattle on a national scale and estimate genetic parameters of these traits. In collaboration with the Canadian Bovine Mastitis Network, 690 Holsteins from 58 herds across Canada were immunized to measure delayed-type hypersensitivity as an indicator of CMIR and serum antibody (AMIR) to putative type 1 and type 2 test antigens. The statistical procedure included the fixed effects of parity and stage of lactation and the random effects of herd-technician, animal and residual. A linear animal model was used to estimate genetic parameters and breeding values using a DMU software package. Heritability of CMIR was 0.18 and for AMIR between 0.14 – 0.41 depending on time and antibody. The genetic correlations between CMIR and AMIR were negative and ranged from −0.13 to −0.45. EBV were used to classify cows as High (H), Average or Low (L) for IR. Health and production records are available for correlation with these diverse immune response profiles. Preliminary results show no difference in 305 d production between IR categories, indicating selection for IR would not impact production. Selective genotyping of H and L immune responders using the Bovine SNP50 BeadChip is underway. Identifying H and L immune responders and determining genetic profiles of these phenotypes may make it feasible to include IR in breeding indices to improve health of dairy cows.

Key words: immune response, genetic parameters, dairy cattle

704 The relationship between measured optical density of uterine lavage samples and clinical endometritis. V. S. Machado*, M. L. S. Bicalho, and R. C. Bicalho, *Cornell University, Ithaca, NY.*

The objective of this study was to evaluate a novel clinical endometritis diagnosis technique using optical density of uterine lavage samples. Clinical endometritis is the inflammation of the endometrium diagnosed by the detection of purulent or mucupurulent uterine exudates after 21 d postpartum, not accompanied by systemic signs. In the present study, the diagnosis of clinical endometritis was evaluated using low-volume uterine lavage technique at 35 ± 3 DIM, examining the presence of purulent or mucupurulent content only in the uterine secretion. The study enrolled 554 cows from a dairy farm located near Ithaca NY from May 4th 2010 until January 17th 2011. After they were cultured for *A. pyogenes*, the uterine lavage samples were frozen in −80°C until they were processed for the assessment of optical density (OD), as follows: hypertonic saline solution (10%) was added to the uterine lavage in a 1:1 proportion, followed by incubation at room temperature for 30 min and centrifugation for 30 min at 3,000 x g at 4°C. The supernatant was collected and an aliquot of 0.2 mL was added to microplate wells. The OD200, OD352, OD620, OD790, OD860 and OD960 were assessed. The prevalence of clinical endometritis in the present study was 16.8% (93 cows). The ROC analysis of the accuracy of ODs in the detection of clinical endometritis was done for several OD wavelengths. The OD620 (optical density at 620 nm) presented the highest area under the curve in the ROC analyzes and was selected for further analysis. The ROC analyzes indicated an optimal cut-off point of 0.049 (OD620); sensitivity was 88.17% and sensitivity was 70.93%. The positive predictive value and negative predictive value for the test were 37.96% and 96.75%, respectively. The mean OD620 for endometritis negative cows was 0.07 (±0.005), which was significantly lower than for cows diagnosed with endometritis 0.24 (±0.03). The OD620 mean for *A. pyogenes* culture negative cows was significantly lower (0.9 ± 0.007) than for *A. pyogenes* culture positive cows (0.17 ± 0.03).

Key words: endometritis, uterine health, dairy cows

705 Survey of individual cow records to identify factors associated with lameness in dairy cattle in New Zealand. C. M. Lira-Diaz[1], J. K. Margerison*[1], and N. Lopez-Villalobos[2], *[1]Massey University, IFNHH, Palmerston North, New Zealand, [2]Massey University, IVABS, Palmerston North, New Zealand.*

This study aimed to assess the main factors associated with the occurrence of lameness of dairy cattle, using 1969 individual cow records from 3 dairy farms in the North Island of New Zealand and monitored cows for locomotion score (LS) using a 5 point scale (1 not lame, 3 tender footed, 4 lame, 5 very lame (not weight bearing on a limb/ limbs)) on a daily basis for a 12 mo period. A total of 9.34% of cows were diagnosed as lame at least once during the year (LS > 3) and assessment of individual claws was recorded using the international foot map (IFM) (0 = inter-digital, 1+2 = white line, 3 = axial lateral sole, 4+5 = sole area, 6 = heel, 10 = inter-digital heel, 11 = other cause of lameness). The incidence of lameness was significantly higher in hind claws 3.73 times more frequently (78.88% of cases) than fore claws (21.12% of cases), with no significant difference (*P*

< 0.8498) between right (Rt) and left (Lt) claws (Lt: 49.40%, O.R.1, C.I.95%; Rt: 50.60%; O.R.1.024, 95% C.I.). Lateral claws had the highest incidence of lameness (55.38%, O.R. 1.24, C.I 95%; $P < 0.05$) from medial claws. Results indicate a significantly ($P < 0.001$) higher percentage of LS 4 (59.20%, O.R. 7.05, C.I.95%), followed by LS 3 (32.40%, O.R.1.83, C.I. 95%), while LS 5 was lowest (8.40%, O.R. 1.00, C.I.95%). Highest incidence related to areas of the sole (IFM 4+5: 23.11%) followed by abaxial (IFM 3: 22.71%) and while line (WL) (IFM 1+2: 16.33%) areas, followed by inter-digital (IFM 0+10: 15.54%) and heel (IMF 6: 10.76%), while in 11.55% of cases the exact area affected was not identified. Claw examination showed the type of lameness most frequently diagnosed was WL disease (26.29%), followed by sole penetration (23.11%), inter-digital necrosis (16.33%), sole ulcer (11.16%), medial claw overgrowth (4.78%), thick hock (3.19%) and 15.14% was other causes. In conclusion, the main claws affected were the hind (88.45% of cases) and the main types of lameness were WL disease and foreign body penetration of the sole.

Key words: lameness, dairy cattle

706 Claw horn disease and claw horn anatomy: A meta-analysis in UK and New Zealand first-lactation dairy cattle. L. A. Lethbridge and J. K. Margersion*, *IFNHH Massey University, Palmerston North, New Zealand.*

In dairy cattle lameness is one of the main economic and welfare issues and claw horn related issues are the main pathogenesis. There is considerable amounts of data exist in many countries, there have been few similarly detailed studies assessing claw horn disease (CHD) and anatomical characteristics in the first lactation completed in New Zealand (NZ). This research used meta analysis to compare studies of CHD in the UK and NZ by the same research methods over a 3 year period. Days postpartum (dpp) significantly affected the number, percentage and total lesion score for both sole and white line, and peak hemorrhaging in NZ occurred at 110 dpp and had declined by 160, a similar pattern where peak lesions were seen at 100 dpp and levels had reduced by 150 dpp (UK). The median locomotion score of 1 with a peak score of 2 occurred between 71 and 98 dpp (NZ), which was a little sooner than the 110 to 120 dpp found in many other studies. A similar pattern for claw lesion score (CLS) to peak approx 110 to 120 d occurs irrespective of location. However the UK based research had far lower CLS (0.3) for both sole and white line lesions than in NZ. Overall, there were no significant relationships found between claw horn growth and wear rates, CLS dpp and PR (growth = Average growth = 5.98 - 0.386 Sole PR + 0.0324 d + 0.0033 CLS Sole R-Sq(adj) = 15.4% $P = 0.402$ and average wear = 9.52 - 0.458 Sole PR + 0.0173 d - 0.0112 CLS Sole R-Sq(adj) = 3.4% $P = 0.600$, and net change Net = - 11.2 + 0.244 Sole PR + 0.0396 d + 0.0303 CLS Sole R-Sq(adj) = 12.6% $P = 0.573$). Monthly growth rates were generally higher in the NZ compared with the UK, while claw horn wear rates were higher in NZ compared with the UK at 100 dpp. NZ heifers maintained a shallower claw angle, shorter dorsal border and higher heel height than UK heifer resulting in a smaller more compact foot and smaller wearing surface. The dorsal borders and heel depth in UK heifers were longer and shallower than those in NZ heifers, but UK foot angle was steeper than NZ.

Key words: claw horn disease, dairy cattle

Breeding and Genetics: Dairy Cattle Breeding II

707 Methods for the assessment of milk coagulation properties: A genetic analysis. A. Cecchinato*, M. Penasa, M. De Marchi, C. Cipolat Gotet, I. Bazzoli, N. Cologna, and G. Bittante, *Department of Animal Science, University of Padova, Viale dell'Università, Legnaro, Padova, Italy.*

Milk coagulation properties (MCP: clotting time, curd firmness) are of great importance because they influence cheese processing, yield and quality. Assessment of MCP can be performed through Formagraph (FMG), which is an instrument based on the tiny forces exerted by pendulums when samples of coagulating milk are exposed to linear oscillations, or Optigraph (OPT), which is based on an optical signal in the near-infrared reflectance spectroscopy. The FMG provides measures of milk clotting time (RCT, min), defined as the time from the addition of rennet to milk until the beginning of coagulation (within a 90-min testing time), and curd firmness (in mm) measured at different time: 30 (a30), 60 (a60), 75 (a75) and 90 (a90) min from the beginning of the test. The OPT provides same measures of MCP by means of particular feature points extracted from optical information acquired in real time. The aim of this study was to estimate heritabilities of and genetic correlations between MCP obtained from FMG and OPT. A total of 1,014 Brown Swiss cows were sampled once in 68 herds from January 2010 to February 2011. Individual milk samples were collected during the evening milking and analyzed for MCP by using FMG and OPT. A Bayesian standard linear model was implemented via Gibbs Sampling. The model included the non genetic effects of days in milk, parity, herd and the additive genetic effect of animals. For RCT measured by FMG, marginal posterior mean (SD) of heritability was 0.30 (0.09). Estimates of heritability for a30, a60, a75 and a90 averaged 0.14 (0.06) and ranged from 0.13 (0.06) to 0.16 (0.07). For OPT, corresponding estimates were slightly lower. Genetic correlations between MCP from FMG and OPT approached 0.90 (0.06). On the basis of the genetic parameters obtained in this study, the improvement of MCP through selection is possible, regardless the method used.

Key words: milk coagulation properties, near-infrared spectroscopy, genetic parameters

708 Genetic relationships between fertility and content of major fatty acids in milk for first-parity Walloon Holstein cows. C. Bastin*[1], N. Gengler[1,2], and H. Soyeurt[1,2], *[1]University of Liège, Gembloux Agro-Bio Tech, Animal Science Unit, Gembloux, Belgium, [2]National Fund for Scientific Research, Brussels, Belgium.*

Fertility traits are difficult to measure and have low heritabilities. Consequently, indicators traits are of interest for breeding value estimation for fertility especially if these traits are easier to measure, have higher heritabilities and are well correlated with fertility. Furthermore, some traits of the milk fatty acid (FA) profile could be considered because they can be related to the energy balance status. Therefore the objective of this study was to estimate genetic correlations between days open (DO) and the contents of 19 individual and groups of milk FA. Fatty acids contents (in g/dl of milk) were estimated by MIR and were: saturated, unsaturated, monounsaturated, polyunsaturated, long chain, short chain, medium chain, C4:0, C6:0, C8:0, C10:0, C12:0, C14:0, C16:0, C17:0, C18:0, C18:1, C18:1 cis, and C18:1 cis-9. Data included 143,332 FA and 29,792 DO records collected from 29,792 Holstein cows in first parity. Co(variances) were estimated using 19 2-trait models that included random regression for FA traits. Overall, genetic correlations between DO and FA contents in milk changed significantly over the lactation. For unsaturated, monounsaturated, long chain, C18:0, C18:1, C18:1 cis, and C18:1 cis-9, genetic correlations with DO were positive in early lactation and became negative after 100 d in milk. For the other fatty acids, genetic correlations with DO were negative along the whole lactation. At 5 d in milk, genetic correlation between DO and C18:1 cis-9 was 0.40 and genetic correlations between DO and C6:0 to C16:0 ranged between −0.55 and −0.20. These results emphasized the relationship between fertility and energy balance status and could be explained by the release of long chain fatty acids in early lactation due to the mobilization of body fat reserves and the consequent inhibition of de novo FA synthesis in the mammary gland. At 200 d in milk, correlations between DO and fatty acid contents ranged between −0.40 for C18:1 cis-9 to −0.10 for C6:0. This research suggested the interest of using FA contents in milk in indirect selection for better fertility in dairy cows.

Key words: fatty acid, fertility, genetic correlation

709 Relationships between mortality and 305-d milk yield of Holstein cows in three regions in US. K. Tokuhisa*, S. Tsuruta, and I. Misztal, *University of Georgia, Athens.*

Several recent research reports have indicated increasing dairy cow mortality over the years; however, the reasons for the increase are unclear. This study aimed to investigate the relationship between mortality and 305-d milk yield. DHI data contained 3 regions: Southeast (SE), Southwest (SW), and Northeast (NE). A total of 3,522,824 records for 3 parities were used: 732,009 (SE), 656,768 (SW), 2,134,047 (NE) from 1999 to 2008. Termination code "6" was regarded as "death" and used for mortality calculation. A 2-trait (305-d milk yield, mortality) animal model fitting fixed effects of herd year, age, DIM, month-of-termination, and random animal genetic effect was used to compute correlations and heritability, separately for each region and parity. Mortality was the highest in August for any parity, and the lowest in spring (i.e., the largest difference between the highest and the lowest mortality in SE was 0.63% in 3rd parity). The highest mortality was observed in SE, and mortality in NE and SW were similar. Mortality increased with parity in all regions. Mortalities in first 3 parities across regions were 3.3%, 4.8%, 7.2% (SE), 2.4%, 3.3%, 5.0% (SW), and 2.2%, 3.7%, 5.4% (NE). The span of mortality between 1st and 3rd parity was the largest in SE (3.9%) and the smallest in SW (2.6%). Genetic correlations between the 2 traits were 0.09, 0.09, 0.17 (SE), −0.03, −0.05, 0.17 (SW), and 0.19, 0.19, 0.00 (NE). The environmental correlations were 0.03, 0.05, 0.06 (SE), 0.03, 0.05, 0.05 (SW), and 0.01, 0.05, 0.06 (NE). Heritability estimates of milk yields were 0.28, 0.19, 0.13 (SE), 0.32, 0.19, 0.16 (SW), and 0.35, 0.24, 0.19 (NE). Heritability estimates of mortality were 0.01 for all 3 parities and all 3 regions. The mortality is the highest in SE and is influenced by season and by parity. Environmentally, high milk producing cows tend to have high mortality. Genetically, effects of high milk production on mortality are less clear. Results may have been influenced by special veterinary care to superior cows.

Key words: US Holsteins, cow mortality, regions

710 Genetic parameters of body condition score and other type traits in Canadian Holsteins. S. Loker*[1], C. Bastin[2], F. Miglior[3,4], A. Sewalem[3,4], L. R. Schaeffer[1], J. Jamrozik[1], and V. Osborne[5], *[1]CGIL, Dept. of Animal and Poultry Science, University of Guelph, Guelph,*

ON, Canada, [2]University of Liège, Gembloux Agro-Bio Tech, Gembloux, Belgium, [3]Guelph Food Research Centre, Agriculture and Agri-Food Canada, Guelph, ON, Canada, [4]Canadian Dairy Network, Guelph, ON, Canada, [5]Centre for Nutrition Modelling, Dept. of Animal and Poultry Science, University of Guelph, Guelph, ON, Canada.

The objective of this research was to estimate the genetic parameters of body condition score (BCS) and other type traits. The data analyzed in this study was from Holstein Canada's new classification system and included BCS, angularity (ANG), chest width (CW), height at front end (HFE), body depth (BD), pin width (PW), and stature (STA), recorded between rounds 72 to 79 (year 2006 to 2010). The model included the fixed effects age of calving × stage of lactation, and herd × round × classifier, and a random additive genetic animal effect. All 7 traits were analyzed together. In general, it was found that larger cows (taller, wider, less angular cows) were genetically inclined to have higher than average BCS, which other studies have linked to better health and fertility. The 2 traits with the strongest genetic correlation with BCS were ANG (−0.70) and CW (0.72). Heritabilities were 0.21, 0.18, and 0.19 for BCS, ANG, and CW, respectively. Genetically, ANG was strongly negatively correlated with BCS (−0.70), whereas CW was strongly positively correlated with BCS (0.72), but ANG and CW were not strongly correlated with each other (−0.16), and so both could be useful as additional information in a genetic evaluation of body condition score. All 3 traits would be useful in conjunction with Valacta's BCS (Sainte-Anne-de-Bellevue, QC, Canada) (collected several times per cow throughout lactation for Québec herds) for a first lactation longitudinal genetic analysis of BCS. A genetic evaluation of BCS would inevitably lead to selection for cattle with improved health and fertility.

Key words: body condition score, type traits, genetic correlation

711 Relationship between body condition score, locomotion and dairy strength with functional longevity in Canadian Holsteins. A. Sewalem*[1,2], F. Miglior[1,2], and G. Kistemaker[2], *[1]Agriculture and Agri-Food Canada, Guelph, Ontario, Canada, [2]Canadian Dairy Network, Guelph, Ontario, Canada.*

The aim of this study was to explore the impact of body condition score (BCS), locomotion and dairy strength on the functional survival of Canadian Holstein cows using a Weibull proportional hazard model. The data set consisted of 490,791 cows from 13,786 herds sired by 8,126 sires. Functional survival was defined as the number of days from first calving to culling, death, or censoring. The statistical model included the effects of stage of lactation, season of production, the annual change in herd size, type of milk recording supervision, age at first calving, effects of milk, fat and protein yields calculated within herd-year-parity deviations, herd-year-season of calving, each type trait and the sire. Analysis was done one at a time for each of 3 type traits. The relative culling rate was calculated for animals in each class after accounting for the above-mentioned effects. BCS showed a curvilinear relationship with longevity. Cows with score of 1 (classified as lean) were 35% more likely to be culled compared with the reference class (score = 5). Similarly, cows with score of 9 (classified as fat) were less likely to stay longer in the herd compared with the reference group. This indicates that neither too lean nor fat cows are desired for breeding purposes. The result also showed that lameness and dairy strength had a clear linear relationship with longevity. Cows classified with score 1(namely cows considered as lame) were more than 34% more likely to be culled than cows classified as intermediate group (score = 5). Additionally, cows with higher score than average were less likely to be culled than cows from the average group (score = 5). Similarly, for dairy strength cows with poor score were nearly 50% more likely to be culled than the reference group (Good Plus). However, cows with excellent score were found to have longer longevity than the other groups.

Key words: functional survival, body condition score, locomotion

712 Modeling of residual feed intake for primiparous dairy cow using orthogonal polynomial random regression. G. Manafiazar*, T. McFadden, E. Okine, L. Goonewardene, and Z. Wang, *Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Alberta, Canada.*

Residual feed intake (RFI) is defined as the difference between an animal′s actual energy intake (AEI) and its expected energy intake (EEI) based on its maintenance and various production requirements. Due to the complexities of multifunctional (maintenance, growth, pregnancy, and lactation) energy requirements, there is no method available for evaluating individual RFI in dairy cows currently. The objective of this study is developing a statistical model to evaluate individual RFI for first lactation dairy cow. Two hundred first lactation cows were used in an experiment at the Dairy Research and Technology Center of the University of Alberta. Individual feed intake was measured daily while individual body weight and body condition score of each animal were assessed at the times of calving and each of DHI milk sampling days. Individual milk yield and composition data were obtained from the official DHI data set. The net energy required for maintenance (NE_M), lactation (NE_L), pregnancy (NE_P); energy balance (EB) and 4% fat corrected milk (FCM) traits for each animal were derived from the data. Twenty 5 alternative Legendre polynomial (LP) models were fitted for each trait with fixed (FP) and random (RP) polynomial regressions of orders from 1 to 5. The best model for each trait was selected using multiple statistical criterion. The selected model for NE_M, NE_L, EB and FCM was FP_1RP_4, FP_2RP_2, FP_1LP_4 and FP_2RP_2, respectively, where the subscript numbers stand for order of LP. An individual conversion coefficient of gained or lost energy for each animal was estimated with a simple linear regression of predicted daily FCM on predicted daily EB in the negative period while AEI on predicted daily EB in the positive period. The individual EEI is calculated as a summation of predicted NE_M, NE_L, NE_P and net gained or lost energy from that individual. The model made it feasible to evaluate dairy RFI while accounting for multi-functional energy requirements.

Key words: dairy, feed efficiency, Legendre polynomial

713 Genetic association of days open with feed intake and efficiency. J. E. Vallimont[1], C. D. Dechow*[1], J.M. Daubert[1], M. W. Dekleva[1], and J. W. Blum[2], *[1]Pennsylvania State University, University Park, [2]University of Bern, Bern, Switzerland.*

The objective of this study was to determine the genetic relationship between feed efficiency and days open in dairy cows. Dry matter intake, body weight (BW), and body condition score (BCS) were collected monthly on 970 cows in 11 tie-stall herds for 6 consecutive months and merged with test-day records. Two methods of feed efficiency were considered. Dry matter efficiency (DME) was the ratio of 305-d fat-corrected milk (FCM) to 305-d dry matter intake (DMI). Residual feed intake (RFI) was the difference between DMI and feed intake predicted from National Research Council equations. High values of RFI represent cows with lower feed efficiency. Associations of DMI, DME and RFI with days open were estimated with 5-trait

animal models that included days open, FCM, BW, BCS and either DMI, DME or RFI. Fixed effects were herd-calving-cluster, age at calving and lactation number. Random effects were animal, permanent environment and error. Analyses of DME and RFI were conducted with and without covariables for BCS and change in BCS from day in milk 5 to 60. Heritability estimates were 0.18 for DMI and DME, 0.05 for RFI, and 0.07 for days open. The genetic correlation of DMI with days open was slightly favorable (−0.15), whereas genetic correlations of days open with DME (0.68) and RFI (−1.0) were more unfavorable than the genetic correlation between days open and FCM (0.49). RFI was genetically correlated with higher BCS (0.41), whereas higher DME was genetically correlated with lower BCS (−0.68). Adjustment of RFI and DME for BCS traits had a modest effect on genetic correlation estimates with days open (−0.85 and 0.58, respectively). Genetic differences among cows for the RFI measure used in this study were small and appeared to partly reflect BCS differences among cows that were not considered in the predicted DMI equations. There were genetic differences among cows in DME, but cows that were more feed efficient were less efficient reproductively.

Key words: feed efficiency, heritability

714 A comparison of six protocols for isolation of high quality and quantity ovine genomic DNA suitable for microarray analysis. A. Psifidi[1], C. I. Dovas[2], G. Bramis[1], G. Arsenos[1], and G. Banos*[1], *[1]Department of Animal Production, Faculty of Veterinary Medicine, Aristotle University of Thessaloniki, Thessaloniki, Greece, [2]Laboratory of Microbiology and Infectious Diseases, Faculty of Veterinary Medicine, Aristotle University of Thessaloniki, Thessaloniki, Greece.*

Isolation of high quality and quantity genomic DNA is a crucial step in large-scale SNP discovery projects using microarrays. Few of the current DNA extraction procedures can be easily adapted to high-throughput operation for microarray genotyping at low cost. In this study, 6 different DNA extraction protocols were evaluated and compared for the isolation of ovine genomic DNA. Blood samples used were taken from 16 ewes of the Chios dairy breed, in 9mL K_2EDTA Vacutainer blood collection tubes. Protocols 1 and 6 were direct applications of commercial kits Nucleospin Blood and Nucleospin Blood L (Macherey-Nagel), respectively. Protocols 2 and 3 were direct applications of extraction kits Nucleospin Blood and Nucleospin Tissue (Macherey-Nagel), respectively, with a buffy coat of 9mL blood being used instead of 200µl whole blood. Protocols 4 and 5 were based on modified protocols of 2 and 3, respectively, aiming at increasing DNA recovery and purity. The key modification was the incorporation of a chloroform extraction step. Spectrophotometer measurements were used as criteria for evaluating quantity and quality (OD260/280 and OD260/230) of the extracted DNA. All samples were subjected to real-time PCR to amplify part of the PRNP gene and test the efficiency of amplification as a measure of DNA sample purity and quality. Processing time and cost were also evaluated. Extraction methods were compared using a model that included the effects of protocol and sample. The model applied separately to DNA concentration, final DNA concentration accounting for volume, OD260/280 and OD260/230. Protocol had a significant ($P < 0.05$) effect on all parameters. Protocols 4, 5 and 6 yielded the highest DNA concentration even after accounting for volume. Method 6 had the lowest values for OD260/280 and OD260/230 suggesting less pure DNA. All samples were amplified with real-time PCR. Incubation time was greater for protocols 2, 3, 4 and 5. Protocol 6 was the most expensive. Based on results, protocols 4 and 5 were selected for further application.

Key words: ovine, DNA extraction, microarrays

715 Association between the ghrelin gene with milk production traits in Murrah buffaloes (*Bubalus bubalis*). F. M. M. Gil, F. R. P. Souza, G. M. F. de Camargo*, P. D. S. Fonseca, D. F. Cardoso, R. R. Aspilcueta-Borquis, G. Stefani, and H. Tonhati, *São Paulo State University, Jaboticabal, São Paulo, Brazil.*

Ghrelin is a gastrointestinal hormone and a potent release stimulator of growth hormone (GH) in the somatotropic cells of the hypophysis and hypothalamus. It also influences the general metabolism of the body. Polymorphisms in the ghrelin gene in dairy cows were associated with milk yield, fat and protein percentage. The characterization of the ghrelin gene (GHRL) in buffaloes is important because it is a gene related to growth, carcass and milk production traits. The aim of this study was to associate a SNP in intron 2 of the GHRL gene in Murrah buffaloes with milk production traits. The SNP is a T/C substitution at position 1456 bp of GHRL. The DNA was extracted from hair of 206 dairy buffaloes from one farm in São Paulo state, Brazil. The animals were genotyped by PCR-RFLP using the restriction enzyme NcoI. For the analysis, the GLM procedure of SAS was used, the model included as fixed effects birth season, birth year and genotype and as a covariable the age of the buffalo. The possible association of the polymorphism with the phenotypic values of milk yield, protein yield, fat yield, protein percentage and fat percentage at a statistical significance of 5% was tested. Three genotypes were obtained. The genotypes CC, CT and TT have the frequencies 0.29, 0.56 and 0.19, respectively. The allelic frequencies of C and T were 0.57 and 0.43, respectively. The results indicate that there is association of the SNP with milk yield ($P = 0.0104$), fat yield ($P = 0.0045$), protein yield ($P = 0.0031$), fat percentage ($P = 0.0403$) and protein percentage ($P = 0.0368$). It indicates that the SNP may be used as a molecular marker for the traits analyzed in dairy Murrah buffaloes. However, further analyses with a bigger number of animals are necessary to confirm the results obtained.

Key words: molecular marker, SNP, PCR-RFLP

716 Relationship between horn fly infestation and polymorphisms in cytochrome P450 and prolactin promoter genes in beef cows. A. R. Boyer*[1], M. A. Brown[2], M. L. Looper[3], A. H. Brown, Jr.[1], C. D. Steelman[1], and C. F. Rosenkrans Jr.[1], *[1]University of Arkansas, Fayetteville, [2]USDA-ARS, Grazinglands Research Laboratory, El Reno, OK, [3]USDA-ARS, Dale Bumpers Small Farms Research Center, Booneville, AR.*

Individual animal variation occurs regarding external parasite infestation in beef cattle. Our objective was to determine if horn fly infestations present on beef cattle are associated with the single nucleotide polymorphism (SNP; T318C) in the cytochrome P450 gene (CYP3A28) and the prolactin (PRL) promoter gene (C1286T). Unrelated beef cows of Angus (A), Brahman (B), and crossbred (BA and AB) breed types were used, and genotyped for the T318C SNP (n = 64) and the C1286T SNP (n = 43). Cattle were on either common bermudagrass (BG) or endophyte-infected tall fescue (E+) throughout the study. Individual horn fly counts on cows were recorded for 21 wks beginning in May. Horn flies were counted by walking around each cow at a set distance of 5 to 10 m. Horn fly numbers ≤25 were counted individually, while numbers >25 were counted in groups of 5. Chemical fly control containing coumaphos was used wk 9 and 16 of the study. Genomic DNA was prepared from buffy coat, and 3 genotypes for the CYP3A28 gene and PRL promoter gene were identified. Results found an effect of week occurred for both the T318C ($P < 0.0001$) and the C1286T ($P < 0.0001$) SNP. Homozygous thymine cows (TT) for T318C SNP had greater ($P < 0.0001$) numbers of horn flies (180.1 ± 10.9 flies) than heterozygous thymine-cystine (TC; 96.7 ± 12.4 flies) and homozygous cystine (CC; 53.5 ± 35.0 flies) cows. Cows homozygous CC for the C1286T SNP had greater ($P = 0.0025$) numbers of horn flies (207.7 ± 21.6 flies) than heterozygous CT (127.9 ± 14.6 flies) and homozygous TT (87.6 ± 27.3 flies) cows. A genotype x week interaction occurred for both the T318C ($P < 0.0001$) and C1286T ($P = 0.0018$) SNP. Cattle grazing E+ tall fescue tended to have fewer horn flies than those grazing BG for both the T318C (86.2 ± 22.4 vs. 134.0 ± 12.8 flies; $P = 0.06$) and C1286T (120.0 ± 18.5 vs. 162.1 ± 17.1 flies; $P = 0.10$) SNP. Different genotypes appear to have an effect on external parasite infestation observed on beef cows, and genetic selection of cows with these SNP could improve external parasite resistance in beef cattle.

Key words: horn fly, genotype, single nucleotide polymorphism

717 Gene expression analysis and fatty acid profiling in concentrate and pasture based beef finishing systems. J. W. Buchanan*[1], A. J. Garmyn[1], G. G. Hilton[1], D. L. VanOverbeke[1], Q. Duan[2], D. C. Beitz[2], and R. G. Mateescu[1], [1]*Oklahoma State University, Stillwater,* [2]*Iowa State University, Ames.*

Expression analysis of genes involved in lipogenesis and lipid desaturation provides understanding about the genetic component controlling intramuscular fatty acid profile in different finishing systems. The health advantages of grass finished beef compared with concentrate finished beef include increased monounsaturated fatty acids (MUFA), polyunsaturated fatty acids (PUFA), conjugated linoleic acid (CLA), and an improved omega-3 to omega-6 fatty acid ratio. Intramuscular (IM) samples were taken at slaughter from 100 heifers finished on a concentrate (CO) diet and 60 heifers finished on pasture (PA). Across treatments, CO heifers had a higher hot carcass weight and higher marbling score ($P < 0.05$) than PA heifers, but no significant differences were found in frame size and fatness due to hot carcass weight, rib eye area, marbling score, and yield grade within treatment. IM fatty acid profiles were characterized using gas chromatography fatty acid methyl ester analysis and data were analyzed using the PROC GLM procedure in SAS (SAS Institute Inc., Cary, NC). IM samples were sorted into healthy and unhealthy groups based on the atheroindex (AI) ($P < 0.001$), and 10 samples from each treatment (n = 20) were selected for gene expression analysis. Differences in fatty acid profile across treatments included a higher AI, and a lower omega-3 to omega-6 ratio, lower percent PUFA, and lower percent omega-3 fatty acids in CO compared with PA ($P < 0.05$). Total RNA was extracted from each sample and gene expression was quantified in real-time using SYBR Green RT-PCR detection. Data were normalized against the geometric mean of the most stable housekeeping genes β actin and RPS15A as determined by the BESTKEEPER software. The transcriptional regulator PPAR gamma was upregulated in PA vs. CO heifers ($P < 0.05$) by 5- and 6-fold in healthy and unhealthy AI groups, respectively. Significant upregulation in PA vs. CO heifers was also detected across AI groups ($P < 0.05$), where DGAT2, ADIPOQ, and FABP4 were upregulated 3-, 7-, and 26-fold in unhealthy vs. 1-, 2-, and 7-fold in healthy samples.

Key words: fatty acid profile, gene expression, grass finished beef

718 Expression analysis of key genes of bovine fat metabolism indicated correlated trans regulatory mechanisms in a bovine resource population segregating for two major genes affecting growth and lipid deposition. Ch. Kuehn*, C. Kalbe, R. Brunner, T. Goldammer, and R. Weikard, *Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany.*

Recently, the mutations NCAPG I442M and GDF8 Q204X were identified as major loci affecting growth and lipid deposition in an F2 resource population from Charolais and German Holstein. Therefore, the effects of both mutations on the expression of key genes in lipid deposition (ADIPOR1, FABP4, SCD and DGAT2) could be comparatively investigated on an identical genetic background. Additionally, genome-wide linkage studies were performed to identify further genomic loci with impact on the expression of those 4 genes involved in regulation of lipid metabolism, fatty acid transport and desaturation and triglyceride synthesis. Our study comprised 150 bulls, which had been generated by consistent application of embryo transfer during generation of the resource population and had been fed a semi ad libitum feed ration of concentrates and chaffed hay until slaughter at 18 mo of age. Tissue samples of skeletal muscle (M. longissimus) were taken immediately after slaughter and snap frozen for further gene expression analysis by quantitative real-time PCR analysis. All F2 bulls and all P0 and F1 ancestors were genotyped for the NCAPG I442M and GDF8 Q204X mutation as well as for 565 further genetic markers (SNPs, microsatellites) distributed across the entire genome. Association studies revealed a significant effect ($P < 0.05$) of the GDF8 Q204X mutation on the expression of the ADIPOR1, SCD, and DGAT2 gene. For the NCAPG I442M mutation, a significant effect was restricted to the SCD gene. This fits the previous observation that the GDF8 Q204X mutation had a larger effect on intramuscular fat deposition compared with NCAPG I442M. Further genome-wide linkage analyses searching for other QTL affecting the expression of the 4 investigated key genes of fat metabolism indicated a trans regulation of their transcription, because none of the QTL detected (most significant QTL for ADIPOR1: BTA12, FABP4: BTA22, SCD: BTA6, DGAT2: BTA1) was located on the chromosome harboring the respective target gene.

Key words: lipid deposition, eQTL, NCAPG

719 Sound and efficient designs and models for RNA-seq experiments with application in animal genomics. J. P. Steibel* and P. Reeb, *Michigan State University, East Lansing.*

Next generation RNA sequencing (RNA-seq) will become the method of choice for high throughput quantification of transcriptomes. In order for an RNA-seq experiment to produce meaningful results, a sound experimental design has to be matched with the corresponding analysis model. Consequently, the objective of this work is to introduce experimental designs and models of RNA-seq experiments with application in animal functional genomics. We separate the experimental design into 2 parts: a) the sampling scheme and b) the sequencing scheme and we show how to efficiently combine the 2 parts. Following features common across RNA-seq platforms, we consider lane effects and barcode effects as blocking factors. We show general design rules that result in efficient designs, but illustrate their use with 3 sampling schemes widely used in animal functional genomics. 1) Tissue differential expression, where RNA is extracted from T tissues in each of N animals, 2) Complete block design where K treatment are applied to N animals, but they are blocked in groups of size K and 3) Repeated measurement experiments, where K treatments are applied to each of N animals and RNA is extracted at S subsequent time points. We show sequencing schemes for the 3 experiments with or without resorting to bar coding. We present the appropriate analysis model using overdispersed Poisson likelihoods. When using a single level sampling scheme (experiments 1 and 2), publicly available R packages (e.g., edgeR, DGEseq) can be used to fit the required models. But in case of multilevel sampling designs (example 3), there is currently no software package available that would produce the required fit. We discuss alternatives (e.g., using SAS or R functions) and their main advantages and disadvantages to perform the analysis. While this technology is still novel and there are not many experimental data sets available, this paper addresses basic issues that should be considered before such data sets are generated to ensure that experimental and nuisance factors can be appropriately accounted for and disentangled to produce meaningful conclusions.

Key words: RNA-seq, experimental design, gene expression

720 Microbial and sensory evaluation of fresh Mozzarella cheese. B. Ganesan*, D. Irish, C. Brothersen, and D. J. McMahon, *Western Dairy Center, Department of Nutrition, Dietetics and Food Sciences, Utah State University, Logan.*

Commercial fresh Mozzarella cheese is made by direct acidification and stored dry or in water without salting. The cheese has a shelf life of ~6 wk, but usually develops off flavor and looses textural integrity by 4 wk, potentially due to the lack of salt that allows outgrowth of undesirable bacteria. We hypothesized that low salt promotes unwanted bacterial survival in fresh Mozzarella cheese thereby altering its quality and safety. To study the impact of salt on the microbial and sensory quality and the ability of pathogen-related bacteria to survive during refrigerated storage, we made fresh mozzarella cheese with high (2%) and low (0.5%) salt. Both cheeses were stored dry and the low salt cheese also in 0.5% brine of which one part was used for sensory evaluation and the rest for microbial studies. Consumers preferred the 1% salt dry cheese to the other cheeses ($P < 0.05$), but found no off flavors at 14 d storage in any cheese and also preferred a salad-style serving (cheese served with a cherry tomato marinated in balsamic vinegar) to fresh cheese. Descriptive panelists perceived higher levels ($P < 0.05$) of bitter, umami, brothy, and salty attributes in 1% salt dry cheese. Coliforms and psychrophiles were not detected in cheeses or brine over 9 wks. Standard plate counts remained at 100–300 cfu/gm up to 2 wks, but increased by 1,000–10,000-fold ($P < 0.05$) between 4 and 6 wks in all cheeses independent of salting, and coincides with the observed reduction in cheese quality. This showed that 2% salt was insufficient to control bacterial growth, and that slow-growing, cold- and salt-tolerant bacteria may survive and spoil fresh mozzarella cheese. *E. coli* and *Enterococcus faecalis* added to the 3 cheeses also increased by 100-fold ($P < 0.05$) over 90 d of storage. Interestingly, *E. coli* added to the cheese brine first grew in the brine by 100-fold ($P < 0.05$) before attaching to the cubes, whereas *Ent. faecalis* attached to the curd within 24 h and grew only in the cubes. These observations suggest that incident bacteria may survive and attach to curd by different mechanisms in fresh mozzarella cheese that need to be collectively addressed to reduce pathogen survival and spoilage.

Key words: fresh Mozzarella, safety

721 CheddarCyc: A database of Cheddar cheese flavor reactions and pathways. B. Ganesan* and K. Brown, *Western Dairy Center, Department of Nutrition, Dietetics and Food Sciences, Utah State University, Logan.*

Cheese flavor is a summation of all microbial enzymatic and chemically spontaneous reactions that sugars, proteins, and lipids and their degradation products undergo during cheese aging. To understand cheese flavor development mechanisms attributable to bacteria we currently host and actively maintain metabolic pathway databases for LAB involved in cheese flavor generation at the ProCyc webserver (www.usu.edu/westcent/procyc). However the flavor-related pathways are scattered among the individual bacterial databases, which also contain metabolic routes that do not generate flavor compounds. Alternately, a large number of chemical reactions that are not captured in bacterial metabolic databases, either spontaneous or yet unattributed to enzymes, also participate in flavor compound production. In the current format, metabolic databases do not unify the diverse routes of cheese flavor compound generation. To that end, we created a cheese flavor enzymatic and chemical reaction database that links uncharacterized compounds and their reactions to flavor development and microbial metabolism and additionally contains selected flavor compound-generating metabolic pathways of bacteria. The database called "CheddarCyc" contains information on ~100 known Cheddar cheese flavor compounds based on current knowledge from literature. Key mechanisms of flavor generation such as carbohydrate metabolism, amino acid metabolism related to Arg, aromatic, sulfur, and branched chain amino acids, mechanisms of free fatty acid generation, and individual reactions demonstrated in literature are connected together. The database provides a chemical context in our ongoing effort to define flavor profiles of Cheddar cheese. Similar databases that are specific to flavor compounds found in other cheeses can be reconstructed relatively quickly using this mechanism. This provides us a resource to comprehensively tackle flavor generation routes and discover solutions to preexisting issues on Cheddar cheese flavor chemistry and enzymology. CheddarCyc will be publicly available at ProCyc and will eventually house the vast majority of Cheddar cheese flavor compound reactions proposed to date.

Key words: Cheddar cheese, flavor, metabolism

722 New approaches to understand cheese ripening. S. Lortal*[1,2], V. Gagnaire[1,2], S. Jeanson[1,2], J. Floury[1,2], and M.-N. Madec[1,2], *[1]INRA, UMR1253, STLO, Rennes, France, [2]Agrocampus-Ouest, UMR1253, STLO, Rennes, France.*

Cheese ripening is usually described in terms of kinetics of proteolysis, lipolysis and aroma compound production, which provides an averaged view of ripening. However, after milk inoculation and rennet action, bacteria are immobilized as colonies into the curd and grow as such. This colonial distribution is a reality in all kind of cheeses. The efficiency of bacteria within these colonies to act on dairy matrices (gene expression and activity of the enzymes produced) will thus depend on local physico-chemical conditions, matrix structure, diffusion limitations and inter-colony distance. The ambition of our team is to understand the ripening mechanisms in situ at a microscopic scale level, considering the colonial distribution. For that purpose, the following fields were explored: i) to characterize the spatial distribution of bacterial colonies according to the level of inoculation by mathematical modelization and by in situ validation using confocal laser microscopy (Jeanson et al., 2011 Appl. Environ. Microbiol. doi:10.1128/AEM.02233-10); ii) to estimate the diffusion rate of small solutes in dairy matrices differing in composition and microstructure. Indeed diffusion of water and salt were extensively characterized (Floury et al., 2010 Dairy Sci. Technol. 90:477–508) but not the diffusion of small solutes which are crucial for the bacterial metabolic activity and the ripening reactions. Moreover, the impact of cheese composition and microstructure on this diffusion is far from being well understood. The diffusion coefficient of a small solute was estimated for the first time by a noninvasive way within a cheese matrix using new imaging approaches, the Fluorescence Recovery After Photobleaching and using fluorescent 4 and 20 kDa dextran molecules. iii) to reveal in situ bacterial enzymes within and around the colonies immobilised in cheese. Cell wall protease and intracellular peptidases were first detected in situ by immunofluorescent antibodies and confocal microscopy.

Key words: cheese ripening, bacterial colony, diffusion of solutes and enzymes

723 In situ proteolytic activity of *Lactobacillus helveticus* and stretchability of Swiss-type cheese. L. Sadat-Mekmene[1,2], R. Richoux[3], L. Aubert-Frogerais[3], M.-N. Madec[1,2], C. Corre[1,2], M. Piot[1,2], J. Jardin[1,2], S. Lortal*[1,2], and V. Gagnaire[1,2], *[1]INRA, UMR1253, STLO, Rennes, France, [2]Agrocampus Ouest, UMR1253, STLO, Rennes, France, [3]Actilait, Rennes, France.*

In contrast to other lactic acid bacteria, *Lactobacillus helveticus* can possess 2 cell-envelope proteinases (CEPs) called PrtH2 and PrtH (Genay et al. 2009, Appl. Environ. Microbiol.. 75:3238–3249; Sadat et al. 2011a, in press Int. J. Food Microbiol.). These CEPs exhibit different cleavage specificity on pure αs1-casein (Sadat-Mekmene et al., 2011b, Appl. Environ. Microbiol. 77(1) 179–186). The aim of this work was to investigate the proteolytic activity of *L. helveticus* strains in cheese matrix according to the number of their CEPs and the cheese stretchability. Two strains were selected, ITGLH77 and ITGLH1 which possess one CEP, PrtH2, and 2 CEPs, PrtH and PrtH2, respectively. The proteolysis was monitored during ripening: i) casein hydrolysis by urea-PAGE; ii) peptide pattern of the cheese aqueous extracts first by SDS-PAGE and second by RP-HPLC. Three chromatographic fractions were collected and peptides identified by RP-HPLC coupled on-line with tandem mass spectrometry. In parallel, the dynamic of stretchability of Emmental cheese was measured to determine the contribution of CEPs in its generation, since *L. helveticus* is known to enhance stretching properties in contrast to other lactobacilli, such as *L. delbrueckii* ssp. *lactis*. The microstructure of the strands of Emmental cheeses was observed by confocal laser scanning microscopy. The stretchability of Emmental was significantly higher in cheese manufactured with strain ITGLH77. By using Principal Component Analyses, the stretching properties were found to be correlated with the presence of peculiar peptides derived from primary proteolysis, hydrophobic peptides, containing more than 20 amino acid residues and derived from αs1-casein, which were accumulated in cheese manufactured using strain ITGLH77. The presence of these peptides suggest their less hydrolysis by this strain, in agreement with results observed in vitro (Sadat-Mekmene et al., 2011b), namely different cleavage specificity of CEPs PrtH et PrtH2 on pure αs1-casein.

Key words: cell envelope proteinase, *Lactobacillus helveticus*, Swiss-type cheese stretchability

724 Influence of Hofmeister salts on the textural and rheological properties of nonfat process cheese. J. A. Stankey* and J. A. Lucey, *University of Wisconsin, Department of Food Science, Madison.*

Hofmeister salts (HS) weaken or strengthen hydrophobic interactions of proteins resulting in salting in or salting out, respectively. Hydrophobic interactions also play a key role in casein particles and gels. In process cheese manufacture emulsifying salts (ES) are used to chelate Ca and disperse the insoluble casein matrix while heating. Since HS modify hydrophobic interactions we investigated the impact of HS on textural and rheological properties of nonfat process cheese (NFPC) made without ES. A directly acidified nonfat cheese base was made with citric acid (pH 5.6) and ripened for 7 d. Cheese was shredded and frozen until use. Two levels (0.1 or 0.3 M) of chaotropic (NaSCN) or kosmotropic (Na_2SO_4, NaCl) types of HS were blended with thawed, nonfat cheese. Cheese and HS were heated in a waterbath to 85°C and mixed using an overhead stirrer (6 min). Molten cheese was poured into plastic molds, sealed and stored (4°C) for 7 d before analysis. Small amplitude oscillatory rheological properties were measured while heating from 5 to 85°C. Moisture contents and pH of NFPC were ~55% and ~5.8, respectively. Calcium concentrations (475 mg/100 g) were similar in all NFPC. Sulfur content increased in NFPC made with increasing concentrations of NaSCN or Na_2SO_4. The NFPC made with 0.3 M NaSCN were shiny, stickier, had lower hardness, higher LT values (indicating higher meltability) and melt occurred at lower temperatures than other treatments. The NFPC made with 0.3 M Na_2SO_4 were tough, very viscous, had increased hardness values and lower LT values (less meltable). At 0.3 M concentrations, hardness increased in cheeses in the following order: NaSCN < NaCl < Na_2SO_4. Cheeses made with 0.3 M NaCl or Na_2SO_4 lost water during processing. Hydrophobic interactions increase with temperature during manufacture; the addition of kosmotropic HS strengthened these interactions resulting in "salting out" (water loss) and a firmer (less meltable) NFPC. Addition of chaotopic HS reduced hydrophobic interactions and resulted in weakened protein-protein bonds and thus created a softer (more meltable) NFPC network.

Key words: rheology, Hofmeister series, nonfat process cheese

725 Impact of reforming on low-fat cheese texture as influenced by pH. C. Akbulut* and J. A. Lucey, *Department of Food Science, University of Wisconsin, Madison.*

Grating of cheese and repressing it to "reform" its shape is an approach that could be used to improve the texture of excessively firm low-fat cheese. Our objective was to study the impact of pH on the properties of low-fat cheese that was reformed after grinding. Low-fat cheese bases having 4 different pH values were produced by direct acidification of milk to pH 6.2 with citric acid and altering the final pH by the addition of glucono-δ-lactone (0, 0.1, 0.3 and 0.4%) to curd, to obtain cheeses with pH values 6.2, 5.8, 5.5 and 5.3, respectively. Cheeses were stored for 2 wk at 4°C, and then ground and reformed by pressing ground cheese into plastic cups using a laboratory hydraulic press for 1 h at 20°C. They were kept at 4°C overnight and then removed from plastic cups, vacuum-sealed and stored for 1 wk before analysis. Hardness was determined at 80% compression. Dynamic moduli and loss tangent was measured during heating from 5 to 85°C. Melt profiles were obtained by the UW-Melt Profiler. Acid-base titrations were used to determine the amount of residual insoluble Ca in cheese. Reforming low-fat cheese reduced its hardness at all pH levels, however the decrease in hardness of high pH cheese was much greater than the decrease obtained when low pH cheese was reformed. As a result, the relatively harder texture of high pH low-fat cheese was softened to a level that could also be accomplished by pH reduction. Meltability increased slightly as a result of reforming. Fluorescence microscopy was used to observe the fusion in the contact region between 2 cheese slices that were held together at 4°C for 1 wk. The pH 6.2 cheese slices remained intact (little fusion). Reducing the cheese pH resulted in a greater fusion between slices. With a decrease in cheese pH, there was a decrease in the insoluble Ca content; cheese became more meltable and softer making it easier to reform. These results showed that reforming cheese with a lower pH didn't alter the texture as much as at high pH since most bonds appeared to reform on storage at low pH. The rubbery and firm texture of the low-fat cheese made at high pH was improved by reforming as the texture became shorter and softer.

Key words: low-fat cheese, texture, pH

726 Recovery of ω-3 fatty acids in Cheddar cheese curd and long-term stability of ω-3 fatty acids in whey powder. B. Ganesan*, C. Brothersen, and D. J. McMahon, *Western Dairy Center, Depart-*

ment of Nutrition, Dietetics and Food Sciences, Utah State University, Logan.

Full-fat Cheddar cheese was made with milk fortified with ω-3 fatty acids and the partitioning of ω-3 fatty acids into curd and whey was determined, along with flavor attributes of ω-3 fatty acid-containing whey powder over storage. ω-3 fatty acids from both animal and plant sources were incorporated into the milk. The encapsulated powder was added to cheese milk or the milled curd during dry salting. The oil form of ω-3 fatty acids was either mixed or homogenized oil in milk or cream, wherein the homogenized milk and cream constituted 10% of fat in cheese milk. The recovery of ω-3 fatty acids from the animal source was 90.5%, significantly higher ($P < 0.05$) than that of the plant source (80.3%). Homogenization provided similar recoveries of ω-3 fatty acids (90–93%, $P > 0.05$) for the 2 sources, whereas homogenized treatments were significantly different from non-homogenized treatments (79–83%, $P < 0.05$). Addition of encapsulated ω-3 fatty acids to the cheese curd during salting provided higher recovery (91–99%, $P < 0.05$) for both animal and plant sources and was the most efficient method of fortifying Cheddar cheese with ω-3 fatty acids. Whey collected during cheese making from the various fortification treatments was further dried into powder using a drum dryer and stored for 9 mo at 4°C or room temperature (18–22°C) to study changes in attributes perceived by a descriptive panel. Sweet taste was perceived higher ($P < 0.05$) at 3, 6, and 9 mo than at 0 mo and perceived at varying levels across the different cheese milk treatments. Bitter, salty, sour, brothy, cooked, and lactone/fatty acid flavor attributes were only perceived higher at 0 and 3 mo; whereas fishy flavor was discerned only at 6 and 9 mo, with all ω-3 fatty acid-incorporated whey powders scoring higher than the unincorporated control ($P < 0.05$). Notably, panelists scored the whey powders similarly for other attributes despite the whey powders containing different levels of ω-3 fatty acids. Commercial preparations of ω-3 fatty acids appear to be prone to develop off flavors in whey powder and lose acceptability during long-term storage.

Key words: Cheddar cheese, omega-3 fatty acids, whey powder

727 Rheology, microstructure and quality of curd made from buffalo milk: A comparison with ultrafiltered cows' milk. I. Hussain*, A. S. Grandison, and A. E. Bell, *Department of Food and Nutritional Sciences, University of Reading, Reading, Berkshire, UK.*

Rennet induced curds were made from buffalo, cows' and ultrafiltered cows' milk (UF cows' was concentrated such that it has chemical composition approximately equivalent to buffalo milk). These milk samples were compared on the basis of rheology, physicochemical characteristics and curd quality. The ionic and soluble calcium contents were similar in all milk samples. The total and casein bound calcium were higher in UF cows' milk than untreated cows' milk, and found to be lower than in buffalo milk. This is due to concentration of colloidal part of milk (casein) during the ultrafiltration process. The rennet coagulation time was almost the same in UF cows' and buffalo milk while it was higher in cows' milk. The dynamic moduli (G', G") values were higher in buffalo and UF cows' milk than cows' milk 90 min after chymosin addition. The loss tangent was the same in UF cows' and buffalo milks and has a lower value as compared with cows' milk. The frequency profile (0.1–10Hz) was recorded 90 min after the enzyme addition; all of treated samples found to be weak viscoelastic frequency dependent gel. The cows' curd was weaker (dynamic moduli) than buffalo and UF cows' curds. The yield stress was measured 95 min after the enzyme addition, and attained a higher value in buffalo milk as compared with other milk samples. The curd yield, curd moisture and curd fat retention were found to be higher in UF cows' milk than for buffalo and cows' milk. The minimum whey fat losses occurred in UF cows' milk. The total mineral contents were also higher in UF cows' milk than in the buffalo and cows' milk. The electron micrographs showed that sizes of casein micelles and fat globule were different in the 2 types of milk. The curd structure appeared to be more "dense" in buffalo milk than cows' milk.

Key words: rheology, curd, ultrafiltration

728 Effect of milk processing on the MFGM proteins and phospholipids. X. ElÍas-Argote* and R. Jiménez-Flores, *California Polytechnic State University, San Luis Obispo.*

MFGM phospholipids (PLs) and proteins have been ascribed antimicrobial and antiviral properties, as well as anticancer and antihypercholesterolemic activities. 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 applied analytical and proteomic techniques to analyze the protein and lipid profile in the MFGM throughout milk processing. Milk was collected/treated at 6 different points: before reaching the storage unit (35°C), storage temperature (4°C), batch, high temperature short time (HTST), and ultra high temperature (UHT) pasteurizations, and by pulsed light treatment. MFGM proteins were analyzed using 1D and 2D-PAGE and LC-MS. Over 117 proteins were identified using HPLC-MS, and their relative quantities at different motilities in the SDS gel were analyzed using Scaffold 3 and Delta2D_4. As the heat treatment increased, more protein aggregates were observed, especially in the UHT milk, where caseins, lactoferrin, and guanine nucleotide-binding proteins were detected in the high molecular weight region (>150 kDa). Also, low heat at a prolonged time (63°C, 30min) resulted in more MFGM proteins being released into the skim milk. In addition, the protein profile for the light pulse treatment was similar to the 4°C and HTST samples. In contrast, variation in the phospholipid composition of the membrane throughout milk processing was not statistically significant ($P > 0.05$). From this study, the best method to preserve milk bioactivity might be HTST, which reduces pathogenic microorganisms and still preserves most of the MFGM proteins. In regard to functionality, formation of aggregates might reduce the full potential of a nutraceutical MFGM protein, thus more studies are needed to create processing methods that retain the proteins' native state, including the consideration of pulsed light treatment as a new pasteurization method.

Key words: MFGM, proteomics, phospholipids

729 Focus on milk fat globule membrane proteins from goat milk. C. Cebo*[1], C. Henry[2], S. Truchet[3], F. Bouvier[4], H. Caillat[5], and P. Martin[1], *[1]INRA, UMR1313 Unité Génétique Animale et Biologie Intégrative, Jouy-en-Josas, France, [2]INRA, Plateforme PAPSSO (Plateforme d'Analyse Protéomique Paris Sud Ouest), F-Jouy-en-Josas, France, [3]INRA, Unité Génomique et Physiologie de la Lactation, Jouy-en-Josas, France, [4]UE332 Domaine de Bourges, Osmoy, France, [5]INRA, UR631 Station d'Amélioration Génétique des Animaux, Castanet-Tolosan, France.*

Fat is present in milk as droplets of triglycerides surrounded by a complex membrane deriving from the mammary epithelial cell and called the Milk Fat Globule Membrane (MFGM). In-depth proteomic studies have been published for bovine MFGM proteins. However, to date, only sparse studies exist on MFGM proteins from non-cow milks. The objective of this study was thus to investigate the protein composition of the goat Milk Fat Globule Membrane. MFGM proteins from goat milk were separated by 6% and 10% SDS-PAGE and Coomassie or Periodic Acid / Schiff (PAS) stained. Most of MFGM proteins (mucin-1, fatty acid synthase, xanthine oxidase, butyrophilin, lactadherin and adipophilin) already described in cow milk were identified in goat milk using peptide mass fingerprinting. A prominent difference between the cow and the goat species was demonstrated for lactadherin. Indeed, we have shown that lactadherin from goat milk appears as a single polypeptide chain in 6% SDS PAGE whereas 2 polypeptide chains are easily identified in cattle. In addition, goat MFGM proteins were subjected to 1D-LC-MS/MS (one dimensional gel coupled to tandem mass spectrometry) analysis. Twenty-five µg MFGM proteins were separated in 10% SDS-PAGE and Coomassie stained. The lane was divided in 20 slices and each slice was digested by trypsin and subjected to LC/MS/MS analysis. This approach led us to identify - with at least 2 unique peptides (Bos Taurus Database)- more than 160 proteins associated with the goat Milk Fat Globule Membrane. Interestingly, integrative analysis of MFGM-associated proteins using DAVID Bioinformatics Resources demonstrated that identified biological processes are not only connected with lipid metabolic processes or exocytosis-related biological processes, but also with G-protein receptor signaling pathway, translation, or regulation of apoptosis, as previously demonstrated for MFGM proteins from bovine milk. These findings may help in the understanding of lipid droplet formation in the goat species, where an apocrine mechanism for milk secretion is hypothesized.

Key words: milk fat globule membrane, goat, lactadherin

730 Identification of major milk fat globule membrane proteins from pony mare′s milk highlights the molecular diversity of lactadherin across species. C. Cebo*[1], E. Rebours[1], C. Henry[2], S. Makhzami[1], P. Cosette[3], and P. Martin[1], *[1]UMR1313 Unité Génétique Animale et Biologie Intégrative, Jouy-en-Josas, France, [2]INRA, Plateforme PAPSSO (Plateforme d'Analyse Protéomique Paris Sud Ouest), Jouy-en-Josas, France, [3]UMR6270 CNRS, Université de Rouen, Plateforme Protéomique de l'IFRMP23, Mont-Saint-Aignan Cedex, France.*

Although numerous studies have been devoted to the soluble fraction, namely caseins and whey proteins, to date, little is known about the milk fat globule membrane (MFGM) fraction from mare′s milk. Using mass spectrometry, most of MFGM already described in cow or goat milks were identified in mare′s milk. Prominent differences through species were highlighted for lactadherin. Indeed, whereas one or 2 polypeptide chains are respectively identified by peptide mass fingerprinting matrix-assisted laser desorption/ionization-time of flight (PMF MALDI-TOF) analysis for caprine and bovine lactadherin, lactadherin from mare′s milk appears as 3 polypeptide chains in 6% SDS PAGE. Digestion of MFGM proteins from mare′s milk with Peptide N-glycosidase F (PNGase F) revealed that the existence of 3 distinct polypeptide chains for equine lactadherin could not be solely explained by differential N-glycosylation of a single polypeptide chain. On the other hand, polymerase chain reaction (PCR) experiments on lactadherin transcripts isolated from milk fat globules revealed that splicing events occur on lactadherin from mammary gland with the existence of 2 distinct lactadherin transcripts in the horse species. Cloning and sequencing of both lactadherin transcripts revealed the existence of a cryptic splicing site usage located at the end of exon 5 of equine lactadherin and liquid chromatography coupled to tandem mass spectrometry (LC-MS/MS) analyses confirmed the existence of 2 lactadherin variants in the MFGM from mare′s milk. Interestingly, this cryptic splicing event led to the suppression of a putative N-glycosylation site in the protein. Whatever, we demonstrate here that expression of lactadherin is species-dependent, therefore questioning about of the precise function of these different isoforms in mammary gland biology across species.

Key words: milk fat globule membrane, lactadherin, cryptic splicing site

731 Effect of methane emission reducing diet on coagulation properties of bovine milk. A. Aprianita*[1], O. N. Donkor[1], P. J. Moate[2], M. J. Auldist[2], J. S. Greenwood[2], W. J. Wales[2], and T. Vasiljevic[1], *[1]School of Biomedical and Health Sciences, Faculty of Health, Engineering and Science, Victoria University, Melbourne, Victoria, Australia, [2]Department of Primary Industries, Ellinbank, Victoria, Australia.*

The effects of methane emission reducing diets on coagulation properties of bovine milk were investigated. The treatment diets included supplementation with fat, tannin or combination of fat and tannin to a normal diet which also served as a control. The obtained milk samples were skimmed, standardized (C/*F* = 0.7), homogenized (25 MPa), and heat treated (60°C; 30 min). Subsequently, glucono-delta-lactone (GDL) (2.2%) or commercially available rennet (0.2 mL/L) was added to induce gel formation. For rennet-gel, calcium chloride (0.02%) was added before rennet addition. Both types of gel were analyzed for rheological parameters (small amplitude oscillatory and large deformation), syneresis, permeability, and microstructural characteristics. This study indicated that fat or tannin supplementation could improve gelatinization characteristics of acid milk gel by increasing storage modulus (G'), gel hardness and reducing time of gelatinization. Addition of tannin enhanced the elastic property of gel greater in comparison to that of fat; while combination of fat-tannin did not alter G' value. Supplementation of fat, tannin, or combination of fat and tannin slightly increased syneresis of acid milk gel. This was confirmed by shift angle and permeability values. The presence of fat during rennet induced coagulation had a substantial impact on the properties of the gel. Addition of fat alone or in combination with tannin increased G' and reduced gelation time. In contrast, tannin supplementation impaired gelatinization by reducing G' and increasing gelation time. All types of diet also slightly increased syneresis of milk gel, with tannin giving the highest impact. This study showed that milk obtained from cows fed a methane emission reducing diet had altered coagulation properties that were apparently dependent on the supplement.

Key words: methane emission reducing diet, milk properties, coagulation

732 Development of a method to determine the susceptibility of raw milk to oxidation. J. K. Amamcharla* and L. E. Metzger, *Midwest Dairy Foods Research Center, Dairy Science Department, South Dakota State University, Brookings.*

The initial quality of raw milk plays a critical role in the consumer acceptability of pasteurized milk. In recent years especially in the Midwest region, numerous cases have been reported where pasteurized milk is susceptible to spontaneous oxidation. The objective of the present work was to investigate the applicability of Ferric Reducing Antioxidant Power (FRAP) assay for identification of raw milk that are susceptible to oxidation. In this study, the FRAP assay was modified for analysis of raw milk. A FRAP working reagent consisting of 300 mmol/L of acetate buffer (pH 3.6), 20 mmol/L of ferric chloride, and 10 mmol/L of 2, 4, 6-tripyridyl-s-triazine made up in 40 mmol/L of hydrochloric acid was used. All 3 solutions were mixed in the ratio 10:1:1. To measure the FRAP value, 0.3 mL of milk was mixed with 4.5 mL of FRAP reagent and incubated at 37°C for 4 min. After the incubation, the sample was filtered using a 0.45µm syringe filter to remove precipitated protein. Absorbance at 593 nm was measured on the filtrate relative to the FRAP reagent as a blank. The FRAP value was calculated using ferrous sulfate calibration standards (50–600µ mol/L). Raw milk samples were collected from 6 individual cows. Each of the 6 samples was divided into 4 sub-samples. Three of the sub-samples were spiked with either 0.1 ppm of copper, 7.5 IU/quart of vitamin E, or both. The remaining fourth sub-sample served as a control. Each of the sub-samples was again divided into 3 equal parts and kept refrigerated. On each experimental day, one sub-sample was withdrawn and analyzed using the FRAP assay. The data was analyzed as repeated measures design using the GLM procedure in SAS. The treatment (presence or absence of copper or vitamin E), time and their interaction significantly ($P \ll 0.05$) influenced the FRAP value of raw milk. Moreover, the average percent reduction in FRAP value by the end of 48 h was found to be 27, 54, 28, and 47% for control, copper, vitamin E, and copper + vitamin E spiked samples, respectively. Overall the FRAP assay shows potential in the identification of milks susceptible to oxidation.

Key words: milk oxidation, ferric reducing antioxidant power (FRAP)

733 Measurement of a milk gelation time constant using laser-scanning fluorescence confocal microscopy and image processing techniques. R. Hennessy*[1] and R. Jimenez-Flores[2], *[1]Cal Poly Biomedical Engineering, San Luis Obispo, [2]Cal Poly, DPTC, San Luis Obispo.*

The gelation kinetics of milk can dictate how nutrients are absorbed after ingestion and are therefore important when determining the nutritional benefit of a dairy product. Current methods to measure gelation kinetics, such as near-infrared spectroscopy and rheology, are destructive and only provide one-dimensional data, while other methods, such as the Berridge clotting time method, are subjective because they depend on an operator's skill. A 2-dimensional, non-destructive, objective measurement technique is needed to accurately quantify the gelation kinetics of milk. The purpose of the present study was to investigate the ability of laser-scanning fluorescence confocal microscopy (LSFCM) to measure gelation kinetics. In this study, a mixture of raw milk and chymosin was imaged using LSFCM. The milk was stained with the fluorescent markers Nile red, which stains lipids, and fast green FCF, which stains proteins. Once chymosin was added to the raw milk, images were captured every 5 seconds for 30 minutes. Because gelation causes the milk to change from a liquid to a solid, the instantaneous gelation rate could be estimated by calculating the mean difference between successive images (R). As the milk begins to gel, the movement of the lipids and proteins eventually ceases, and the mean difference between successive frames eventually reaches zero. R was plotted versus time and fit to the curve B=e exp-kT[Ch]t, where B is the initial value of R, T is the temperature of the milk at the time the images were acquired, [Ch] is the concentration of chymosin, t is the time, and k is the gelation time constant of the milk. The gelation time constant, k, was then used to characterize the gelation kinetics. Because this method is able to account for the initial rate of the gelation process, the chymosin concentration, and the temperature when calculating the gelation time constant, it shows promise as a technique to measure and compare the intrinsic gelation characteristics for different milk varieties.

Key words: milk coagulation, gelation kinetics, confocal microscopy

734 Mid-infrared predictions of lactoferrin content in bovine milk. H. Soyeurt*[1,2], C. Bastin[1], F. Colinet[1], V. Arnould[1,3], D. Berry[4],

E. Wall[5], N. Gengler[1,2], P. Dardenne[6], and S. McParland[4], *[1]University of Liège, Gembloux Agro-Bio Tech, Animal Science Unit, Gembloux, Namur, Belgium, [2]National Fund for Scientific Research, Brussels, Brussels, Belgium, [3]CONVIS Herdbuch, Ettelbruck, Luxembourg, [4]Animal and Grassland Research and Innovation Centre, Teagasc, Fermoy, Cork, Ireland, [5]Animal and Grassland Research and Innovation Centre, Teagasc, Penicuik, Midlothian, UK, [6]Agricultural Walloon Research Centre, Quality Department, Gembloux, Namur, Gembloux.*

Lactoferrin (LF) is a glycoprotein present in milk and active in the immune system of cows and humans. Therefore, an inexpensive and rapid analysis to quantify this protein is desirable. A previous study reported the potential to quantify LF from the mid-infrared (MIR) spectrometry from 69 milk samples. Through the European Robust-Milk project (www.robustmilk.eu), 3,606 milk samples were collected in Belgium, Ireland, and Scotland from individual cows and analyzed using a MIR MilkoScanFT6000 spectrometer. Milk LF content was quantified using ELISA in duplicate. Average ELISA data with a CV lower than 5% were used. After the detection of spectral and ELISA outliers, the calibration set contained 2,499 samples. An equation to predict LF content from MIR was developed using partial least squared regression. A first derivative pre-treatment of spectra was used to correct the baseline drift. To improve the repeatability of the spectral data, a file which contained the spectra of samples analyzed on 5 spectrometers was used during the calibration. The lactoferrin mean was 159.28 mg/l of milk with a SD of 97.21 mg/l of milk. The calibration (C) coefficient of determination (R^2) was equal to 0.73 with a standard error (SE) of calibration of 50.54 mg/l of milk. A cross-validation (CV) was used to assess the robustness of the equation. R^2 CV was 0.72 with a SE-CV of 51.16 mg/l of milk. An external validation (V) was conducted on 150 milk samples collected in Belgium. The SE of prediction (SEP) was 59.17 mg/L of milk. The similarity between R^2 C and R^2CV as well as between SE-C and SE-CV and between SE-CV and SEP confirms the equations developed are robust. The correlation between predicted and measured LF values was 0.71. This lower value compared with the one obtained from the calibration set (0.85) could be explained by the low ELISA reproducibility (16.24% ± 25.51%). If the developed equation is used to clean the validation data set, a total of 16 samples can be deleted. The validation coefficient for these 134 samples increased to 0.82. From these results, the developed equation could be used for screening the dairy cow population for breeding purposes.

Key words: milk, lactoferrin, infrared

735 First assessment of diffusion coefficients in model cheese by fluorescence recovery after photobleaching (FRAP) analysis. J. Floury*[1,2], M. N. Madec[2], M. H. F. Famelart[2], S. Jeanson[2], and S. Lortal[2], *[1]Agrocampus Ouest, UMR1253, Rennes, France, [2]INRA, UMR1253, Rennes, France.*

In cheese technology, mass transfer of solutes like salt, moisture and metabolites, is very important for the final quality of cheese, through the control of the brining and ripening processes. Numerous studies have reported salt and water transfer in cheese, but very few have dealt with the mass transfer properties of other solutes in cheese. Most of the reported diffusion coefficients have been obtained by macroscopic and destructive methods. The objective of the study was to develop, for the first time, the FRAP technique that allows in situ measurements of diffusion properties at the microscopic scale inside cheese. The effect of the matrix microstructure on mass transfer properties of small solutes was also studied. A model matrix based on ultrafiltrated milk, mimicking soft-type cheese, was used. Its structure was modified by adding gelatine and analyzed by confocal microscopy and rheological measurements. Two different sizes of FITC-dextran molecules (4 and 20 kDa) were chosen as models of small migrant solutes. Diffusion coefficients were estimated with a new modeling approach which allows to take into account diffusion of the molecules during the bleach phase. The two FITC-dextrans were able to migrate in the model cheese network, but their mobility is reduced compared to water: diffusion coefficient values were equal to 68 ±9 $\mu m^2/s$ for the 4kDa and 23±3 $\mu m^2/s$ for the 20kDa dextran. The composition of the matrix has a great influence on the mass transfer properties. The diffusion coefficients of the dextrans were reduced by a factor 3 in the model cheese with gelatin. This result was explained by structural measurements: gelatin led to a more heterogeneous microstructure than the UF model cheese that increased the global length path of the migrating solutes. This study shows the power and the potentiality of the FRAP technique to study mass transfer properties of fluorescent solutes in complex food matrices such as cheeses.

Key words: mass transfer, FRAP, modeling

736 Repeated transport influences feed intake, but not feed efficiency in Holstein calves. A. L. Adams*, G. A. Holub, T. H. Friend, A. J. Krenek, S. M. Garey, C. L. Terrill, and M. J. Carter, *Texas A&M University, College Station.*

Previous studies have determined that stress causes decreases in feed intake and efficiency in cattle, but the effect of repeated transport on these parameters has not been well studied. This study determined how repeated transport affected feed intake and growth in calves. Thirty-six 4-mo-old Holstein steer calves were housed in groups of 6 with each group randomly assigned to either transport (T) or control (C) treatments. Each calf was assigned to an individual feed bunk and feed intake was recorded daily. Transported and control calves did not have access to feed during treatment. Calves were transported for 6 h in their group of 6 in a 7.3 m x 2.4 m goose-neck trailer divided into 3 compartments, at an average density of 0.87 m^2/calf, every 7 d for 5 consecutive wk. Feed intake was analyzed as a repeated measure in an autoregressive covariance mixed model ANOVA. Average daily gain (ADG) and feed efficiency were analyzed using a diagonal mixed model ANOVA. Control calves had a higher feed intake than transported calves overall (C: 7.29 ± 0.23 kg, T: 6.91 ± 0.23 kg, P = 0.012), on the day of treatment (C: 6.78 ± 0.43 kg, T: 6.01 ± 0.43 kg, P = 0.0074), and the day after treatment (C: 7.83 ± 0.45 kg, T: 7.08 ± 0.45 kg, P = 0.015). On days of treatment, feed intake for transported calves significantly decreased during wk 2, but increased with each successive transport (P < 0.0001). Overall, control calves had higher ADG than transported calves (C: 1.53 ± 0.12 kg/day, T: 1.36 ± 0.12 kg/day, P = 0.024). The largest difference in ADG occurred during wk 2 (C: 1.69 ± 0.41 kg/day, T: 1.10 ± 0.41 kg/day, P = 0.031). Transported calves tended to have decreased feed efficiency during wk 2 and 3, but increased feed efficiency during wk 4 and 5 (P = 0.072). These results suggest that calves exposed to repeated transport may decrease feed intake as an initial response to stress, however, overall feed efficiency is not affected and calves may quickly acclimate to repeated transport.

Key words: calf, feed intake, transport

737 Effects of serum protein-based arrival formula and serum protein supplement (Gammulin) on plasma metabolites in transported dairy calves. A. Pineda*[1], J. K. Drackley[1], J. M. Campbell[2], and M. A. Ballou[3], *[1]University of Illinois, Urbana, [2]APC Inc., Ankeny, IA, [3]Texas Tech University, Lubbock.*

Adequate nutrition is important to provide all nutrients for proper health and growth of young calves, especially in the presence of stressors like cold and transport. Serum protein products have been proposed to improve health and diminish effects of stress in dairy calves. Previously we reported that a commercial serum protein supplement (G; Gammulin, APC Inc.) in milk replacer decreased mortality (P = 0.007) in transported male calves. The aim of this portion of the study was to assess the effects of a serum protein-based arrival formula (AF) and use of G in milk replacer on plasma indicators of nutritional adequacy and acute-phase response. Nine-3 male Holstein calves were stratified by arrival BW and plasma protein, and then randomly assigned to 1 of 4 treatment groups. Treatments were 1 = control electrolyte, milk replacer with G (n = 24); 2 = control electrolyte, milk replacer without G (n = 25); 3 = AF, milk replacer with G (n = 22); and treatment 4 = AF, milk replacer without G (n = 22). At first feeding, calves were fed either AF or a control electrolyte solution. Six h later, 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). Blood samples were taken at d 0 (before treatments), 2, 7, 14, and wk 4. Calves remained in the experiment until d 56, below the low critical temperature. Data were analyzed using the MIXED procedure of SAS. IgG concentrations at d 0 were not different (P > 0.17) among treatments. Cortisol tended to be greater (P = 0.06) for calves that received AF. Concentrations of haptoglobin, acid-soluble protein, albumin, and zinc did not differ among treatments. Supplementation with G resulted in greater total protein (P = 0.04) and urea N (P = 0.01) in plasma at wk 4 (2 wk after G supplementation ended). Despite the marked reduction in mortality of transported cold-stressed male calves fed the serum protein product, indicators of acute-phase response were not affected; however, protein status of calves may have been improved.

Key words: calf, acute phase response, serum protein

738 Digestive function and plasma oxidative status of intra–uterine growth retarded fully weaned piglets. J. Michiels*[1,3], M. De Vos[2], J. Missotten[3], A. Ovyn[3], S. De Smet[3], and C. Van Ginneken[2], *[1]Faculty of Biosciences and Landscape Architecture, University College Ghent, Ghent, Belgium, [2]Laboratory for Veterinary Anatomy, Embryology and Pathology, Department of Veterinary Sciences, University of Antwerp, Wilrijk, Belgium, [3]Laboratory for Animal Nutrition and Animal Product Quality, Department of Animal Production, Ghent University, Melle, Belgium.*

Intra–uterine growth retarded (IUGR) pigs, relative to normal birth weight (NBW) littermates, have lower birth weights and vitality scores, both of which are associated with a higher incidence of postnatal mortality and a lower growth rate in surviving IUGR pigs. To better understand developmental differences, digestive function and plasma oxidative status of fully weaned IUGR and NBW pigs were studied. Newborns from 13 hyper–prolific sows were weighed. At weaning (26.3 ± 1.2 d after parturition) pairs (n = 21) of IUGR and NBW littermates were selected and fed a commercial starter diet until sampling day (22.3 ± 4.3 d post-weaning). An IUGR piglet was defined as having a birth weight <1 kg and < mean litter birth weight – 1.5 SD. For each piglet 97 variables were determined including anatomy of digestive organs, digesta characteristics, small intestinal morphology, secretory and absorptive capacity, barrier function, brush–border enzyme activities, cytokines and density of growth-factor receptors, serum IGF-I, and plasma oxidative status. Data were analyzed using the paired Student′s T-test (continuous variables) or the Wilcoxon rank test (categorical). Few parameters showed significant differences. However, in the IUGR pig, the structural and functional maturation of the digestive tract post–weaning was delayed: lower small intestinal weight to length ratio (P < 0.001) due to a thinner Tela submucosa and Tunica muscularis (both P < 0.001) and a higher numerical secretory capacity in the distal jejunum. These observations might be a consequence of lower circulating IGF–I concentrations (126 ± 43.7 vs. 152 ± 44.9 ng/mL, P = 0.034 for IUGR and NBW, respectively) and a lower density of IGF–I receptors in proximal jejunal tissues (P < 0.05). Additionally, the plasma antioxidant capacity was lower for the IUGR pigs (ferric reducing ability, 106 ± 14.4 and 114 ± 9.7 μmol Fe^{2+}/L, P = 0.042 and glutathione-peroxidase enzyme activity, 0.29 ± 0.054 and 0.33 ± 0.047 U, P = 0.001 for IUGR and NBW, respectively). The

described changes in fully weaned IUGR pigs resemble those reported for IUGR neonates.

Key words: intra-uterine growth retardation, gastrointestinal tract, pig

739 Effect of dietary energy manipulation on mares and their foals: Glucose and insulin dynamics. 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, North Dakota State University, Fargo.*

To investigate the effect of dietary DE manipulation of mares in the last third of pregnancy on mare and foal glucose and insulin dynamics, 30 Quarter Horse mares (538 to 695 kg BW and 4 to 19 yr) were blocked by expected foaling date. All mares were allowed ad libitum access to bermudagrass (*Cynodon dactylon*) hay and randomly assigned within block to dietary treatment: forage (F), or forage + grain (FG; grain fed at 0.75% BW as-fed). Treatments began 110 d before expected foaling date and terminated at parturition. A modified frequent sampling i.v. glucose tolerance test (FSIGT) was performed on mares 20 d before expected foaling date and on foals at 80 and 160 d of age. Jugular catheters were placed 1 h before FSIGT, and horses were allowed ad libitum access to bermudagrass hay and water throughout. A baseline plasma sample was harvested, then glucose bolus of 0.3 g/kg BW administered. An insulin bolus of 30 mU/kg BW was given 20 min after the glucose bolus. Blood samples were harvested at 1, 2, 3, 4, 5, 6, 7, 8, 10, 12, 14, 16, 19, 22, 23, 24, 25, 27, 30, 35, 40, 50, 60, 70, 80, 90, 100, 120, 150, and 180 min into tubes containing sodium heparin, immediately placed on ice, and centrifuged within 20 min. Glucose concentrations were analyzed using a colorimetric assay and insulin concentrations determined using a commercial RIA kit. All data were analyzed using the PROC MIXED procedures of SAS. Mare glucose area under the curve (AUC) was greater for FG compared with F ($P < 0.01$). Mare insulin AUC and peak insulin were also greater for FG compared with F ($P \leq 0.05$). Foal glucose AUC and peak glucose were not influenced by maternal treatment ($P \geq 0.82$), but both increased with age ($P \leq 0.05$). Foal insulin AUC and peak insulin were influenced by maternal treatment with foals from FG mares having greater peak insulin compared with foals from F mares ($P \leq 0.10$ and $P \leq 0.05$, respectively). An influence of age was observed on foal insulin AUC ($P \leq 0.05$), with all foals decreasing from d 80 to d 160. In summary, dietary treatments affected both mare and foal glucose and insulin dynamics.

Key words: glucose, insulin, maternal nutrition

740 Expression of key transcription factors during differentiation of equine bone marrow mesenchymal stem cells into osteoblast cells. E. R. Ackell*[1], A. Sanchez[2], C. Mora[1], S. A. Zinn[1], T. A. Hoagland[1], and K. E. Govoni[1], *[1]Department of Animal Science, University of Connecticut, Storrs, [2]Cummings School of Veterinary Medicine, Tufts University, North Grafton, MA.*

A novel method to improve fracture healing in horses is the use of equine bone marrow mesenchymal stem cells (eBMSC). Additional research is needed to identify optimal culture conditions and determine the mechanisms involved in regulating eBMSC differentiation into osteoblasts. We hypothesize that eBMSC have greater proliferation potential in allogenic serum and expression of key transcription factors is required for optimal differentiation. The eBMSC were isolated from the sternum of 3 Morgan horses (3.4 ± 0.3 yr of age). Cells were treated with fetal bovine serum (FBS) or horse serum (HS) and cell proliferation was determined by alamarBlue assay and bromodeoxyuridine (BrdU) incorporation. To induce osteoblast differentiation, cells were incubated with L-ascorbic acid-2-phosphate and glycerol-2-phosphate in the presence or absence of human bone morphogenetic protein 2 (hBMP-2), dexamethasone (DEX), or both. Alkaline phosphatase (ALP) activity, an indicator of osteoblast differentiation, was determined by ELISA in these cultures. Total RNA was isolated from cells at d 0, 3, 6, 9, 12, 15, and 18 of culture to determine expression of RUNX2 and Tbx3 using real-time RT-PCR. Data were analyzed by ANOVA using SAS and expressed as mean ± SE. Relative to control (CON) (serum-free media), FBS and HS increased cell number (133 ± 5 and 116 ± 5%, respectively; $P < 0.001$) and BrdU incorporation (173 ± 16 and 172 ± 16%, respectively; $P < 0.001$). Treatment with DEX (1,638 ± 38%; $P < 0.001$), but not hBMP-2 ($P > 0.05$) increased ALP activity compared with CON. Osteocalcin expression increased 260-fold by d 18 of culture ($P < 0.001$) demonstrating differentiation into osteoblasts. By d 6 of culture RUNX2 expression increased 3-fold ($P < 0.001$). Tbx3, a gene involved in regulating osteoblast function, increased 1.8-fold at d 3 ($P < 0.01$), however expression was 4-fold less at d 18 ($P < 0.01$). In summary, FBS induced greater proliferation of eBMSC, DEX is essential for differentiation into osteoblast cells, and inhibition of Tbx3 may be required for optimal differentiation of eBMSC.

Key words: bone marrow mesenchymal stem cell, osteoblast, transcription factor

741 Inter-relationship of BW with linear body measurements in Hissardale sheep at different stages of the life cycle. M. Abdullah*, U. Younas, J. A. Bhatti, T. N. Pasha, M. Nasir, and M. A. Jabbar, *University of Veterinary & Animal Sciences, Lahore, Punjab, Pakistan.*

Determining animal live BW, linear body measurements, and their inter-relationship and correlation is imperative for determining genetic potential, breed standards, and improved breeding programs for greater meat production. Hissardale is the only fine wool sheep breed maintained in Pakistan and developed by crossing exotic Merino with a local carpet wool sheep Bikaneri. Monthly BW data from 314 Hissardale sheep and linear body measurements including heart girth (HG), height at wither (HAW), body length (BL), ear length (EL), ear width (EW), neck length (NL), neck width (NW), tail length (TL), and tail width (TW) were analyzed after random selection at the Livestock Experiment Station, Jahangirabad, Khanewal, Pakistan to determine the appropriate model for estimating BW at different ages of life cycle including pre-weaned and post-weaned sheep. Animals were categorized according to their age (≤6, 7 to 12, 13 to 18, 19 to 24, and > 24 mo). The BW (mean ± SD) of animals was found to be 10.87 ± 1.82, 16.40 ± 1.40, 21.04 ± 1.44, 25.57 ± 2.94 and 47.10 ± 4.41 kg in all age groups (≤6, 7 to 12, 13 to 18, 19 to 24, and > 24 mo, respectively). Body weight was found to be significantly ($P < 0.001$) and positively correlated with HAW for all 5 age groups (0.79, 0.85, 0.67, 0.73, and 0.54, respectively), BL (0.69, 0.83, 0.53, 0.82, and 0.46, respectively) and HG (0.58, 0.85, 0.70, 0.76, and 0.42, respectively). However, the relationship between BW and other linear body measurement like EL, EW, NL, NW, TL, and TW were found significant ($P < 0.05$) but comparatively less correlated except for neck width in 0 to 6- and 7 to 12-mo age groups; neck length, neck width, tail length, tail width in 13 to 18- and 19 to 24-mo age groups. The recorded body measurements had a strong positive correlation with BW, indicating that they can be

used to estimate BW in Hissardale sheep of varying ages under field conditions.

Key words: Hissardale sheep, live body weight, linear body measurements

742 Gene expression of Red Angus sired steers and heifers evaluated for residual feed intake. C. M. Welch*[1], G. K. Murdoch[1], C. S. Schneider[1], K. C. Chapalamadugu[1], K. J. Thornton[1], J. K. Ahola[2], J. B. Hall[1], and R. A. Hill[1], *[1]University of Idaho, Moscow, [2]Colorado State University, Fort Collins.*

To improve our mechanistic understanding of variation in residual feed intake (RFI), gene expression studies have been suggested. In the present study, 42 progeny (25 steers, 17 heifers) of Red Angus sires divergent for maintenance energy (ME) EPD were RFI–tested during an 84-d post-weaning period. Subsequently, biopsy samples were collected from the biceps femoris muscle and mRNA expression of key genes in various regulatory pathways was evaluated through quantitative real-time PCR. A 2-sample t-test at a 2-tailed $P < 0.05$ was used to identify differentially expressed genes in the 2 extreme RFI quartile groups. Fatty acid synthase (FASN) was expressed in greater abundance in inefficient (high RFI) compared with efficient (low RFI) animals ($P = 0.03$). Gene expression of C/EBPα ($P = 0.06$) and PPARγ ($P = 0.13$) also tended toward greater abundance in inefficient animals. When these data were analyzed by sex, inefficient heifers showed a similar expression pattern for C/EBPα ($P = 0.003$) and PPARγ ($P = 0.08$), while FASN tended to be up-regulated in inefficient steers ($P = 0.11$). These patterns of gene expression in skeletal muscle suggest that lipogenesis was up-regulated in inefficient heifers, while fatty acid synthesis was up–regulated in inefficient steers. In addition, IGFBP5 ($P = 0.06$) tended to be up-regulated in inefficient animals although there was no difference ($P > 0.05$) in expression of the type 1 IGF receptor, IGFBP2, IGFBP3 or growth hormone receptor (GHR). When analyzed by sex, inefficient heifers tended to show higher expression of IGFBP2 ($P = 0.12$), IGFBP3 ($P = 0.15$), IGFBP5 ($P = 0.08$), and GHR ($P = 0.13$), thus muscle anabolic processes may be altered. No differences in expression of these genes were detected in steers. Thus, differential gene expression provides a tool to suggest metabolic pathways that may be involved in RFI variation of beef cattle.

Key words: IGF, C/EBPα, PPARγ

743 Effects of timing of an initial implant on performance of feedlot heifers. M. R. McDaniel*[1], W. C. Murdock[1], K. M. Taylor[1], N. P. Miller[1], B. H. Carter[1], F. Castillo[1], N. A. Elam[3], D. U. Thomson[2], and C. A. Loest[1], *[1]New Mexico State University, Las Cruces, [2]Kansas State University, Manhattan, [3]Nutrition Services Associates, Hereford, TX.*

Calves affected by disease repartition nutrients to support immune function, which could interact with anabolic implant modulation of growth. This study evaluated effects of timing of an initial implant on performance of 408 Angus-cross heifers (200 ± 0.8 kg BW). Heifers were assigned to 24 pens and 3 treatments in a completely randomized design. Treatments were: 1) no implant (CON); 2) an implant (Revalor-H; 140 mg trenbolone acetate and 14 mg estradiol; Intervet/Schering-Plough Animal Health) at initial processing (IMP0); and 3) an implant (Revalor-H) 21 d after initial processing (IMP21). Heifers were fed once daily a 68% concentrate diet from d 0 to 21, a 75% concentrate diet from d 22 to 63, and an 82% concentrate diet from d 64 to 126. Statistical analysis used the mixed procedure of SAS and differences of least squares means. From d 0 to 21, DMI of heifers was not affected ($P = 0.34$), and ADG was greater ($P < 0.05$) for IMP0 (1.03 kg/d) than CON (0.86 kg/d) and lesser ($P < 0.05$) for IMP21 (0.65 kg/d) than CON. Also, G:F was greater ($P < 0.05$) for IMP0 (0.299) than CON (0.247) and lesser ($P < 0.05$) for IMP21 (0.196) than CON from d 0 to 21. From d 0 to 42, DMI of heifers was not different among treatments ($P = 0.31$), ADG was greater ($P < 0.05$) for IMP0 (1.23 kg/d) than CON (1.04 kg/d) and intermediate for IMP21 (1.15 kg/d), and G:F was greater ($P < 0.05$) for IMP0 (0.245) and IMP21 (0.238) than for CON (0.211). From d 0 to 63, DMI was not different among treatments ($P = 0.38$), ADG was greater ($P < 0.05$) for IMP0 (1.39 kg/d) and IMP21 (1.36 kg/d) than for CON (1.21 kg/d), and G:F was greater ($P < 0.05$) for IMP0 (0.238) and IMP21 (0.236) than for CON (0.212). From d 0 to 126, DMI was greater ($P < 0.05$) for IMP0 (7.01 kg/d) and IMP21 (7.00 kg/d) than for CON (6.75 kg/d), ADG was greater ($P < 0.05$) for IMP0 (1.31 kg/d) and IMP21 (1.33 kg/d) than for CON (1.24 kg/d), and G:F was not different ($P = 0.28$) among treatments. In summary, heifers that received IMP0 and IMP21 had similar performance by d 42, which implies that delaying the initial implant for 21 d does not affect overall feedlot performance. Authors acknowledge Texas Cattle Feeders Association funding.

Key words: implant, performance, heifer

744 Effect of feeding 25-hydroxycholecalciferol on porcine fetal myoblast proliferation and differentiation. E. A. Hines[1], J. D. Coffey[1], M. A. Vaughn[1], C. W. Starkey[1], T. K. Chung[2], and J. D. Starkey*[1], *[1]Texas Tech University, Lubbock, [2]DSM Nutritional Products Asia Pacific Pte. Ltd., Singapore.*

Little is known regarding the effects of maternal supplementation of different vitamin D sources on fetal muscle development. To determine the effects of feeding the circulating metabolite of vitamin D, 25-hydroxycholecalciferol (25OHD3, Hy•D, DSM Nutritional Products), on fetal myoblast proliferation and differentiation, 38 PIC C22 gilts in 4 replicates were randomly assigned to 1 of 2 corn-soybean meal-based diets. The control diet (CTL) was formulated to contain 2,500 IU D3/kg diet, while the experimental diet (25OHD3) contained 500 IU D3/kg diet + 50 µg 25OHD3/kg diet. Gilts were fed 2.7 kg of their assigned diet once daily beginning 42 d before breeding. Gilts were artificially inseminated with PIC 337-G semen 12 and 24 h after exhibiting estrus. At gestational d 90 (±1), pregnant gilts were harvested (CTL n = 12; 25OHD3 n = 13), fetuses were extracted, and the right semitendinosus muscles of all fetuses from each litter were pooled and used for myoblast isolation. Myoblasts were cultured and proliferation index was measured at 24, 48, 72, and 96 h post plating using bromodeoxyuridine labeling and fluorescence microscopy. Myoblast differentiation capacity was determined by enumerating nuclei fused into myotubes 12 d post plating. Data were analyzed using the GLIMMIX procedure of SAS. The percentage of proliferating myogenic cells observed at 48 h was not different ($P > 0.05$) among treatments. However, at 24 ($P = 0.08$), 72 ($P = 0.07$), and 96 ($P < 0.05$) h post plating the percentage of proliferating myogenic cells was greater in the 25OHD3 cultures compared with CTL. Additionally, the differentiation capacity of myoblasts (percentage of nuclei fused into myotubes after 12 d in culture) was not different among treatments ($P > 0.05$). These results indicate that the proliferation phase of myoblasts derived from fetuses from 25OHD3 gilts may be extended. Extension of the proliferative phase of myoblasts in fetal muscle at gestational d 90, when muscle fiber hyperplasia is complete, could result in greater

capacity for muscle fiber hypertrophy and ultimate meat yield in the offspring of gilts fed 25OHD3.

Key words: myoblast, cell proliferation, vitamin D

745 Early postnatal myofiber increase in pig muscle results from myofiber elongation and tertiary myofiber formation. J. Bérard*[1,3], D. Loesel[1], A. Tuchscherer[2], C. Rehfeldt[1], and C. Kalbe[1], *[1]Leibniz Institute for Farm Animal Biology (FBN), Research Unit Muscle Biology and Growth, Dummerstorf, Germany, [2]Leibniz Institute for Farm Animal Biology (FBN), Research Unit Genetics and Biometry, Dummerstorf, Germany, [3]Institut Agricole Régional, Aosta, Italy.*

Myogenesis in pigs is commonly considered a biphasic phenomenon with the formation of primary and secondary fibers. Hyperplasia is accomplished around 90 d of gestation. However, some studies suggest a substantial increase in the total fiber number (TFN) from birth to 4 to 5 wk of age, but the origin is uncertain. Few studies indicate that early after birth tertiary myofibers of very small diameter expressing embryonic/fetal isoforms of myosin heavy chains (MyHC) appear. On the other hand, maturation and elongation of existing myotubes may contribute to muscle growth after birth. The aim of this study was to establish in which way TFN increases after birth and whether this increase is imputable to tertiary myofibers and(or) fiber elongation. The semitendinosus muscle of 128 German Landrace piglets was examined by histological and (immuno-)histochemical techniques at d 1 (n = 63), 7 (n = 12), 21 (n = 12), and 28 (n = 41) of age. Birth weight groups (BWG) were established on the basis of the 25 and 75% quartiles of birth weight frequency distribution of all piglets; low (L-BW ≤1.16 kg), medium (M-BW >1.16 to 1.52 kg), and heavy (H-BW ≥1.52 kg). Data were analyzed by ANOVA using PROC MIXED of SAS including the fixed effects age, BWG and age x BWG. Least squares means were pair-wise tested by Tukey Kramer or Dunnett test. Eosin-stained muscle cross sections allowed determining muscle cross-sectional area and TFN. TFN was increased at d 7, 21, and 28 of age compared with d 1 of age ($P < 0.01$). From d 1 to 28 of age TFN increased from 463×10^3 to 825×10^3 on average and amounted 85% in L-BW, 91% in M-BW, and 61% in H-BW piglets ($P < 0.001$). Microscopy of longitudinal and consecutive (every 110 μm) transversal sections revealed that at d 7 of age very small fibers expressing the embryonic MyHC isoform were apparent all over the muscle. In addition, intrafascicular endings of normal-sized fibers expressed embryonic MyHC. These results suggest that the TFN is not fixed at birth and its postnatal increase may be related both to the elongation of existing muscle fibers and to the genesis of tertiary myofibers.

Key words: skeletal muscle, myogenesis, total fiber number

Meat Science and Muscle Biology: Lamb and Pork Quality and Muscle Biology and Meat Products

746 Carcass and meat attributes of Red Sokoto buck goats as influenced by post-slaughter processing methods. A. B. Omojola*[1], E. S. Apata[1], and O. O. Olusola[1], *[1]University of Ibadan, Ibadan, Oyo State, Nigeria, [2]Olabisi Onabanjo University, Ago Iwoye, Ogun State, Nigeria, [3]University of Ibadan, Ibadan, Oyo State, Nigeria.*

A total of 27 good grade Red Sokoto buck goats weighing between 18.25 and 19.50kg were purchased from a specialized goat market, quarantined and stabilized on a standard diet for 20 one days. The goats were sacrificed to evaluate the effects of scalding, singeing and skinning on their yield, carcass and meat attributes in a completely randomized design. The animals were well rested, starved of feed for 16 h, weighed, stunned mechanically and slaughtered in batches of 3 under commercial conditions. The samples for shear force, cooking loss and water holding capacity (WHC) were taken from the loin. The result showed that the dressing percentage was highest ($P < 0.05$) in scalded carcasses (58.29%) and least in skinned carcasses (46.27%). The carcass length was least ($P < 0.05$) in singed carcass (34.35cm) and highest (44.76cm) in skinned carcasses. Singeing imposed a higher degree ($P < 0.05$) of toughness (6.61 kg/cm^3) on the meat as against 5.20 and 4.12 kg/cm for meat from scalded and skinned carcasses respectively, while the cooking loss was highest ($P < 0.05$) in singed carcasses. WHC was highest ($P < 0.05$) in meat from skinned carcasses (68.76%) followed by skinned (62.70%) and least in meat from singed carcasses (53.80%). The visual color score was highest ($P < 0.05$) for singed carcasses (7.45), followed by scalding (6.16) and least in skinned (5.30). The rib eye area and the depth of chest were not significantly ($P > 0.05$) affected by the post slaughter processing methods however, width and length of leg were highest ($P < 0.05$) in skinned carcasses and least in singed carcasses. Skinning elicited higher ($P < 0.05$) meat quality attributes and the leather industry will benefit immensely as the skin of Red Sokoto goats are highly priced. Post slaughter processing methods (dressing) were found to affect the quality of meat from Red Sokoto goats.

Key words: skinning, scalding, singeing

747 Yield of West African dwarf buck goats slaughtered at different weights. A. B. Omojola*[1], S. Attah[2], and O. O. Olusola[1], *[1]University Of Ibadan, Ibadan, Nigeria, [2]University of Agriculture, Markurdi, Nigeria, Markurdi, Nigeria, [3]University of Ibadan, Ibadan, Nigeria.*

Goat meat is highly relished and forms a major item of food in Nigeria and other developing African countries however there is no proper documentation on its yield as affected by different slaughter weights. A total of 36 male West Africa Dwarf goats with initial live weight between 5.47 and 8.82 kg were reared on a 16.8% crude protein concentrate diet until they reached the pre-determined slaughter weight (SW) of 10, 15 and 20 kg. Each carcass was split into two halves along the back bone. The right side of each carcass was separated into wholesale cuts and weighed while the left half was split into trunk, pelvic and pectoral limbs. Each part was subsequently dissected into lean, fat and bones. The result obtained showed that the hot carcass weight (HCW), chilled carcass weight (CCW) and the dressing percentage (DP) increased ($P < 0.05$) as the SW increased while there was an inverse relationship between the SW and the percent chilling loss. The percent external offal (head, skin and feet) reached maximum weight at 15 kg SW. The liver and the empty stomach gave highest values for goats slaughter at 15 kg, while the relative weight of organs such as lung, heart, kidney, pancreas and spleen were not significantly ($P > 0.05$) affected by the SW. The leg cut gave the highest percentage (25.53-28.18%), followed by shoulder (21.43-23.24%), rack (11.11-12.34%) and loin (10.07-40.7%). The percentage weight of the leg and shoulder were highest ($P < 0.05$) at 15 kg SW while that of rack was highest ($P > 0.05$) at 10 kg SW. Goats slaughtered at 15 kg SW has the highest proportion of lean, external and internal offal.

Key words: slaughter weight, offal, carcass

748 Fatty acid composition of muscles from Sarda suckling lamb reared indoor and outdoor. A. Nudda*, M. G. Manca, G. Battacone, R. Boe, M. Sini, N. Castanares, and G. Pulina, *University of Sassari, Dipartimento di Scienze Zootecniche.*

In dairy sheep farms the production of meat by milking lamb is an relevant source of income. The knowledge of the fatty acid composition of lamb meat is important for its economic value. The aim of this work was to study the effect of rearing system on the fatty acid composition of 2 muscles from suckling lambs of Sarda breed. Forty-eight suckling lambs were divided into 2 groups subjected to different rearing system: 24 lambs raised indoor (Group IN) and fed only dam's milk during the night when they were kept together; while 24 lambs followed their mothers also in outdoor pasture (Group OUT). Lambs were weighed weekly and finally slaughtered at 28 d of age. After 24 h of refrigeration, at 4°C, the tight muscles (TM) and longissimus dorsi (LD) were dissected from each right half-carcass. Intramuscular fatty acid composition (FA) of each sample was determined by gas-chromatography. Data were analyzed by 2 ways ANOVA with rearing system, muscle type and their interaction as fixed factors. The weight gains of lambs were not affected by rearing system. The intramuscular fat content was significantly higher in TM than in LD muscle, while this variable was not affected by rearing system. The type of muscle influenced significantly almost all FA concentration, except the C18:1 c9 content.The PUFA n3 were higher in LD, because of the highest content of C18:3 n3 and very long chain FA (EPA, DPA and DHA), compared to TM. The content of PUFA n6 was also higher in LD than in TM sample, due to the highest content of C18:2 c12,c15 and C20:4 n6. Concentrations of C16:0, C18:1 t11, and CLA c9,t11 were higher in TM than in LD samples. The rearing system of lambs does not seem to affect significantly the FA composition of intramuscular fat, except for C18:0 content. The comparison between two rearing system performed in this trial did not show effect on FA composition of intramuscular fat of suckling lambs. Moreover, results suggest that muscle type should be take in to account when examining FA profile in meat.

Key words: lamb muscles, fatty acid, rearing system

749 Nutritive and organoleptic characteristics of kilishi as affected by meat type and ingredient formulation. O. O. Olusola*, A. B. Omojola, and A. O. Okubanjo, *University of Ibadan, Ibadan, Oyo, Nigeria.*

Kilishi is a ready-to eat-intermediate moisture meat which is highly relished. The product is traditionally prepared from beef infused with spices and defatted groundnut paste. It contains about 46% meat and

54% non meat ingredients. This study tried to appraise the eating quality of kilishi as affected by meat types and ingredient formulation. Three different kilishi recipes viz fresh, frozen and oven dried groundnut paste representing recipes 1, 2 and 3 respectively were formulated and used for the preparation of pork and beef kilishi in a completely randomized design. The nutrient composition and eating qualities of each kilishi type were evaluated. The results obtained showed that kilishi from the recipes were similar in crude protein content with a value ranging from 55.47 – 62.33%. These differed significantly from the crude protein content of the dried raw pork (46.1%) and the dried raw beef (35.85%) which were not infused in the mixture of spices and groundnut paste. The ash content was highest ($P > 0.05$) in beef kilishi from recipe 1 with a value of 10.31 percent and least (6.96%) in pork kilishi from recipe 2. The color rating was highest in all pork kilishi irrespective of the recipe. The panelist also rated pork kilishi higher in juiciness with a value range of 3.50 – 4.30 as against values of 1.80 – 4.40 for beef kilishi. Beef kilishi from recipe 1 had the highest flavour rating while the overall acceptability was highest in both products from recipe 1 with values of 6.30 and 5.20 for beef and pork kilishi respectively. The plant ingredients in the recipes highly contributed to the crude fiber values of 2.96 – 4.42% obtained in products across the recipes. The results obtained in this study showed that the non meat ingredients contributed substantially to the nutritive value of kilishi produced from the three recipes, however the use of recipe 1 with fresh groundnut paste was better in product qualities than frozen or oven dried groundnut paste.

Key words: groundnut paste, kilishi, pork/beef

750 Over-nutrition during pregnancy increases collagen content in the skeletal muscle of mature male offspring. Y. Huang*, M. J. Zhu, R. J. McCormick, N. M. Nathan, S. P. Ford, and M. Du, *Department of Animal Science, University of Wyoming, Laramie.*

Collagen and its crosslinking in meat contribute to the background toughness. However, mechanisms regulating collagen accumulation has not been well studied. We hypothesized that the fetal stage of development would have dramatic effects on the muscle collagen content of offspring meat. To test, ewes were fed a control diet (CON, fed 100% of NRC, n = 7) or an over-nourished diet (OB, fed 150% of NRC, n = 7) from 60 d before conception to lambing. After weaning, male offspring were penned together and fed to requirements to 2 −3 years old when the Longissimus dorsi (LD) muscle was sampled. An increase of 37.8 ± 19.0% ($P < 0.05$) was observed in collagen content in OB offspring LD muscle compared with Con offspring. The mRNA expression of Collagen I and Collagen III, the major types of fibrillar collagen in muscle, also tended to elevated ($P < 0.10$) in OB offspring (80.7 ± 49.8 and 42.2 ± 21.6%, respectively) when compared with CON offspring. Matrix metalloproteinases (MMPs) and tissue inhibitors of metalloproteinases (TIMPs) are involved in collagen remodeling. There was an increase in MMP1 expression in OB offspring LD muscle compared with CON offspring (52.6 ± 25.0%, $P < 0.05$), but CON offspring expressed more MMP13 (91.7 ± 35.4%, $P < 0.05$) than OB offspring. The mRNA expression of TIMP1 and TIMP3 in LD muscle tended to increase ($P < 0.10$) in OB offspring compared with CON offspring (49.7 ± 21.1 and 94.6 ± 45.8%, respectively). Lysyl oxidase is a key enzyme catalyzing collagen cross-linking; the expression of lysyl oxidase was higher in OB offspring compared with the CON offspring LD muscle (74.0 ± 32.3%, $P < 0.05$). In summary, our data demonstrate that over-nutrition during pregnancy increased collagen content in the muscle of mature male offspring. This increase is associated with both enhanced collagen synthesis and decreased connective tissue remodeling (Supported by USDA-2008–35206–18826, NIH 1R01HD067449, and INBRE #P20RR016474).

Key words: collagen, offspring, muscle

751 Intrauterine crowding impairs formation as well as growth of secondary myofibers. C. E. Pardo[1,2], A. Koller-Bähler[1], M. Kreuzer[2], and G. Bee*[1], *[1]Agroscope Liebefeld Posieux, Posieux, Switzerland, [2]Department of Agricultural and Food Science, Zurich, Switzerland.*

There is evidence that intrauterine crowding is linked to intrauterine growth retardation and impaired myofiber hyperplasia. The aim of the study was to determine the impact of differences in uterine space using unilateral hysterectomized-ovariectomized (UHO) and unilateral oviduct ligated (OL) sows on reproduction performance, organ and muscle development of selected progeny at birth. In the study 8 UHO and 10 OL Swiss Large White third parity sows were used. At farrowing litter size and litter birth weight (BtW) were determined. Subsequently, within each litter 2 male and 2 female progeny with the lowest (L) and highest (H) BtW were sacrificed and internal organs and the LM were collected and weighed. To determine the number and diameter of primary (Prim) and secondary (Sec) myofibers and to calculate the Sec:Prim ratio, histological analyses were performed on the LM using mATPase staining after pre-incubation at pH 4.3 and 10.2. The litter size was similar (8.0 vs. 7.6; $P > 0.75$) for the 2 sow groups. However, as expected progeny born from UHO sows were lighter (1.43 vs. 1.85 kg; $P \leq 0.01$) than those from OL sows. When expressed per 100 g BtW, the heart, liver, kidney and spleen of UHO and OL progeny were of similar ($P \geq 0.36$) weight whereas the brain was heavier (2.52 vs. 1.92%; $P < 0.01$) and the brain:liver ratio was greater (1.03 vs. 0.75; $P < 0.01$) in UHO than OL piglets. Due to a numerically higher ($P = 0.13$) number of Prim but not ($P = 0.92$) Sec myofibers, the Sec:Prim myofiber ratio was lower (27.1 vs. 29.6; $P = 0.05$) in the LM of UHO than OL progeny. The Sec but not the Prim myofibers were smaller (8.1 vs. 9.1 μm; $P < 0.01$) in diameter in the LM of UHO than OL piglets. In L piglets a brain sparing effect was observed as their relative brain weight (2.4 vs. 2.0%) and brain:liver ratio (0.99 vs. 0.79) was higher ($P < 0.01$) than in H piglets. Only Prim myofiber number, which tended ($P = 0.06$) to be higher in L than H piglets, was affected by BtW. The current data suggest that regardless of BtW and gender, in individuals born from a crowded environment, formation as well as growth of Sec myofibers in the LM was impaired.

Key words: intrauterine crowding, muscle development, pig

752 Microarray analysis of the differentially expressed genes in adipose tissues between Jinhua pigs and Landrace pigs. T. Wu*, Z. Yuan, Y. Wang, and T. Shan, *Institute of Feed Science, Zhejiang University, Hangzhou, Zhejiang province, China.*

This study was conducted to detect the gene transcriptional expression profiles and further screen out the differentially expressed genes in subcutaneous fat between Jinhua pigs (at age of 90 d) and landrace (at age of 90 d) by Microarray. A total of 458 genes at least 2.0-fold significant difference were screened out including 223 higher expressed genes (77 genes with annotation available) and 235 lower expressed genes (58 genes with annotation available) in subcutaneous fat tissues of Jinhua pig compared with that of landrace. Furthermore, semiquantitative PCR and real-time quantitative PCR were used to confirm the 9 differentially expressed genes (Leptin, salivary lipocalin, heat shock 27kDa protein 8, Cyclin B2, Carboxylesterase 1, phosphoglycerate

mutase 2, Short/branched chain specific acyl-CoA dehydrogenase, apolipoprotein D, Cellular retinoic acid binding protein 1). The PCR depicting results showed great consistency with the microarray. Six categories including fat metabolism, energy metabolism, transcription, splicing factor, protein synthesis, protein degradation were classified through bioinformatics analysis. Taken together, this research demonstrates previously unrecognized changes in gene transcription of subcutaneous fat between Jinhua pigs and landrace pigs, and some potential candidate cascades identified in the study merit further investigation.

Key words: adipose tissue, differential expressed gene, microarray

753 SIFT-MS identifies unique volatile masses in 24 h postmortem loins from Berkshire- and Landrace-influenced swine. S. Taylor*, C. A. Wick, J. Harper, M. Wick, K. Shircliff, and S. J. Moeller, *The Ohio State University, Columbus.*

The objective of this preliminary study was to test the efficacy of using Selected Ion Flow-Tube Mass Spectrometry (SIFT-MS) as a novel device for the discrimination of swine of different maternal genetic composition that have previously been observed in our laboratory to differ in pork quality. Berkshire-sired market pigs, derived from matings to one purebred Berkshire (BB, n = 5), one purebred Landrace (BL, n = 5), and one Berkshire-Saddleback crossbred (BS, n = 5) dam were raised on straw with access to outdoor concrete from 30 kg through harvest (~5 mo of age, ~100 kg). A 3 phase feeding program was followed, providing ad libitum access to feed and water. Pigs were harvested following a 15-h fast. Pork loin quality was assessed at 24 h postmortem and a 2.54 cm diameter core removed from carcass and placed in LN2 for subsequent analysis. Warner-Bratzler Shear Force (WBSF) was assessed on one chop after a 7 d aging period. Loin 24 h pH was greater (0.14 units, $P < 0.05$) in BB and BS pig when compared with BL pigs, and chops from BB (3.01 kg) and BS (2.84 kg) exhibited less WBSF when compared with chops from BL pigs (4.67 kg). Each sample was divided into 3 equal parts, pulverized in LN2 and analyzed by SIFT-MS analysis. Sixty-one masses were identified and the relationships of the masses to maternal background determined by SIMCA. The BB and BS were not different from each other ($P > 0.05$); however, the BL loins were different from both the BB and BS loins ($P < 0.05$). These data support our hypothesis that rapid analysis by SIFT-MS is able to discriminate Berkshire from Landrace genetic influences in the present study. Future analysis by SIFT-MS will allow for the identification of the primary components unique to the different genetic lines and assess implementation as a tool for product characterization.

Key words: swine, pork quality, SIFT-MS

754 A partial replacement of soybean meal by whole or defatted algal meal in diet for weanling pigs does not affect their plasma biochemical indicators. E. Isaacs*[1], K. Roneker[1], M. Huntley[2], and X. G. Lei[1], *[1]Cornell University, Ithaca, NY, [2]Cellana, Kailua-Kona, HI.*

Marine algae have recently emerged as a new exciting source of biofuel. Our objective was to determine effect of supplemental defatted algal biomass from biofuel production on biochemical indicators of protein metabolism in plasma of weanling pigs. A total of 27 weanling pigs (BW = 10.69 ± 0.22 kg) were divided into 3 groups (n = 9/group), and fed a corn-soybean meal basal diet (BD), the BD plus 6.6% whole algal meal, or the BD plus 7.2% defatted algal meal (provided by Cellana, Kailua-Kona, HI) for 6 wk. Plasma urea nitrogen concentration, an indicator of dietary protein utilization efficiency, was not affected by the treatments as the 3 groups of pigs had similar values (mg/L) at Wk 3 (112.4 ± 9.4, 93.3 ± 11.0, and 102.1 ± 9.1) and Wk 6 (163.0 ± 22.1, 170.8 ± 14.7, and 155.9 ± 16.9). There was no group difference in plasma alanine aminotransferase or alkaline phosphatase activity at either time point. Ultrasound scan of vertebral fat and muscle depth of individual pigs at Wk 3 and Wk 6 predicted similar body lean yield (%) among all the 3 groups (Wk 3: 50.7 ± 0.2, 50.8 ± 0.2, and 50.7 ± 0.1; Wk 6: 52.2 ± 0.2, 52.1 ± 0.4, and 52.4 ± 0.1). In conclusion, adding 6.6% of whole algal meal or 7.2% of defatted algal meal into a corn-soy basal diet for weanling pigs effectively replaced the same amount of soybean meal without adverse effect on the biochemical indicators of protein metabolism or health.

Key words: algae, biofuel, pigs, protein, ultrasound

755 Effects of soybean meal of different origins and micronization of high protein soybean meal on nutrient digestibility and productive performance of weanling pigs. J. D. Berrocoso, E. A. Monteserín, L. Cámara, M. P. Serrano, R. P. Lázaro, and G. G. Mateos*, *Universidad Politécnica de Madrid, Madrid, Spain.*

The effects of the inclusion in the diet of a regular soybean meal (R-SBM, 44% CP) or a high protein SBM (HP-SBM, 49% CP), and the degree of grinding of the HP-SBM, on apparent total tract digestibility and growth performance of piglets from 27 to 56 d of age were studied. There were 6 diets in pellet form with similar nutrient content based on 6 different sources of SBM that supplied in all cases, 6.5% of dietary CP. There was a diet that included 15.8% R-SBM, a diet that included 10% soy protein concentrate (SPC) in substitution of the R-SBM, and 4 additional diets arranged factorially with 2 sources of HP-SBM (USA or Argentinean origin) ground or micronized (geometric mean diameter of 881 or 60 μm). Each treatment was replicated 8 times (6 pigs per pen). Adequate orthogonal comparisons were performed to test the effects of SPC, type of SBM, and the micronization of the HP-SBM on the traits studied. From 28 to 56 d of age, diet did not affect growth performance, but piglets fed the micronized HP-SBM had better G:F ($P \leq 0.05$) from 28 to 35 d of age and ADFI ($P = 0.06$) from 35 to 42 d of age than piglets fed the ground HP-SBM. In general, nutrient digestibility was higher for the SPC than for the R-SBM with the HP-SBM being intermediate. In fact, N digestibility was higher (84.1 vs. 81.4%; $P \leq 0.01$) for the SPC than for the R-SBM containing diets and that of DM (82.2 vs. 81.1%; $P \leq 0.05$) and OM (86.0 vs. 84.9%; $P \leq 0.05$) was higher for the HP-SBM than for the R-SBM. However, micronization of the SBM did not affect nutrient digestibility. It is concluded that the inclusion of SPC in the diet in substitution of R-SBM improved N digestibility but did not affect growth performance. Micronization of SBM did not affect nutrient digestibility but improved G:F during the first wk post-weaning but not thereafter. Under the conditions of the present experiment, the inclusion of added value soy products in piglet diets presents slights advantages over the use of R-SBM but further economical studies are required.

Key words: nutrient digestibility, soy products, piglet performance

756 Effects of adding cracked corn to a pelleted supplement for nursery and finishing pigs. C. B. Paulk*[1], A. C. Fahrenholz[1], J. M. Wilson[1], L. J. McKinney[1], J. D. Hancock[1], K. C. Benhke[1], J. C. Ebert[2], and J. J. Ohlde[2], *[1]Kansas State University, Manhattan, [2]Key Feeds, Clay Center, KS.*

Two experiments were completed to determine the effects of feeding ground and cracked corn with a pelleted supplement to nursery and finishing pigs. For both experiments, treatments were corn-soybean meal-based and fed as mash, pellets, and pellets with 50% of the corn (ground or cracked) blended into the diet after the rest of the formulation (the supplement) had been pelleted. In Exp. 1, a total of 224 nursery pigs (avg BW of 7.4 kg) were used with 7 pigs/pen and 8 pens/treatment. For the 28-d experiment, pigs fed mash had greater ($P < 0.03$) ADG and G:F compared with pigs fed the other treatments. However, this resulted from adding ground or cracked corn outside the pellets (complete pellets vs corn and pelleted supplement, $P < 0.001$). In Exp. 2, a total of 252 finishing pigs (avg BW of 40 kg) were used with 7 pigs/pen and 9 pen/treatment. For the 80-d experiment, pigs fed mash had lower ($P < 0.03$) ADG compared with pigs fed diets with pellets. Pigs fed complete pellets had greater ($P < 0.03$) ADG and G:F compared with pigs fed corn and the pelleted supplement and pigs fed the supplement blended with cracked corn had greater ($P < 0.02$) ADG than pigs fed the supplement blended with ground corn. With hot carcass weight used as a covariate, dressing percentage of pigs fed mash was greater than for pigs fed the other treatments with no differences for fat thickness or percentage fat free lean index among pigs (FFLI) fed the various treatments ($P > 0.13$). In conclusion, adding ground or cracked corn to a pelleted supplement had negative effects on growth performance compared with feeding a complete pellet.

Table 1.

Item	Mash	Pellet	Ground Corn	Cracked Corn	SE
Nursery (d 0 to 28)					
ADG, g	510	498	487	473	12
G:F, g/kg	719	759	660	643	12
Finishing					
ADG, g	1,045	1,107	1,055	1,094	11
G:F, g/kg	393	408	384	380	6
Dress, %	74.5	74.1	74.5	73.8	0.1
Fat thickness, mm	18.9	19.5	19.9	18.7	0.5
FFLI, %	52.2	51.7	51.6	52.2	0.3

Key words: cracked corn, pellet, pig

757 Inulin, alfalfa and citrus pulp in diets for piglets: Effects on digestibility and metabolism of N. S. Brambillasca*[1], E. Menezes[1], P. Zunino[2], and C. Cajarville[1], *[1]Departamento de Nutrición Animal, Facultad de Veterinaria, UdelaR, Montevideo, Montevideo, Uruguay, [2]Departamento de Microbiología, Instituto de Investigaciones Biológicas Clemente Estable, MEC, Montevideo, Montevideo, Uruguay.*

The addition of fibrous components in the diet of pigs may reduce the N output in feces and urine. So, the aim of this work was to evaluate the effect of the inclusion of inulin, alfalfa, and citrus pulp in diets for piglets on N digestibility and metabolism. Twenty 4 cross-breed piglets (12.1 ± 1.7kg BW) in a randomized complete block design were housed in metabolic cages and assigned to one of 4 treatments: corn and soybean meal based diet (CO; 3.56% N), 97% CO+3% inulin (IN; 3.08% N), 95.5% CO+4.5% fresh alfalfa (AL; 3.06% N) and 95.5% CO+4.5% fresh citrus pulp (CP; 2.94% N) in DM basis. The experiment consisted of an 11 d adaptation period followed by 5 d of feces and urine collection. Diets, feces and urine were analyzed for N, and digestibility, fecal and urinary output, retention, excretion and utilization of N were calculated. Data were analyzed by PROC MIXED considering treatment effect and means were separated by orthogonal contrasts. Pigs fed CO presented the highest intake, digestibility, retention and utilization of N; these parameters were reduced when aditives were included to diets. Urinary N output and total N excretion was higher for animals consuming AL. The low N utilization when animal received AL could be related to a higher N urinary output. Lower N digestibilities could be associated to the inclusion of fibrous components in AL and CP diets. Acknowledgments: ANII for scholarship of the first author.

Table 1. Effect of diets on N digestibility and balance

	Treatment					*P*-value		
	CO	IN	AL	CP	SEM	CO vs ADDIT	IN vs AL+CI	AL vs CI
N intake (g/d)	24.1	20.3	18.6	19.5	1.97	0.05	ns	ns
N digest.	0.86	0.82	0.79	0.80	0.02	0.03	ns	ns
Fecal N output (g/d)	3.5	3.6	3.8	3.7	0.40	ns	ns	ns
Urinary N output (g/d)	1.9	1.8	4.0	2.0	0.59	ns	ns	0.02
N retention (g/d)	18.7	15.0	10.9	13.8	1.77	0.01	ns	ns
N excretion (g/d)	5.5	5.4	7.7	5.7	0.72	ns	ns	0.05
N utilization (%)	77.1	74.1	57.0	69.8	4.21	0.02	0.03	0.02

ADDIT: additives; P: probability of contrasts ($P \leq 0.05$).

Key words: fiber, nitrogen balance, swine

758 *Nannochloropsis oculata* meal did not alter nutrient usage and had no adverse health effects when fed to rabbits as a protein source. 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.*

Twenty-four adolescent male New Zealand White rabbits were used (n = 12/treatment) to evaluate the safety and potential animal feed use of *Nannochloropsis oculata* algae meal that remained after oil extraction for biodiesel production. Algae meal was included at 10% (DM basis) to a test diet that was isocaloric and isonitrogenous to the control diet (with no algae meal). Rabbits had ad-libitum access to feed for 45 d, including a 7 d. transition period to the Control and Algae diets. Body weights were recorded every 7 d. Blood was drawn via an ear puncture on d 0 and 28 of the study and analyzed for metabolites. A nutrient balance trial was conducted from d 28 through 35. On d 45 of the study, the rabbits were euthanized, blood was collected via a heart puncture, organs were weighed, and histological samples were collected. Intake of DM (194.9 v. 180.3 g/d), N (6.21 v. 5.68 g/d) and NDF (83.6 v. 76.8 g/d) were similar ($P > 0.05$) across treatments. Intake of ADF (53.41 vs. 42.72 g/d) was greater ($P < 0.01$) for the rabbits fed the Control diet than those fed the Algae diet. Subsequently, apparent ADF digestibility was decreased ($P = 0.03$) for rabbits consuming the Algae diet compared with the Control. Total N excretion (4.41 v. 3.95 g/d) was not different ($P > 0.05$) between the diets, however total P excretion (0.99 v. 0.78 g/d) was greater ($P < 0.01$) for rabbits fed the Control diet. There were no differences ($P > 0.10$) in final BW, blood glucose ($P > 0.10$), or serum urea N ($P > 0.10$). No differences ($P > 0.10$) were observed in kidney, liver or spleen histology of animals fed either the control or diet with algae meal. These data indicate that the algae meal of *Nannochloropsis oculata* may be a safe alternative protein source for herbivorous animals, yet the digestibility may be limited by the increased fiber content of the algae meal.

Key words: algae, biodiesel, digestibility

759 Comparative efficacy of meal and extracts of *Aspilia africana* leaf in laying quails. O. O. K. Oko*, *University of Calabar, Calabar, Cross River State, Nigeria.*

The study evaluated the mode of action of *Aspilia africana* leaf meal and extracts as potential phytogenic feed additives compared with an antibiotic growth promoter. Three forms of *Aspilia africana* leaf; meal, aqueous and ethanolic extracts were tested against a negative control and a standard antibiotic growth promoter (oxytetracycline) in a 70 d study employing 540 (7 wk-old) growing quails. Each *Aspilia africana* leaf form was supplemented at 2.5%, 5.0%, 7.5% or 10.0% into the basal diet, while oxytetracycline (positive control) was supplemented at 0.002%. Fourteen dietary treatments of 30 birds per treatment with 10 birds per replicate of 3 were studied in a RCB design. Traits measured included; production performance, egg composition, internal and external egg qualities. A 2-way ANOVA at $P < 0.05$ was conducted. Results showed that the impact of dietary supplementation with *Aspilia africana* leaf were similar to or better than ($P < 0.05$) those of the antibiotic growth promoter. Egg production characteristics were form and dose-dependent. While hen-day production increased up to 86.24% in birds on *Aspilia africana* leaf compared with those on oxytetracycline (69.20%) and basal (61.38%) diets; their egg shell thickened up to 0.35 mm, yolk color intensified ($P < 0.05$) from 3.03 to 6.25 whereas, percentage crack comparatively decreased. Crude extracts of *Aspilia africana* leaf exhibited higher ($P < 0.05$) phytogenic effects than the meal at supplementation levels of 5–7.5%. The aqueous extract further demonstrated higher egg boosting potentials. Therefore, an inclusion level of 5% aqueous extract of *Aspilia africana* leaf in layer diet is recommended as an alternative growth promoter.

Key words: phytobiotic, egg booster, plant extract

760 Effect of mycotoxin inhibitor (sim wall) on mold colonized feed in broiler chicken. S. Aikore[1], D. Eruvbetine*[1], R. Bandyopadhyay[2], J. Atehnkeng[2], M. A. Oyekunle[1], and A. M. Bamgbose[1], *[1]University of Agriculture, Abeokuta, Ogun State, Nigeria, [2]International Institute of Tropical Agriculture, Ibadan, Oyo State, Nigeria.*

To determine the effect of mycotoxin inhibitor (Sim wall) on mold colonized feed, broiler chickens were divided into 9 treatment groups in a factorial arrangement. Maize grains were colonized with either *A. flavus* 3228 strain (aflatoxin producer) or *A. flavus* 3229 strain (non afalatoxin producer). Non treated maize was used as a control. Sim wall was included at 3 levels (0, 1000 and 2000 ppm). Standard broiler starter followed by broiler finisher diets composed of the treated and untreated maize with and without Sim wall were fed to the birds for 8 wk. Records of BW, feed intake and mortality were kept. Blood samples were collected for determination of blood parameters and enzyme levels. After slaughtering, liver samples were examined for histopathological changes. Data was analyzed using ANOVA (SAS2009). Results revealed that the birds fed atoxigenic maize treated diets had BW, feed intake and feed conversion values similar to that of the control diet ($P \geq 0.05$). However, the birds fed diets containing aflatoxigenic maize had lower BW and less efficient feed conversion and the highest level of mortality ($P \leq 0.05$). Inclusion of 2000 ppm Sim wall had the best result in terms of BW. Among the blood parameters measured, serum total protein, albumin, globulin and enzymes alanine amino transferase and aspartate amino transferase the best results were obtained in the control group, the atoxigenic treated group and the group fed 2000ppm Sim wall ($P \leq 0.05$). Lesions of the liver were pronounced in the birds fed aflatoxigenic treated diets showing severe fatty changes, necrosis and fibrosis. However, inclusion of 2000 ppm Sim wall recorded mild lesions of the liver. It can be concluded that the deleterious effects of aflatoxin contaminated maize in diets for broilers can be ameliorated by the inclusion of 2000 ppm Sim wall.

Key words: aflatoxin, mycotoxin inhibitor, broilers

761 Impact of tylosin phosphate and ractopamine hydrochloride alone or in combination on growth performance, feed efficiency and water intake in finishing pigs. C. M. Pilcher*[1], R. Arentson[2], and J. F. Patience[1], *[1]Iowa State University, Ames, [2]Elanco Animal Health, Greenfield, IN.*

Ractopamine hydrochloride (RAC) is a nutrient repartitioning agent added to diets in late finishing to increase weight gain, feed efficiency and carcass leanness. Tylosin phosphate (TP) is used in swine diets to control diseases such as ileitis and swine dysentery and to improve growth performance. There is very limited information on the impact of these 2 products when used in combination. The objective of this study was to evaluate the impact of TP and RAC alone or in combination on growth performance, feed efficiency and water intake in finishing pigs fed corn-soybean meal or corn-soybean meal-dried distillers grains with solubles (DDGS) based diets. A total of 72 PIC gilts (start BW = 107.4 ± 0.50 kg) were blocked by weight and randomly assigned to a 2 × 2 × 2 factorial arrangement of treatments: TP (0 or 44 ppm), RAC (0 or 5 ppm), and DDGS (0 or 30%). Pigs were housed individually and fed treatment diets for 17 d. TP treated pigs were administered 66 mg tylosin per liter of water for 3 d before receiving treatment diets. Feed was provided twice daily, as much as the pigs could consume within 1 h per meal (ADFI = 2.98 ± 0.045 kg/d). Water was provided to the pigs between feeding periods, ad libitum (ADWI = 7.76 ± 0.23 kg/d). Data were analyzed with the MIXED procedure of SAS. There were no significant interactions ($P > 0.10$) among any of the treatments. RAC improved ADG (1.31 vs. 1.11 kg/d; $P < 0.0001$) and G:F (0.446 vs. 0.368; $P < 0.0001$) and had no effect on ADFI. TP had no effect on ADG, ADFI or G:F. DDGS inclusion reduced ADFI (2.80 vs. 3.18; $P < 0.0001$) and ADG (1.15 vs. 1.27 kg/d; $P = 0.001$) and had no effect on G:F. There was no significant effect of dietary treatment on water intake ($P > 0.10$); however, pigs fed RAC or DDGS increased water to feed ratio (2.77 vs. 2.47; $P = 0.03$ and 2.79 vs. 2.49; $P = 0.02$, respectively). In conclusion, under the conditions of this experiment, TP did not affect growth performance, RAC enhanced growth performance, and there were no interactions between the response to TP and RAC. The inclusion of DDGS did not affect the responses to either TP or RAC.

Key words: ractopamine, tylosin phosphate, swine

762 Dietary nucleotides as an alternative to antibiotic growth promoters (AGP) for nursery pigs. R. Patterson*[1], E. McMillan[2], O. Jones[1], and B. A. Slominski[3], *[1]Canadian Bio-Systems Inc., Calgary, Alberta, Canada, [2]Nutreco Canada Agresearch, Burford, Ontario, Canada, [3]University of Manitoba, Winnipeg, Manitoba, Canada.*

The potential of dietary nucleotides to replace AGP in nursery pig diets was evaluated using 168 mixed-sex pigs weaned at 17 ± 2 d of age in a completely randomized design. The test article, Maxi-Gen Plus, is a nucleotide-rich yeast product (NP) containing a mixture of mononucleotides. Pigs were randomly assigned to the following dietary treatments: Positive control (PC; containing 110 ppm chlortetracycline HCl and 31.2 ppm tiamulin per kg of feed); Negative control (NC; no antibiotics); NC + 0.1% NP; NC + 0.2% NP. Diets were fed ad libitum for 28 d. On d 14, 0.2% NP pigs had greater BW than NC pigs (9.32 vs 8.76 kg, $P = 0.005$) but did not differ ($P > 0.1$) compared with PC (9.32 kg) or 0.1% pigs (9.11 kg). On d 28, pigs fed the 0.1% NP diet were heavier than NC pigs (16.52 vs 15.40 kg, $P = 0.028$) and weighed the same as PC (16.31 kg) and 0.2% pigs (16.30 kg). FCR was not affected by dietary treatments during the study. From d 7–14, pigs fed the 0.2% NP diet had greater ADG (332 vs 284 g/d, $P = 0.048$) and ADFI (406 vs 349 g/d, $P = 0.034$) than NC pigs but did not differ compared with PC or 0.1% pigs. ADG was not affected by dietary treatments from d 14–21, however during this period, pigs fed a diet supplemented with 0.1% NP had an ADFI of 641 g/d, which tended ($P = 0.09$) to be greater than that of NC pigs (569 g/d). Although ADFI was not affected by dietary treatments from d 21–28, pigs given the 0.1% NP diet had an ADG of 623 g/d which was the same as that of PC (572 g/d) and 0.2% (565 g/d) pigs and greater than that of NC pigs (537 g/d, $P = 0.041$). Overall, no differences were observed for ADFI between either NP treatment. However, pigs fed the 0.1% NP diet had greater ADG than NC pigs (379 vs 335 g/d, $P = 0.05$) and the same ADG as 0.2% (379 g/d) and PC pigs (379 g/d). This study indicates that AGP can be withdrawn from nursery pig diets without a loss of performance when diets are supplemented with 0.2% nucleotides from d 0–14 and with 0.1% nucleotides from d 15–28. It thus appears that dietary nucleotides have the potential to replace AGP in nursery pig diets as pigs receiving dietary nucleotides performed the same as pigs receiving AGP.

Key words: nucleotides, piglets, antibiotic replacement

763 In vitro fermentative characteristics of citrus pulp, apple pomace and inulin combined in increasing levels with a predigested dog food. S. Brambillasca*, C. Deluca, A. Britos, L. Reyes, and C. Cajarville, *Departamento de Nutrición Animal, Facultad de Veterinaria, UdelaR, Montevideo, Montevideo, Uruguay.*

The fermentation characteristics of citrus pulp (CP), apple pomace (AP) and inulin (IN) mixed with a pre-digested dog food was studied. A commercial dog food was predigested (pepsin+pancreatin) and mixed with AP, CP or IN to obtain 3 different mixtures: 3, 5 and 7% in DM basis. 0% level consisted in the pre-digested food incubated as sole substrate. In vitro gas production was performed using diluted feces from 3 dogs fed the same dog food and gas volume was recorded at 2, 4, 6, 8, 10, 12, 18, 24, 48, 67 h after inoculation. Organic matter disappearance (OMD) was determined by ashing the fermentation residues. Asymptotic gas production (A, mL/g OM), time to reach 50% of the asymptote (B, h), maximal rate of gas production (Rmax, mL/h) and time of occurrence of Rmax (Tmax, h) were determined. Data were analyzed by PROC MIXED considering fiber source, inclusion level and its interaction, and means were separated by Tukey test. No source x level interaction was detected. IN produced more gas with a faster rate than the other 2 fiber sources. A and Rmax were the highest for the 5 and 7% levels, whereas Tmax for the 0% level was the lowest. OMD was affected by inclusion level and highest for 0 and 7% levels. The fermentative parameters of CP and AP were similar to those produced when IN was included in the mixtures. This suggests that these by-products can be included at 5 to 7% levels in diets for dogs and enhance the fermentative activity of the colonic microbiota as a recognized commercial prebiotic do. Acknowledgments: CIDEC–Fvet for the financial support of this work.

Table 1. In vitro fermentation parameters according to fiber source and inclusion level

	A (mL/g OM)	B (h)	Rmax (mL/h)	Tmax (h)	OMD (%)
Fiber					
CP	82.8^{b}	1.10	7.06^{b}	0.58	26.9
AP	86.5^{ab}	1.11	8.55^{ab}	0.51	27.5
IN	92.8^{a}	1.10	10.19^{a}	0.44	29.0
SEM	2.70	0.03	0.60	0.12	1.50
P	≤0.05	ns	≤0.01	ns	ns
Level					
0	54.5^{c}	1.01^{b}	8.32^{ab}	0.08^{b}	30.3^{a}
3	91.0^{b}	1.17^{a}	6.97^{b}	0.85^{a}	23.6^{b}
5	102.9^{a}	1.11^{a}	9.37^{a}	0.48^{a}	27.7^{ab}
7	101.1^{a}	1.13^{a}	9.75^{a}	0.64^{a}	30.1^{a}
SEM	3.11	0.03	0.70	0.14	1.71
P	≤0.001	≤0.01	0.02	≤0.01	0.03

^{a,b,c}Values within a column with different superscript differ ($P \leq 0.05$).

Key words: canine, fiber, fermentation

Nonruminant Nutrition Symposium: Nutrition and Gut Microbiome

764 Whole-body systems approaches for gut microbiota-targeted, preventive healthcare. L. Zhao*, *Shanghai Jiao Tong University, Shanghai, China.*

Humans are superorganisms whose phenotypes are dictated by 2 integrated genomes, the genetically inherited human genome (23,000 genes) and the environmentally acquired human microbiome (over 1 million genes). The 2 genomes must work in harmonious integration to maintain health. Gut microbiota constitutes the majority of the human microbiome. Bioactive substances (antioxidants, vitamins or various toxins) produced by particular members of gut microbiota may get into bloodstream via enterohepatic circulation or impaired gut barrier to affect host immunity and metabolism. Undigested nutrients from the diet or drugs that arrive in the colon play a dominating role in shaping the structure of the gut microbiome. For example, accumulating evidence supports the new hypothesis that obesity and related metabolic diseases develop because of low-grade, systemic and chronic inflammation provoked by increased antigen load from a diet-disrupted gut microbiota. On the other hand, changes of host health induced by biotic or abiotic perturbations may also disrupt gut microbiota which in return can further deteriorate host health. Due to the tight integration of gut microbiota into human global metabolism, molecular profiling of urine metabolites and gut microbiome can provide an ideal window for reflecting physiological functions of the host. Variations in gut microbiota and urine metabolites can thus be employed as emergent functions for quantitative assessment and monitoring of health at the whole-body level with the advantage of measuring human health based on the results of interactions between the 2 genomes and the environment rather than just host genomic sequences. Large-scale, longitudinal cohort studies in conjunction with these whole-body systems approaches will generate pre-disease biomarkers with predictive power, thus making preventive health management of populations with rapidly changing disease spectrums possible through re-engineering of the imbalanced gut microbiome with specially designed drugs/diets.

Key words: gut microbiome, host health, additives

765 Dietary modulation of the gut microbiota by prebiotics and probiotics. G. R. Gibson*, *University of Reading, Reading, UK.*

The human large intestine is an intensively colonized area containing bacteria that are health promoting, as well as pathogenic. This has led to functional food developments that fortify the former at the expense of the latter. Probiotics have a long history of use in humans as live microbial feed additions. In contrast, a prebiotic is a non digestible food ingredient that beneficially affects the host by targeting indigenous components thought to be positive. Dietary carbohydrates, such as fibers are candidate prebiotics but most promise has been realized with oligosaccharides. As prebiotics exploit non-viable food ingredients, their applicability in diets is wide ranging. Main prebiotic targets at the moment are bifidobacteria and lactobacilli (although this may change as our knowledge of the flora diversity and functionality expands). Any dietary component that reaches the colon intact is a potential prebiotic, however much of the interest in the development of prebiotics is aimed at non-digestible oligosaccharides such as inulin type fructooligosaccharides (FOS) and trans-galactooligosaccharides (TOS). Other prebiotics are emerging. Some prebiotics occur naturally in several foods such as leek, asparagus, chicory, Jerusalem artichoke, garlic, artichoke, onion, wheat, banana and oats. However, these foods contain only trace levels, so developments have taken the approach of removing the active ingredients from such sources and adding them to more frequently consumed products to attain levels whereby a prebiotic effect may occur, e.g., cereals, confectionery, biscuits, infant feeds, yogurts, table spreads, bread, sauces, drinks, etc. The rationale for using probiotics and prebiotics to reduce risk will be reviewed. On the contrary, the role of the gut flora in various clinical states will be briefly discussed. Building upon this information, research will be presented on the generation and testing of a novel prebiotic (TOS) which has led to the development of products designed to improve immune health in the elderly, reduce the symptoms of Irritable Bowel Syndrome and help prevent traveler's diarrhea.

Key words: gut microbiome, host health, pro pre biotic

766 Effect of dietary change on equine and swine gut microbiota. K. Daly*[1], A. Darby[2], N. Hall[2], C. Proudman[3], D. Bravo[4], and S. P. Shirazy-Beechey[1], *[1]Department of Molecular and Cellular Physiology, University of Liverpool, Liverpool, UK, [2]Department of Functional and Comparative Genomics, University of Liverpool, Liverpool, UK, [3]Equine Division, Department of Veterinary Clinical Sciences, University of Liverpool, Liverpool, UK, [4]Pancosma, Geneva, Switzerland.*

The large intestinal tracts of mammalian species contain vast populations of microorganisms that interact with each other and co-exist with their host in a mutually beneficial relationship. The total number of these microorganisms (~10^{14}) exceeds the number of cells in the body by 10-fold. It is becoming increasingly evident that intestinal microbiota play an important role in maintaining the health and well being of the host. Several environmental factors such as age, disease, antibiotics and diet are known to influence the composition of the microbiota, and subsequent microbial metabolites produced. By far the biggest influence on the composition and activity of the gut microbiota is diet. Domesticated animals, such as the horse, are often fed diets that differ significantly to their natural forage. Indeed, dietary change and the amount of grain fed to horses are two important variables that have emerged from a number of studies as risk factors for acute intestinal disease. Our studies, using molecular biological strategies, have indicated that there are significant modifications in microbiota and fermentation products when horses were maintained on grain based diets, compared to horses maintained on traditional forage; these changes became much more exaggerated in horses affected by a form of dietary-induced intestinal disease. To determine any alterations in gut microbiota that occur during development in piglets, from suckling to weaning, and in response to changes in diet, from hydrolysable to fermentable carbohydrates and addition of nutritional supplements, we have employed a combination of 454 pyrosequencing and 16S rRNA-oligonucleotide hybridization using samples of colonic contents taken from piglets weaned onto various controlled diets. We shall report on the characteristics of microbial transformations that occur.

Key words: gut microbiome, host health, pyrosequencing

767 Dietary manipulation of canine and feline microbiota. K. S. Swanson*, *Department of Animal Sciences and Division of Nutritional Sciences, University of Illinois, Urbana.*

The canine and feline colon is inhabited by a complex and dense community of bacteria, archaea, fungi, protozoa, and viruses. A signifi-

cant hindrance to the field has been the inability to effectively identify and quantify microbial species, their metabolic end products, and mechanisms by which they affect host health. Molecular tools, including qPCR, FISH, DGGE, RFLP, and DNA sequencing, have overcome many of the limitations of culture-based techniques. Recently developed high-throughput techniques (e.g., 16S rRNA microarrays; next-generation sequencing) have dramatically changed the research landscape in regards to gastrointestinal microbiology. These techniques are now being used to characterize canine and feline gastrointestinal microbiota and identify the effects of diet, age, and disease on these communities. Continued use of DNA-based techniques to characterize microbial phylogeny and metabolic capacity, along with other technologies to analyze microbial RNA (gene expression), protein, and metabolite profiles, will increase our understanding of host-microbe relationships in pets. Composition of the commensal microbiota is dependent on several factors, including host genotype, age, and diet. The main energy source of colonocytes (i.e., SCFA) is derived primarily from microbial fermentation of carbohydrate-based energy substrates reaching the large bowel. Dietary proteins may also serve as fermentable materials, but result in the production of putrefactive compounds such as ammonia, biogenic amines, and phenols that are implicated as the major odor components of feces and may have negative influences on gut health. The supplementation of dietary fibers, prebiotics, or probiotics has become a popular strategy for improving gut health in humans and pets. In the past couple decades, over 50 peer-reviewed publications have reported the effects of these dietary ingredients in dogs and cats, with many demonstrating beneficial changes in gastrointestinal microbiota, fecal fermentative end products, and stool characteristics. Our current understanding and future research opportunities in this field will be reviewed.

Key words: gut microbiome, feline, canine

768 Rumen microbiota, assessed by evolving techniques. R. J. Wallace*, *Rowett Institute of Nutrition and Health, University of Aberdeen, Aberdeen, UK.*

Our present understanding of ruminal microbiology was built initially upon a few epoch-changing advances made many years ago: Gruby and Delafond's (1843) microscopic observations of protozoa; Hungate's (1947) appreciation of the anaerobic nature of the rumen that led to novel culture techniques for the bacteria; Orpin's (1975) realization that some flagellate protozoa were in fact zoospores of anaerobic fungi, until then a contradiction in terms. Isolation and study of pure cultures was invaluable in understanding the likely role of different species of bacteria, protozoa or fungi in the overall fermentation. Cultivation techniques could not deal with more than a very small number of samples, however, in attempting to assess the effects of diet or manipulation on rumen ecology. Even then, it was known that such analyses were flawed by cultivation bias. We have since passed through a period of evolving molecular techniques, based mainly on ss-rRNA gene analyses. Cloning and sequencing provided community analyses that were free from the biases imposed by cultivation techniques. Related techniques for microbiome analysis quickly followed (DGGE, TGGE, RFLP, ARISA). qPCR and FISH enabled groups or species to be quantified. Now, next-generation sequencing has exploded onto to the scene. A bacterial genome can be sequenced in an afternoon, and sequencing of the entire community's DNA – the metagenome - is about to become routine. Are these seismic increases in information that we can generate about the rumen microbiota as epoch-changing as the historic discoveries? And can they be used to improve the efficiency of animal production, animal welfare and environmental impact? Very recent genomic and metagenomic results confirm that there is a huge amount that we do not understand about genes and organisms that break down plant fiber. Other studies on fatty acid biohydrogenation have come to a similar kind of conclusion, reaching almost an impasse in identifying key genes and species. We now need equally innovative thinking and technology to ensure that the answer to both questions will be yes.

Key words: rumen microbiome, host health

769 Effect of short-term supplementation and temporary weaning in hepatic gene expression in Hereford cows grazing native pasture. A.L. Astessiano*[1], F. Bialade[1], M.P. Grignola[1], J. Laporta[1], C. Viñoles[2], and M. Carriquiry[1], *[1]School of Agronomy, UDELAR, Montevideo, Uruguay, [2]National Research Institute for Agriculture, Tacuarembo, Uruguay.*

Short-periods of improved nutrition associated with temporary weaning increased early pregnancy rates in grazing conditions, but the underlying mechanisms involved in this response remain unknown. Primiparous beef cows (n = 25; 388 ± 7 kg BW and 3.6 ± 0.2 units BCS) in anestrus were used in a randomized block design with a 2x2 factorial arrangement of short-term supplementation, with 2.5 kg/cow of whole rice middlings (90.3%DM, 10%CP, 9%EE, 14%NDF; SUP, n = 12 vs. CON, n = 13) for 23 d, and temporary weaning, by applying nose plates to calves for 14 d (with, n = 13 vs. without, n = 12), before initiation of the breeding period (103 ± 1 d postpartum) to study hepatic expression of GH-IGF axis genes. Liver biopsies were obtained at the initiation and end of the treatment period. The abundance of mRNA of growth hormone receptor (GHR), GHR-1A, insulin-like growth factor-I (IGF-I), IGF binding proteins-2 (BP2),-3 (BP3), and insulin receptor (INSR) were measured by real time RT-PCR normalized by hypoxanthine phosphoribosyltransferase and β-actin as endogenous control genes. Means from a mixed model analysis were considered to differ when $P < 0.05$. Neither short-term supplementation nor temporary weaning affected cow BCS. Expression of GHR and IGFI mRNA were not affected by any of the factors evaluated in this study while the expression of INSR mRNA tended be greater ($P = 0.11$, 2.96 vs. 1.83 ± 0.55) in temporary weaned than suckled cows. Expression of BP3 and BP2 mRNA was greater in SUP than CON cows (1.38 vs. 0.85 ± 0.003 and 18.50 vs. 12.63 ± 0.04, respectively). In addition, BP2 mRNA was less in temporary weaned than suckled cows (12.60 vs. 18.53 ± 0.04). The BP3/BP2 ration was not affected by short-term supplementation but was greater in temporary weaned than suckled cows. Short-term supplementation and temporary weaning before initiation of the breeding season could affect IGF availability through changes in hepatic IGFBP synthesis.

Key words: mRNA, suckling management, nutritional treatment

770 Feeding distillers grains as an energy source to gestating and lactating heifers: Impact on ovarian function and reproductive efficiency. P. J. Gunn*[1], J. P. Schoonmaker[1], R. P. Lemenager[1], and G. A. Bridges[2], *[1]Purdue University, West Lafayette, IN, [2]University of Minnesota, Grand Rapids.*

Angus-cross beef heifers pregnant to a single sire (n = 80; BCS = 5.1 ± 0.03; BW = 518 ± 6 kg) were used to assess the effects of feeding dried distillers grains with solubles (DDGS) as an energy source during late gestation and early lactation on follicular development, cyclicity and fertility. At 192 d in gestation, heifers were stratified and allotted by BW and BCS to receive one of 2 isocaloric dietary treatments: a control diet of corn silage and haylage (CON; 10% CP prepartum; 11.8% CP postpartum) or corn residue and DDGS (DG; DDGS at 1.2% BW per d; 15.7% CP). Treatments concluded and cattle were commingled 30 d after synchronization with the 5 d CO-Synch + CIDR timed-AI protocol (118 ± 0.1 d postpartum; DPP). BW and BCS were assessed every 28 d during treatment. At 32 ± 0.2 DPP, 1 follicular wave was mapped via ultrasonography in 10 anestrous heifers per treatment. Starting 40 DPP, blood samples were taken every 10 d until synchronization to determine return to cyclicity via progesterone. Plasma urea nitrogen (PUN) was assessed in blood samples taken at AI. Categorical and continuous data were analyzed with the GLIMMIX and MIXED procedures of SAS, respectively. Dominant (15 ± 0.7 vs. 13 ± 0.6 mm) and secondary (11 ± 0.5 vs. 9.0 ± 0.4 mm) follicle diameter was greater ($P \leq 0.05$) and wavelength (8.9 ± 0.6 vs. 7.5 ± 0.5 d) tended ($P = 0.08$) to be greater in DG than CON, respectively. Percentage of cyclic heifers at estrous synchronization did not differ (89%), but DG (58 ± 2 d) tended ($P = 0.10$) to resume estrous activity at fewer DPP than CON (63 ± 2 d). PUN concentrations at AI were greater ($P < 0.01$) in DG (17.1 ± 0.6 mg/dL) than CON (6.6 ± 0.3 mg/dL). Timed-AI pregnancy rates were numerically ($P = 0.30$) greater in DG (28/36, 78%) than CON (22/33, 67%). Breeding season pregnancy rates did not differ between treatments (99%). In summary, feeding DDGS at 1.2% of BW per d to first-parity heifers resulted in greater dominant follicle growth during the postpartum anestrous period, marginally hastened resumption of estrous cycles, and did not detrimentally impact AI pregnancy rates.

Key words: beef heifer, DDGS, fertility

771 Comparison of Brahman females evaluated for residual feed intake (RFI) as heifers and reevaluated for RFI as gestating cows. B. L. Bradbury*[1,2], S. L. Morgan[1,2], A. N. Loyd[1,2], D. A. Neuendorff[1], A. W. Lewis[1], J. P. Banta[1], D. G. Riley[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.*

Use of residual feed intake (RFI) as a tool to identify feed efficient beef cattle is increasing. This study was designed to examine the relationship between postweaning RFI and mature RFI in Bos indicus females. Mature cow RFI data was collected over 2 years on 2 different cohorts of cows that were previously evaluated for RFI postweaning. In 2009 and 2010, 37 (3–7 yr of age) and 41(2–3 yr of age) cows, respectively, in their first trimester of gestation (affirmed by palpation) were retrained to eat from Calan gates system and evaluated for RFI. Cows were fed twice daily (0800 h and 1600 h) at 2.6% BW for 70 d with BW recorded weekly. Body condition scores were recorded weekly in 2009 and at d 0 and d 70 in 2010. Females were classified according to their RFI values, with a negative RFI = efficient and a positive RFI = inefficient. Residuals for average daily feed intake (ADFI) by heifer and cow (n = 78) were generated using a mixed model. Sire (n = 16) was included as a random effect in both models. Fixed effects included year of record for heifers (2004–2009: $P < 0.001$) and for cow (2009 and 2010; $P < 0.001$). Heifer pen (n = 11: $P = 0.0008$) was nested within year. Cow age (2, 3, 4, 5, 6, or 7 yr; $P < 0.001$), lactation status (lactating or not; $P = 0.07$), and pen (n = 11; $P < 0.001$) were included as nested within year. Regression coefficients of ADFI on ADG and mid-test weight (MTW) for heifers were −0.15 ± 0.03 kg ($P = 0.0002$) and 0.13 ± 0.002 kg ($P < 0.0001$), respectively. Regression coefficients of ADFI on MTW, ADG, and days pregnant were 0.09 ± 0.02 kg ($P < 0.001$), 0.76 ± 0.29 kg ($P = 0.01$), 0.01 ± 0.003 kg ($P = 0.007$), respectively for cows. The Pearson correlation coefficient (r = −0.24, $P = 0.0348$) indicates that heifer RFI may not be an accurate predictor of RFI as a mature cow in the first trimester of gestation.

Key words: RFI, cow, repeatability

772 Effect of temperament on response to cannulation and glucose challenge in Brahman heifers. B. L. Bradbury*[1,2], L. C. Caldwell[2], A. W. Lewis[1], D. A. Neuendorff[1], R. C. Vann[3], T. H. Welsh Jr.[2], and R. D. Randel[1], *[1]Texas AgriLife Research, Overton, [2]Texas AgriLife Research, College Station, [3]MAFES-Brown Loam Experiment Station, Raymond, MS.*

Temperamental cattle have greater serum concentrations of cortisol (CS) which mediates glucose (GLU) metabolism. The objective was to determine the effects of temperament on blood GLU and insulin (INS) following a stressor and a subsequent infusion of dextrose. Brahman heifers (200–300 kg) were evaluated for temperament and 6 calm (C) and 6 temperamental (T) heifers were fitted with jugular catheters and placed in individual stalls. Blood samples were collected at cannulation and then at 0, 30, 60, and 90 min. At 90 min after cannulation dextrose was infused via the cannula at 0.5 mg/kg BW. Blood samples were collected at −5, 0, 10, 15, 20, 30, 40, 60, 80, 100, 120, 140, 160, 180 min relative to the time of dextrose infusion. CS and INS were assayed by RIA and GLU by colorimetry. CS, GLU, INS, insulinogenic index and their interactions with time and temperament were analyzed by GLM for repeated measures. Peak INS concentration, time to peak, GLU disappearance and time to half life were analyzed using GLM procedures. Following cannulation T heifers had elevated GLU (P = 0.0005) and CS (P = 0.0238). There was a significant temperament by time interaction (P = 0.0434) influencing INS following cannulation. During the challenge a temperament by time interaction affected CS (P = 0.0041), GLU (P = 0.0428), and INS (P = < 0.0001). Glucose concentrations were significantly higher in T heifers (P = 0.0011) at half life (P = 0.0092), and time to half life was significant (P = < 0.0001) between temperaments. Peak INS concentrations (mIU/mL) for the C and T heifers were 54.5 ± 7.6 and 27.2 ± 7.6, respectively. Insulinogenic index was affected by temperament (P = 0.0173) and there was a temperament by time interaction (P = 0.0003). These data indicate that temperament (P = 0.0282) has an impact on CS secretion following cannulation stress which subsequently results in elevated GLU and INS concentrations. Temperament modifies metabolic regulatory responses in heifers and this altered metabolism of temperamental cattle may partially explain their decreased productivity.

Key words: cattle, temperament, glucose

773 The role of parathyroid hormone and calcitonin in the prevention of hypocalcemia under induced metabolic acidosis in cattle. E. M. Rodríguez*[1], A. Bach[1,2], and A. Arís[1], *[1]Department of Ruminant Production, IRTA, Caldes de Montbui, Spain, [2]ICREA, Barcelona, Spain.*

Metabolic acidosis ameliorates parturient hypocalcemia by increasing plasma concentrations of 1,25-dihydroxyvitamin D (1,25-D) in cows. Under acidosis, it has been reported in other mammals that parathyroid hormone (PTH) function is enhanced through an upregulation of PTH receptor (PTHR) and increasing 1,25-D levels. The objective of this study was to evaluate the PTH/PTHR concentrations under an acidic state in cattle and to assess changes in calcitonin (CALC), also involved in calcium homeostasis with opposite effects to PTH. Twenty-four Holstein bulls (497 ± 69 kg of BW and 341.5 ± 10.5 d of age) were randomly assigned to 2 treatments [acidosis (ACI), or control (CON)]. Acidosis was induced by oral administration of ammonium chloride (2.5 Eq/day) during 10 d and animals were then slaughtered following commercial practices. Blood samples were taken before slaughter, and samples of urine, kidney, and thyroid gland were harvested immediately after sacrifice. Blood and urine pH were measured immediately after collection. Expression of CALC, CALC receptor (CALCR), PTH and PTHR from kidney and thyroid gland was measured by qRT-PCR. CALC activity under acidotic conditions was tested in vitro using human breast T47D cultures expressing CALCR. Data was analyzed with an ANOVA using the treatment as the main effect. As expected, blood pH was lower (P<0.001) in ACI than CON bulls (7.57 vs. 7.64 ± 0.02). Urine pH was lower (P<0.01) in ACI than CON bulls (5.95 vs. 7.38 ± 0.13). No differences were detected on CALC and PTH expression or on PTH serum concentrations. Expression of PTHR in kidney was greater (P<0.05) in ACI than CON bulls. Furthermore, CALC activity in vitro at pH 7.4 was greater (P<0.01) than that found at more acidic or alkaline pHs. In conclusion, PTH function is enhanced in metabolic acidosis by an increased expression of PTHR in kidney, and whereas CALC/CALCR expression is not affected, its binding activity may be hampered. These findings demonstrate that, in an acidic state, PTH and CALC are complementary hormones promoting increased blood calcium levels.

Key words: hypocalcemia, calcitonin, parathyroid hormone

774 Molecular control of puberty as affected by nutrition and leptin infusion in zebu heifers. J. Diniz-Magalhães*, M. V. Carvalho, A. B. S. Machado, M. A. V. Silva Júnior, and L. F. P. Silva, *Universidade de São Paulo, Pirassununga, São Paulo, Brazil.*

Leptin has been proposed to affect several genes 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 oxytocin (OXT), β-arrestin 1 (ARRB1), and insulin-like growth factor binding protein-2 (IGFPB2). 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: H (high-energy diet), L (low-energy diet), and LL (low-energy diet + oLeptin). Diets were formulated to promote weight gains of 0.4kg/day (groups L and LL) or 1.2kg/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. Expression of transcripts of OXT, ARRB1 and IGFBP2 was quantified by real-time PCR. Changes in gene expression were calculated by relative quantification with the ΔΔCt method, using the gene 18S ribosomal RNA as the reference gene. ANOVA used the MIXED procedure of SAS considering the fixed effects of treatment, gene and trt × gene, and the random effects of heifer(trt), and heifer × trt(gene). There was no effect of leptin, or of nutrition on expression of OXT and IGFBP2 (P > 0.10) at the time of puberty. Also, leptin infusion did not alter ARRB1 expression. However, high energy intake reduced expression of ARRB1 by 1.5 folds (P = 0.02). ARRB1 acts inhibiting protein-G receptors, such as the neuropeptide Y receptors. Therefore, downregulation of ARRB1 could be associated with lower sensibility of the hypothalamus to NPY action, and consequently with hastening of puberty.

Key words: beta arrestin, hypothalamus, *Bos indicus*

775 Energy balance alters leptin but not adiponectin mRNA in Holstein cows. D. A. Koltes* and D. M. Spurlock, *Iowa State University, Ames.*

Adipokines are recognized as important signaling molecules secreted by adipose tissue that alter metabolic activity in multiple target tissues. Thus, adipokines likely play a critical role in homeorhetic adaptations that occur throughout the transition period and lactation cycle in dairy cows. Currently, the regulation of adipokines in response to changing energy balance is not well characterized. Therefore, the objective of this research was to determine if changes in energy balance status alter the mRNA abundance of 2 important adipokines, leptin and adiponectin, in lactating Holstein cows. Three models of altered energy balance were investigated, including transition from pregnancy to lactation, feed restriction, and administration of recombinant growth hormone (GH), Posilac. Adipose tissue was collected from 26 cows before calving, and at 5, 21, and 150 d in milk. In different experiments, adipose tissue was collected before treatment, and on d 1 and 4 of feed restriction (n = 19) and d 3 and 7 following administration of GH (n = 20). For all experiments, net energy balance was calculated from daily individual feed intake and milk production, and weekly body weight and milk component analysis. Cows in early lactation and under feed restriction experienced a similar decline in net energy balance with a nadir of –7.38 and –8.09 MCal, respectively ($P < 0.01$). Net energy balance also declined with GH administration ($P < 0.01$), but to a lesser degree (0.23 MCal on d 7). Leptin mRNA abundance decreased with the onset of lactation and with feed restriction ($P < 0.05$), and there was a trend for its decrease with GH administration ($P = 0.08$). In contrast, a significant change in adiponectin mRNA abundance was observed only with GH administration, where adiponectin mRNA increased on d 3, but not d 7 relative to pre-treatment ($P < 0.05$). These results show that leptin mRNA consistently decreased with declining energy balance, while changes in adiponectin mRNA were not associated with energy balance status. Thus, altered leptin, but not adiponectin, may represent a mechanism by which adipose tissue signals a need for physiological change during times of negative energy balance.

Key words: growth hormone, feed restricted

776 Effect of a high-energy diet after weaning on luteinizing hormone secretion in Holstein bulls. M. Maquivar*[1], L. A. Helser[2], M. D. Utt[1], L. H. Cruppe[1], F. M. Abreu[1], G. E. Fogle[1], J. M. DeJarnette[2], and M. L. Day[1], *[1]The Ohio State University, Columbus, [2]Select Sires Inc., Plain City, OH.*

Feeding a high energy diet to beef heifers weaned at 2 to 3 mo of age prematurely activates the reproductive axis and results in precocious puberty. The objective of the present study was to evaluate the impact of a high energy diet, initiated approximately 2 mo of age, on secretion of LH in Holstein bull calves. Male calves received 1 of 2 diets beginning at 58 ± 0.7 d of age. Diets were designed to contain the same amount of protein (14.1% CP) but different amount of energy: high energy diet (n = 9, HIGH, 2.2 Mcal/kg NEm and 1.37 Mcal/kg NEg) targeting for ADG of 1.5 kg/d and control diet (n = 10, CONT, 1.70 Mcal/kg NEm and 1.09 Mcal/kg NEg) targeting for ADG of 0.75 kg/d. Monthly serial blood samples (10 min intervals for 8 h) were collected via jugular catheters from 6 bulls in each treatment, to assess patterns of LH secretion at 69, 97, 125, 156, 181 and 210 d of age. The ADG differed among treatments (1.47 ± 0.05 HIGH vs. 0.95 ± 0.04 kg/d CONT, $P < 0.01$). Body weight tended ($P < 0.1$) to differ at 118 and 134 d of age and differed ($P < 0.05$) from 146 to 218 d. At 125 d of age, concentration of LH was greater in the HIGH (1.83 ± 0.05 ng/ml) than CONT (1.50 ± 0.07 ng/ml) treatment and was lesser ($P < 0.01$) at 181 (1.07 ± 0.04 vs. 1.43 ± 0.08, respectively) and at 210 (1.00 ± 0.03 vs. 1.34 ± 0.06, respectively) days of age (trt x age, $P < 0.01$). Number of LH pulses did not differ between treatments at 69, 97, 156 and 181 d of age but was greater ($P < 0.01$) in the HIGH than CONT treatment at 125 d (8.33 ± 0.95 vs. 3.00 ± 0.44, respectively) and tended ($P = 0.07$) to be greater at 210 d of age (trt x age, $P < 0.01$). The amplitude of LH pulses was greater ($P < 0.05$) in the CONT than HIGH treatment at 125, 181 and 210 d of age and a tended ($P < 0.1$) to be greater at 97 and 156 d of age. These data suggest that a high energy diet initiated at 2 mo of age induces a rapid activation of the gonadotropic axis in Holstein bulls expressed as increased frequency of LH pulses of a lesser amplitude which results in a greater mean concentration of LH. This alteration in LH secretion may accelerate maturation of the reproductive axis in bulls.

Key words: reproductive axis, LH, male calves

777 Effects of volatile fatty acid infusions on angiopoietin-like protein 4 concentration in plasma and ruminal papillae of cattle. S. H. Li*, B. J. Bradford, and L. K. Mamedova, *Kansas State University, Manhattan.*

Angiopoietin-like protein 4 (ANGPTL4), a plasma regulator of energy and lipid metabolism, may be influenced by microbial populations. Microbes could influence ANGPTL4 production via changes in volatile fatty acid (VFA) production. The objective of this study was to evaluate the effects of VFA on plasma and papillae ANGPTL4 concentrations. Six ruminally cannulated lactating Holstein cows were randomly assigned to treatment sequence in replicated 3x3 Latin squares and fed a standard lactation diet ad libitum. Cows were initially infused with 10 mol/d acetate, propionate, or butyrate for 2d, provided as bolus infusions every 4 h. However, during period (P) 1, both DMI and calculated ME intake were decreased by infusions ($P < 0.001$) relative to pre-treatment. Therefore, in P2 and P3, infusion rates were decreased to 5 mol/d. Blood and ruminal fluid samples were collected immediately before and after infusions. Ruminal papillae samples were collected after infusions and ruminal pH data were collected every 5 min during treatment with an indwelling pH probe. Five d were allowed between treatment periods. Period 1 results were analyzed independently from P2 and P3 data using mixed model analysis. There were no treatment effects on DMI, ME intake, or ruminal pH at either infusion rate ($P > 0.12$). Plasma ANGPTL4 concentration was determined by ELISA, which revealed no treatment effects at either infusion rate ($P > 0.14$). Papillae ANGPTL4 concentration was determined by Western blot, and no effects of treatment were observed at either infusion rate ($P > 0.51$). Furthermore, no correlations were observed between ANGPTL4 and ruminal VFA concentration. However, papillae ANGPTL4 was positively correlated with both ruminal pH ($P = 0.02$) and ME intake ($P = 0.03$). Conversely, plasma ANGPTL4 had an inverse relationship with ruminal pH ($P < 0.01$), with regression estimates ranging from 5.6 to 1.9 ng/mL as mean ruminal pH increased from 6.0 to 6.2. Consistent with previous findings, ruminal ANGPTL4 abundance is positively associated with ruminal pH, but is not associated with plasma ANGPTL4 concentrations.

Key words: ANGPTL4, cattle, volatile fatty acids

778 Incorporation of essential and non-essential fatty acid into distinct lipid classes in cultured bovine and porcine small intestine and muscle explants. C. Caldari-Torres* and B. A. Corl, *Virginia Polytechnic Institute and State University, Blacksburg.*

In foregut fermenters, microbial biohydrogenation leads to saturation of essential fatty acids (EFA) and a loss in their biological function. Despite no literature reporting EFA-deficiency in ruminants, EFA conservation mechanisms in these animals are not well understood. The aim of this study was to examine fatty acid (FA) esterification patterns in ruminant and non-ruminant small intestine (SI) and muscle explants. We performed in vitro culture of bovine and porcine SI and muscle explants with radiolabeled FA to track esterification of EFA and non-EFA into lipid classes. Tissue explants 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). Porcine SI explants incorporated more non-EFA than EFA (17.9 vs 12.4 ± 2.0 nmol•2 h^{-1}•150 mg $tissue^{-1}$, $P = 0.002$). Bovine muscle explants incorporated more EFA than non-EFA (8.73 vs 6.32 ± 0.86 nmol•2 h^{-1}•150 mg $tissue^{-1}$, $P < 0.001$). Pig muscle explants and cattle SI explants did not exhibit preferential esterification of non-EFA compared with EFA. Cattle SI explants esterified more FA into triglycerides (TG) compared with phospholipids (PL) (3.54 vs 2.42 ± 0.35 nmol•2 h^{-1}•150 mg $tissue^{-1}$, $P = 0.01$). Muscle explants from both species incorporated EFA into PL more readily than non-EFA (Cow: 1.98 vs 1.27 ± 0.39 nmol•2 h^{-1}•150 mg $tissue^{-1}$, $P = 0.02$, Pig: 0.98 vs 0.77 ± 0.13 nmol•2 h^{-1}•150 mg $tissue^{-1}$, $P = 0.004$). An increase in PL/TG ratio was observed when measuring incorporation of EFA compared with non-EFA in bovine muscle explants (1.71 vs 0.61 ± 0.19 nmol•2 h^{-1}•150 mg $tissue^{-1}$, $P < 0.001$). There was no difference in PL/TG ratio in porcine muscle explants or bovine or porcine SI explants when quantifying incorporation of EFA compared with non-EFA. Results suggest that muscle esterification patterns of cattle facilitate greater EFA incorporation into PL, while SI esterification patterns of FA seem to have no preference for EFA in ruminants. Support provided by NSF grant IOS-0920491.

Key words: fatty acid, muscle, small intestine

779 Hepatokine, growth hormone, and PPARα-regulated gene network expression in liver of peripartal cows fed two levels of dietary energy prepartum. J. Khan*[1], D. Graugnard[1], D. H. Keisler[2], B. J. Bradford[3], L. K. Mamedova[3], J. K. Drackley[1], and J. J. Loor[1], *[1]University of Illinois, Urbana, [2]University of Missouri, Columbia, [3]Kansas State University, Manhattan.*

Fibroblast growth factor 21 (FGF21) and angiopoietin-like 4 (ANGPTL4) are hepatokines under control of PPARα. During starvation or fasting, liver FGF21 increases leading to inhibition of STAT5ab and impaired growth hormone (GH) action. We examined the expression of 40 genes associated with the network encompassing FGF21, GH, long-chain fatty (LCFA) oxidation, and PPARα in cows (n = 6/diet) assigned to a control (CON; NEL = 1.34 Mcal/kg DM) or moderate-energy (OVER; NEL = 1.62 Mcal/kg DM) diet during the entire dry period. All cows were fed a common lactation diet (NEL = 1.69 Mcal/kg DM) postcalving. A percutaneous liver biopsy was collected at −14, 7, 14, and 30 d relative to parturition (DIM) for transcript profiling via quantitative PCR. Estimated prepartal energy balance (EBAL) was greater (~159% vs. 102%, $P < 0.05$) in OVER vs. CON, but during the first wk postpartum cows fed OVER prepartum were in more negative EBAL. Prior to calving, CON cows had greater ($P < 0.05$) serum FGF21 which corresponded with greater ($P < 0.05$) liver FGF21 expression. Concentration of FGF21 decreased ($P < 0.05$) gradually postpartum regardless of diet. Along with more severe negative EBAL, cows fed OVER vs. CON prepartum had greater ($P < 0.05$) postpartal serum NEFA, BHBA, and GH, and greater liver triglyceride concentrations. Those data agreed with greater expression of ACOX1, CPT1A, ACADVL, HMGCS2, FGF21, and ANGPTL4 in OVER vs. CON at 7–14 DIM. Serum ANGPTL4 concentration was not affected by diet or time. Despite the gradual increase in serum GH after calving, at 7–14 DIM liver from cows fed OVER prepartum had greater ($P < 0.05$) IGFALS potentially to counteract the temporal decrease in hepatic GHR, STAT5ab, and IGF-1. Our results revealed a link between prepartal energy overfeeding and postpartal negative EBAL leading to greater serum NEFA coupled with transcriptional adaptations in liver. Those encompassed not only LCFA oxidation and GH signaling but also hepatokine production. The apparent lack of relationship between liver mRNA of FGF21 and ANGPTL4 with blood concentrations merits further study.

Key words: transition cow, metabolism, growth factors

Production, Management and the Environment: Dairy Facilities

780 Herd turnover and mortality in low profile cross-ventilated and naturally ventilated dairy barns in the Upper Midwest. K. M. Lobeck*, M. I. Endres, S. M. Godden, and J. Fetrow, *University of Minnesota, St. Paul.*

The objective of this study was to describe herd turnover and mortality rates in low profile cross-ventilated barns (CV) compared with conventional naturally ventilated (NV) freestall barns. The study was conducted in 12 commercial dairy farms in Minnesota and eastern South Dakota. All farms had deep sand freestalls and had been in operation for at least 1 year before the beginning of the study. Farm records were collected from January to December 2008. Herd size was stable except 1 CV herd expanded from 1300 to 1600 cows in the summer. One NV and 1 CV barn were excluded at the end of the study because of substandard records. Sold and died events were examined. Herd turnover rate was calculated as the number of animals that were sold or died during the year, divided by the average herd size. Mortality rate was calculated as the number of animals that died divided by average herd size. Seventeen categories were created for sold and died reasons: abortion, udder conformation, Johne's positive, mastitis, low milk production, reproduction, lame, metabolic problems, metritis, animals that were unable to rise, calving problems, injury, sick, miscellaneous, unknown, and no reason stated. Overall herd turnover rate was 26.8 ± 3.2 and mortality was 5.4 ± 0.8. Herd turnover rates (LSMeans ± SE) were 24.6 ± 4.6 and 29.0 ± 4.6, and mortality rates were 5.8 ± 1.2 and 5.0 ± 1.2 in CV and NV barns, respectively. There were no differences between the 2 systems. Top 3 reasons for cattle to die on farm were sickness (33.6 ± 0.4), metabolic disease (9.5 ± 0.03), and injuries (8.6 ± 0.02) with no differences between CV and NV barns. Top reasons to be sold from the herd were low production (10.3 ± 0.1), mastitis (9.6 ± 0.1) and reproduction (8.6 ± 0.1). Cows housed in NV barns were more likely to be sold due to low milk production (21.9 ± 0.1 vs. 12.9 ± 0.1; $P < 0.001$) than cows housed in CV barns. The CV barns reported selling more animals due to reproductive problems (16.0 ± 0.1 vs. 7.6 ± 0.1; $P < 0.001$) and mastitis (10.2 ± 0.1 vs. 6.0 ± 0.1; $P = 0.02$) than NV barns, respectively. Based on these results, CV and NV barns appeared similar for mortality and turnover rates.

Key words: dairy cattle, mortality, turnover

781 Mortality and herd turnover rates in dairy herds utilizing recycled manure solids for bedding freestalls. A. W. Husfeldt*, M. I. Endres, J. A. Salfer, and J. K. Reneau, *University of Minnesota, St. Paul.*

The objective of this study was to evaluate mortality and herd turnover rates in Midwest dairy herds utilizing recycled manure solids in deep bedded or mattress based freestalls. The study included 34 commercial dairy operations with herd sizes ranging from 100 to 3700 lactating cows. Forty 5 percent of the herds had mattresses and 55% had deep bedded stalls. Sold and died events were examined. Herd turnover rate was calculated as the number of animals that were sold or died during the year, divided by the average herd size. Mortality rate was calculated as the number of animals that died divided by average herd size. Overall mortality rate (mean ± SD) was 8.2 ± 3.1%. Deaths were categorized as mastitis, injury, lameness, euthanasia, pneumonia, and miscellaneous or unknown reasons. Main causes of death were miscellaneous or unknown reasons (63.6 ± 15.5), injuries (15 ± 8.9), and mastitis (12 ± 6.9). Overall herd turnover rate was 38.2 ± 6.9%. Reasons for turnover were categorized as injury, low production, mastitis, reproduction, udder conformation, feet and legs, sick, aborted, dairy, and miscellaneous or unknown reasons. Main reasons for turnover were mastitis (19.5 ± 10.9), reproduction (15.8 ± 10.2), and low production (14.3 ± 14.8). Turnover rate during the first 60 DIM was 9.9 ± 3.4%. There was no association between stall surface and mortality. Mortality rates (LSmeans ± SE) were 8.2 ± 0.7 and 8.6 ± 0.9 for deep bedded and mattress herds, respectively. Herd turnover rates were 37.2 ± 1.7 and 38.6 ± 1.9 for deep bedded and mattress herds, respectively. No association was found between turnover rates and stall surface. There was a trend for stall surface to be associated with voluntary (dairy) and involuntary (other) reasons for removal ($P = 0.054$). Voluntary turnover was 16.7 ± 2.5 and 8.8 ± 3.1 for deep bedded and mattress, respectively. Sixty DIM turnover rates were 10.4 ± 0.09 for deep bedded herds and 9.5 ± 1.0 for mattress herds. Stall surface was not associated with 60 DIM turnover rates. Results indicate stall surface had a relatively minor association with mortality and turnover rates in dairy herds utilizing recycled manure solids as bedding.

Key words: mortality, herd turnover, manure solids

782 Effectiveness of fly traps and baits at three primary fly sites on Florida dairy farms. M. E. Sowerby*[1] and J. A. Hogsette[2], [1]*University of Florida, Gainesville,* [2]*USDA-ARS-CMAVE, Gainesville.*

The house fly, *Musca domestica* L., is a ubiquitous pest on dairies. They can cause production losses from fly worry, disperse from farms to nearby towns, transmit diseases like pinkeye, and carry pathogens like *E. coli* O157:H7. The calf raising, commodity barn/feed storage, and feeding barn areas tend to attract and support large house fly aggregations on dairies. If flies could be successfully managed in these areas, farm-wide populations might be significantly reduced. Traps or toxic baits would be the best management tools because house flies are resistant to most pesticides applied as space and residual sprays. Our objective was to evaluate the relative effectiveness of a trap, a toxic scatter bait and a toxic bait strip for house fly managment in high-density fly congregation areas. Three dairies having the aforementioned fly aggregation areas were selected. Treatments were the Farnam Captivator trap (baited with Terminator Fly Attractant), the QuickStrike Bait Strip (nithiazine 1% AI) and QuikStrike Scatter Bait (dinotefuran 0.5% AI). Treatments were placed, one at each area, on all 3 dairies according to a pre-arranged random rotational schedule. After 24 h, flies were counted and devices were rotated to the next area. A complete rotation constituted one replication in a 3 × 3 Latin square design and a test was composed of 6 replications. Data were normalized with $\log_{10} + 1$, subjected to ANOVA, and means separated with the Ryan-Einot-Gabriel-Welsch Multiple Range Test ($P < 0.05$). The mean numbers of flies captured by treatment were: Captivator trap (1624)>QuikStrike Scatter Bait (138)>QuikStrike Strip (95). The mean numbers of flies captured at each area, treatment overlooked, were: commodity barn/feed storage area (1050)>the calf pens (558)>the feeding barn (249). The Captivator trap captured significantly more flies than the bait strip and the scatter bait at all areas. Thus the Captivator trap is recommended for management of flies at the three fly aggregation areas, and the most attractive area, based on our research, is the commodity barn/feed storage area.

Key words: house flies, bait strips, dairy farms

783 Chemical and bacteriological characteristics of digested, composted, and separated raw manure solids prior to use as freestall bedding. A. W. Husfeldt*, M. I. Endres, K. A. Janni, J. A. Salfer, and J. K. Reneau, *University of Minnesota, St. Paul.*

The objective of this study was to investigate the chemical and bacteriological characteristics of digested, composted, and separated raw manure solids. The study included samples of recycled manure solids from 38 Midwest dairy herds collected before use as freestall bedding. Twenty-five composite samples of digested solids, 9 samples of separated raw solids, and 4 samples of composted solids were collected once and analyzed for chemical and bacteriological characteristics. Chemical analyses included moisture, pH, fiber, fat, non-fiber carbohydrates (NFC), ash, nitrogen, phosphorous, potassium, carbon, and C:N ratio. Bacterial counts (colony forming units per mL) of bacillus, coliforms, environmental streptococci, staph species, and yeasts were performed. Moisture content (LSmeans ± SE) was different ($P <$ 0.001) between composted (60.3 ± 1.6)and both digested (72.9 ± 0.7) and raw (72.6 ± 1.1) solids. The pH, nitrogen, phosphorous, NFC, and total ash content were different ($P < 0.001$) between digested and separated raw solids. The pH was 9.3 ± 1.0 for digested solids and 8.9 ± 1.0 for raw manure solids. Nitrogen (%) was 1.50 ± 0.03 and 1.17 ± 0.05% for digested and raw solids, respectively. Phosphorus (ppm) was 5,451 ± 240 for digested and 2,321 ± 415 for raw solids. The NFC (%) was 3.8 ± 0.26 for digested and 6.2 ± 0.45 for raw solids. Ash (%) was 10.2 ± 0.32 and 8.1 ± 0.56 for digested and raw solids, respectively. Differences in coliform ($P < 0.001$) and environmental streptococci ($P =$ 0.002) populations were also found between digested and raw manure solids. Log-transformed coliform bacterial counts in digested and raw solids were 4.0 ± 0.4 and 9.4 ± 0.7, respectively. Coliforms were not found in composted solids. Environmental streptococci counts were 9.4 ± 0.7 in digested solids and 14.8 ± 1.2 in raw solids. Other minor differences between digested and composted manure solids as well as composted and separated raw manure solids were also observed. These results indicate that anaerobic digestion of manure may affect the characteristics of recycled solids before use as bedding for freestalls.

Key words: recycled manure solids, freestall bedding, bacterial counts

784 Chemical and bacteriological characteristics of digested, composted, and separated raw manure solids used as freestall bedding. A. W. Husfeldt*, M. I. Endres, K. A. Janni, J. A. Salfer, and J. K. Reneau, *University of Minnesota, St. Paul.*

The objective of this study was to investigate the chemical and bacteriological characteristics of digested, composted, and separated raw manure solids used as freestall bedding. The study was conducted on 38 dairy farms in the Midwest. Composite bedding samples from each lactating pen and one dry pen collected at one visit were analyzed for bacterial counts of bacillus, coliforms, environmental streptococci, staphyloccocus species and yeasts. Total number of samples for bacterial analysis included 199 digested, 38 composted, and 71 separated raw solids. Subsamples from high and low production groups as well as first parity and dry cow groups were analyzed for moisture, pH, NDF, non-fiber carbohydrates (NFC), ash, N, C, and C:N ratio. Total number of samples for chemical analysis included 85 digested, 14 composted, and 29 separated raw solids. Bedding moisture adjusted for bedding frequency (LSmeans, % ± SE) of composted solids was 40.0 ± 1.1. Composted solids moisture was different ($P < 0.001$) than digested (54.3 ± 1.0) and raw (56.5 ± 1.1) solids. The NDF (%) in digested solids (70.6 ± 0.55) was different than composted (75.0 ± 1.1, $P < 0.001$) and raw solids (73.1 ± 0.9, $P = 0.012$). The NDF content was not different between composted and raw solids. Ash (%) in composted solids was 7.7 ± 1.1 and was different than digested (12.3 ± 1.0, $P < 0.001$) and raw solids (9.7 ± 1.1, $P = 0.024$). In addition, ash content was different between digested and raw solids ($P < 0.001$). Nitrogen (%) was different between raw and digested solids (1.7 ± 1.1 and 2.0 ± 1.0, respectively; $P = 0.001$). There were no differences among the bedding types for coliform counts. Environmental streptococci counts were different ($P < 0.001$) between digested and raw, and digested and composted solids; however, this was a minor biological difference. Environmental streptococci counts (log-transformed colony forming units per mL) were 14.1 ± 0.11, 15.2 ± 0.18, and 15.4 ± 0.24 for digested, raw, and composted solids, respectively. In conclusion, we found only minor differences among digested, composted, and separated raw manure solids when used as bedding in freestalls.

Key words: bacterial counts, freestall bedding, manure solids

785 Temperature and humidity in cross-ventilated and naturally ventilated dairy barns in the upper Midwest. K. M. Lobeck*, M. I. Endres, S. M. Godden, and J. Fetrow, *University of Minnesota, St. Paul.*

The objective of this study was to describe barn temperature, humidity, and some measurements of cow comfort in low profile cross-ventilated barns (CV) compared with conventional naturally ventilated freestall barns (NV). The study was conducted on 12 commercial dairy farms in Minnesota and eastern South Dakota from January to December 2008. Herd sizes ranged from 400 to 1600 lactating cows. All herds had stalls bedded with sand. All NV barns used fans and soakers and all CV barns used evaporative cooling pads for heat abatement. Cow respiration rates were measured on 75 cows from the high production pen on each farm twice during the summer visit. Morning observation was the baseline respiration rate with the second observation taken a minimum of 3 h later in the afternoon. Temperature and humidity were collected hourly inside the facility with data loggers and from the nearest weather station for the entire year. Cow comfort index (CCI) was calculated as the number of animals lying down in the stalls divided by total number of animals touching a stall (lying, 2 feet in a stall, or standing with all 4 feet in the stall) and it was measured 3 times during each visit. The CV barns were warmer in the winter than the NV barns (3.9 vs. −1.7°C; $P < 0.001$). There were no differences in temperature between CV and NV barns in spring, summer, or winter. However, summer temperature-humidity index (THI) was lower in CV than NV barns (65.9 vs. 68.5; $P < 0.001$). Respiration rates were not different between CV and NV barns (55.6 vs. 56.6 breaths/min, respectively). Outside THI was similar for CV and NV barns during respiration rate measurement (73.8 vs. 73.6). Each 1 unit increase in outside THI increased respiration rates by 0.26 ± 0.09. Overall CCI were 84.2, 85.2, 79.7, and 84.6 for winter, spring, summer, and fall, respectively. The CV barns had higher CCI than NV barns (84.2 vs. 75.3; $P = 0.047$) during the summer, with no differences in the other seasons. In conclusion, CV barns had greater CCI and lower THI during the summer than NV barns (possible indicators of improved cow comfort) although respiration rates did not differ.

Key words: temperature, cross-ventilated barn, humidity

786 A one-year comparison of house fly and stable fly populations at three different types of dairy facilities in the Texas Panhandle. S. L. Swiger*[1], K. J. Lager[2], T. R. Bilby[1], B. R. Henderson[2], R. G. S. Bruno[2], and E. R. Jordan[3], *[1]Texas AgriLife Extension and*

Research, Stephenville, [2]Texas AgriLife Extension, Canyon, [3]Texas AgriLife Extension and Research, Dallas.

Throughout the years work has been done to construct the most efficient and economical dairy facility that increases production, eliminates health issues and disease risks. Three main types of dairy facilities are currently utilized in the United States; open dry-lot, free-stall and cross ventilation. Each style of facility has a unique impact on the fly populations on and around a dairy. The objective of this study was to determine the effect of 3 different dairy facility types on number of house flies and stable flies present during summer. House flies were collected with 4 dinotefran baited scatter bait traps and stable flies were collected with 4 Olson sticky traps within each of the 3 dairy facility types. The fly traps were placed throughout each facility and flies were collected weekly for 12 wks from May until August 2010. The 3 facilities were found to contain both house flies and stable flies. The open dry-lot barn had more ($P < 0.05$) stable flies (n = 18,067) than either the free-stall (n = 5,423) or cross ventilation barns (n = 1,130) and the free-stall barn had more ($P < 0.01$) stable flies than the cross ventilation barn. There were more ($P < 0.05$) house flies in the free-stall barn (n = 5,270) than the open dry-lot (n = 418) or cross ventilation barn (n = 2,438) and the cross ventilated barn had more ($P < 0.01$) than the open dry-lot. In conclusion, results show that using a cross ventilated barn reduced stable but not house fly populations compared with a free-stall or open dry-lot facility. Further studies are needed to assess the ability of different facility types to reduce the negative effects of different fly populations on dairy cattle.

Key words: dairy, house fly, stable fly

Ruminant Nutrition: Dairy: Minerals, Vitamins, and Other Stuff

787 Effect of sodium chloride intake on urea concentration in milk from dairy cows. J. W. Spek*[1], J. Dijkstra[1], J. J. G. C. van den Borne[1], and A. Bannink[2], *[1]Wageningen University, Wageningen, the Netherlands, [2]Wageningen UR Livestock Research, Lelystad, the Netherlands.*

A reliable indicator of nitrogen (N) excretion by dairy cattle is required to easily estimate N excretion on farm and to evaluate N excretion mitigation strategies. Milk urea nitrogen (MUN, mg/dl) has been shown to be positively correlated to excretion of urea and total N in urine in dairy cows. However, a significant proportion of variation in urine N-excretion (UN) remains unexplained by MUN content. In the present experiment, it was hypothesized that urine volume is affected by dietary salt intake and affects MUN content and the relationship between MUN and UN. Twelve lactating Holstein Friesian cows (milk production 25.4 ± 2.53 kg/d and 207 ± 41.3 DIM), of which 4 were fitted with catheters in the urine bladder, were randomly assigned to 4 dietary levels of salt (3, 9, 13, and 18 g Na/kg DM) in a 4 × 4 Latin square design. Cows were fed at 95% of ad libitum feed intake to ensure equal N-intake across dietary levels of Na. During the last 2 d of each one-week treatment period, milk was sampled and analyzed for MUN. Urine and feces of catheterized cows were collected quantitatively during the last 2 d of each treatment week. Urine was analyzed for total N and urea, and feces for total N and DM. Data were analyzed with the PROC MIXED procedure of SAS in which the blocking factors cow and period were included as random and fixed effects, respectively. Dry matter and N intake were 21.4 ± 1.24 kg/d and 522 ± 32.0 g/d, respectively, and equal across treatments. A significant negative linear correlation was found between intake of Na and level of MUN: MUN = 12.8 ± 0.44 - 0.70 ± 0.075 × 100 g Na/d. Based on the 4 catheterized cows, for every 100 g increase in Na consumption, a significant linear increase was found for urine production (13.7 ± 0.87 L/d), UN (5.3 ± 2.07 g/d) and urinary non-urea N excretion (4.2 ± 0.57 g/d). However, excretion of urinary urea N was unaffected (1.2 ± 1.62 g/d) by Na intake level. It is concluded that salt intake level affects MUN without an effect on urinary urea excretion. Level of salt intake should hence be considered when using MUN as an indicator of urinary urea excretion or UN.

Key words: milk urea nitrogen, urinary nitrogen excretion, sodium chloride

788 2010 National survey of barriers related to precision phosphorus feeding. J. H. Harrison*[1], R. James[2], C. Stallings[2], E. Whitefield[1], M. Hanigan[2], and K. Knowlton[2], *[1]Washington State University, Puyallup, [2]Virginia Tech, Blacksburg.*

A national survey was conducted in cooperation with ARPAS to document barriers related to phosphorus feeding. The electronic survey link was sent to all ARPAS members with a dairy emphasis. Approximately 130 respondents replied to 8 questions. 53% of respondents indicated that balancing for ration P was a priority (rank of 7–10 out of 1–10 rank). 75.2% of respondents indicated that they perceived current NRC recommendations for P as adequate, while 8.5% indicated that they are too low, and 16.3% indicated they are too high. When asked to identify the most challenging aspect of reducing P in the diet, 54.8% indicated uncertainty of P content of feedstuffs, 36.8% indicated cost, and 9.6% indicated uncertainty of ration ingredients. 52 of approximately 130 respondents replied when asked if their recommendations were above those of NRC. They indicated: concern about negative impact on metabolic diseases (46.2%), mastitis (9.6%), foot problems (7.7%), heat detection efficiency (55.8%), conception rate (63.5%), and retained placenta (23.1%). Most respondents (99%) indicated that they had reduced their recommendations for dietary P content over the last 3 to 5 years. When asked what information is needed to assist them in ration formulation for P, 69.7% indicated availability of P from different sources; 56.3% indicated updated requirements for maintenance, production and reproduction; and 45.4% indicated that more documentation was needed that current NRC recommendations for P are adequate. Additional questions were asked about target level of P in the key production groups, and what sources of P were included in diets. Information collected from the survey indicate that more progress needs to be made to assure the P availability from feedstuffs and assure that no impairment of reproduction would be expected from feeding NRC recommended levels of P.

Key words: phosphorus, feed management, nutrition

789 Evaluation of ruminally protected niacin on thermal regulation and productivity of high-producing dairy cows during summer heat stress. S. R. Wrinkle*[1], P. H. Robinson[1], and J. E. Garrett[2], *[1]Department of Animal Science, University of California, Davis, [2]Quali Tech Inc., Chaska, MN.*

Heat stress resulting in animal production losses costs the dairy industry hundreds of millions of dollars annually in the USA, especially in southern areas such as California. Niacin as a dietary supplement typically induces "flushing," or increased blood flow to the skin, causing a decrease in core body temperature which has been shown to reduce heat stress in dairy cows. Our objective was to determine if feeding ruminally protected niacin (RPNi) is effective in alleviating heat stress in dairy cows. Two 2x2 factorial experiments, each with 28 d periods, were conducted in the summer of 2010. In Expt. 1, 2 pens, each ~180 early lactation multiparity cows were used, and in Expt. 2, 2 pens of ~180 mid-lactation mixed parity cows were used. The basal total mixed ration, of 17% CP, 33% aNDF and 15% starch, was the same for all cows with the exception of RPNi added to RPNi diets. Treatment cows received 19 g RPNi/cow/d, estimated to deliver ~7 g of intestinally absorbable niacin/cow/d as determined by ruminal in sacco incubation. In Expt. 1, respiration rate (RR) and panting score (PS) were measured 4 times/d. RR was lower ($P = 0.02$) at 09:00 h, but not impacted at other times, while PS was lower ($P \leq 0.01$) at 04:30, 09:00 and 20:30, but not impacted at 16:30 h, in cows fed RPNi. Side udder (SU) and back udder (BU) temperatures did not differ at 14:15 or 22:15, but BU was lower ($P = 0.03$) at 06:00 h in cows fed RPNi. There was no difference in DM intake or milk and milk component yields, but milk fat % for RPNi cows was lower ($P < 0.01$). In Expt. 2, where PS, RR, SU and BU were not measured, DM intake and milk yield did not differ between treatments, and there were no differences in milk yield, or milk protein or lactose %. However, fat % was higher in RPNi cows ($P = 0.01$). While symptoms of heat stress were reduced for cows fed RPNi, the increase in cow comfort did not result in increased productivity. Differences in the milk fat % response between stages of lactation suggests that niacin affects metabolism differently if cows are in negative (early lactation) or positive (mid-lactation) energy balance.

Key words: niacin, heat stress, milk fat

790 Effects of feeding a rumen protected lysine (AjiPro-L) from calving to the fourth week of lactation on production of high-producing dairy cows. J. E. Nocek*[1], T. Takagi[2], and I. Shinzato[2], *[1]Spruce Haven Farm and Research Center, Auburn, NY, [2]Ajinomoto Co., Inc., Tokyo, Japan.*

Sixty-five multiparous Holstein cows were used to examine the effects of feeding a rumen protected lysine (AjiPro-L, Ajinomoto Co., Inc., Japan) from calving to the 4th week of lactation on production of dairy cows. Cows were balanced across treatments based on the previous ME305 and body condition score at 21 d pre-partum and assigned to 3 dietary treatments. The experimental diets contained either 0 (Control), 100 or 200g/d of AjiPro. Cows were individually housed in tie-stalls and were fed the experimental diets for 4 weeks from calving, and all cows were moved to free-stall barns and fed a common lactation TMR from 5th to 12th week of lactation to see the carry-over effects. Individual milk yield was measured daily, and milk component contents were measured weekly throughout the study. Individual dry matter intake (DMI) was measured daily during the first 4 weeks of lactation. During the supplementation period, mean yields of milk, FCM and fat were significantly higher ($P < 0.01$) for cows receiving 100 or 200g AjiPro than Control, but neither DMI nor milk protein yield differed between treatments. Milk production efficiency was significantly higher for cows receiving 200g AjiPro than the other 2 treatments. In the post-supplementation period, 100g AjiPro resulted in significantly higher yields of FCM and fat than 200g AjiPro with Control being intermediate. Protein yield was higher ($P < 0.01$) for Control and 100g AjiPro than 200g AjiPro. MUN was higher for 200g AjiPro ($P < 0.05$) than Control. In this study, 100g AjiPro supplementation resulted in increased milk production during the supplementation period and showed a numerical tendency for positive carry-over effects in the post-supplementation period compared with Control, whereas an over-feeding (200g AjiPro) had slight adverse effects in the post-supplementation even if it resulted in the best performance during the supplementation period. These results suggest that optimal lysine supplementation maybe involved with triggering nutrient (both energy and protein) partitioning in early lactation cows.

Key words: rumen protected lysine, milk production, early lactation

791 Feeding a C16:0-enriched fat supplement increased the yield of milk fat and improved feed efficiency. A. L. Lock*, C. L. Preseault, K. E. DeLand, and M. S. Allen, *Michigan State University, East Lansing.*

Previous work has indicated that dietary palmitic acid (C16:0) may increase milk fat yield over and above expected values either without additional fat supplementation or compared with other dietary fatty acids. The effect of dietary C16:0 on feed intake, yield of milk and milk components, and feed efficiency was evaluated in an experiment with a crossover arrangement of treatments with 25 d periods. A fermentable starch challenge (FSC) on the last 4 d of each period was utilized as a split-plot within period. Sixteen midlactation Holstein cows (249 ± 33 DIM) were assigned randomly to treatment sequence. Treatments were either a C16:0-enriched (~85% C16:0) fat supplement (FAT, 2% DM) or a control diet (CON) containing no supplemental fat. Diets containing dry ground corn grain were fed from d 1 through 21 of each period. On the last 4 d of each period, dry ground corn was replaced by high-moisture corn grain on an equivalent DM basis. Response variables were averaged for d 18 to 21 for the dry corn diet and d 22 to 25 for the FSC. There were no treatment effects on milk yield (32.0 kg/d) or milk protein yield (1.1 kg/d). FAT increased milk fat concentration from 3.88 to 4.18% and fat yield from 1.23 to 1.33 kg/d compared with CON ($P < 0.001$). Consequently FAT increased 3.5% fat-corrected milk yield by 1.7 kg/d ($P < 0.05$). FAT decreased DMI by 0.7 kg/d ($P < 0.05$) and increased feed efficiency (3.5% fat-corrected milk yield/DMI) 7.5% ($P < 0.001$) compared with CON. The FSC did not affect milk fat, DMI or feed efficiency. The increase in milk fat yield by FAT was entirely accounted for by an increase in C16:0 output into milk. Data demonstrates the potential for a dietary C16:0-enriched fat supplement to improve milk fat concentration and yield as well as efficiency of feed conversion into milk. Further studies are required to verify and extend these results and to determine whether responses are similar across different diets and levels of milk production.

Key words: palmitic acid, milk fat, feed efficiency

792 Characterizing the effect of Amaferm on forage NDF digestibility. J. E. Nocek*[1] and H. Jensen[2], *[1]Spruce Haven Farm and Res. Ctr, Auburn, NY, [2]Biozyme Inc., St Joseph, MO.*

Amaferm is a fermentation extract shown to stimulate ruminal bacterial and anaerobic fungal growth and enzymatic activity. Our aim was to evaluate the effect of Amaferm on extent and rate of ruminal NDF digestion from a random samplings of corn silage, haylage and hay . Samples (~75 each) of corn silage, haylage and hay of various NDF concentrations and digestibilities were subjected to in situ digestion. Limited sample size restricted cow numbers and rumen residence times used. Two lactating, ruminally cannulated cows (40–120 DIM) were used to determine rumen digestibility: one received control diet only with no Amaferm, the other received the same diet with Amaferm. A standardization procedure with grass hay was used to evaluate cow variation before and after Amaferm supplementation. Rumen polyester bag residence times were 12, 24 and 36 h which allowed time point calculation of rumen NDF disappearance and linear digestion rate determination. Grass hay DM digestibility was not ($P > 0.10$) affected by cow in time. Twelve and 24 h of ruminal incubation of corn silage demonstrated no difference in residual NDF between Control and Amaferm. However at 36 h, Amaferm supplementation resulted in a 8.2% increase ($P < 0.01$) in NDF disappearance, which translated into an increased (15.2%, $P < 0.01$) rate of corn silage NDF digestion. Amaferm supplementation had little effect on Hay NDF digestion at 12 h, however, at 24 h of ruminal exposure, NDF disappearance was higher (11.5%, $P < 0.05$) with Amaferm supplementation. Haylage NDF disappearance at 12, 24 and 36 h was increased by 13.3, 12.6 and 10.0% respectively with Amaferm supplementation. Linear NDF rate of haylage digestion was 16.6% higher ($P < 0.01$) with Amaferm supplementation compared with Control. In summary, Amaferm affected NDF digestibility differently for each forage type evaluated. All forage types tested experienced a significant enhancement in extent of NDF digestibility at some point through 36 h of ruminal exposure when supplemented with Amaferm.

Key words: forage, fermentation extract, NDF digestibility

793 Methionine availability to dairy cows when added to mechanically extracted soybean meal with soy gums. D. W. Brake*[1], E. C. Titgemeyer[1], B. J. Bradford[1], J. F. Smith[1], and C. A. Macgregor[2], *[1]Kansas State University, Manhattan, KS, [2]Grain States Soya Inc., West Point, NE.*

We investigated availability of supplemental DL-Met fed to dairy cows when added to soy gums before application to a mechanically extracted soybean meal (meSBM) at the time of manufacture. Holstein

cows (25) were assigned to treatment sequences in 5 replicated 5 × 5 Latin squares with 14-d periods. Cows were fed 1 of 5 treatment diets as TMR supplemented with 0, 2.5, or 5 g/d metabolizable Met provided as a commercially available ruminally protected (RP) Met (MetiPEARL brand, Kemin Industries, Des Moines, IA) or with 4.2 or 8.4 g/d DL-Met added as part of a meSBM product. For the diets providing added Met from meSBM, a product containing 0.3% Met replaced one-half or all of a meSBM product containing no added Met (Soy Best®, Grain States Soya, Inc., West Point, NE). Diets were designed to be first-limiting in metabolizable Met and contained (DM) 14.3% CP. The diet without added Met was estimated to deliver 6.53% of MP as Lys and 1.76% of MP as Met. Diets contained (DM): 35% ground sorghum grain, 25% corn silage, 15% alfalfa hay, 10% soybean hulls, 9% meSBM, and RP-Lys (LysiPEARL brand, Kemin Industries) to provide 0.055% of diet DM as metabolizable Lys. Plasma Met and Ser concentrations increased with supplemental RP-Met ($P < 0.05$), but were not affected by Met supplied in meSBM. Yields of milk (45 kg/d), protein, fat, and lactose were not different among treatments. Concentrations of milk protein were increased ($P \leq 0.05$) by RP-Met, and concentration of SNF tended to increase with RP-Met. Intakes of DM (25.4 kg/d) and N were not different among treatments nor were apparent digestibilities of DM or N. Milk N:N intake was not different among treatments. Increases in BCS were greater ($P < 0.05$) and N retention was numerically greater when Met was supplied by meSBM. Milk protein yield was not responsive to metabolizable Met supply, but based on concentrations of plasma Met and of milk protein there was little evidence to suggest that supplemental Met provided as meSBM markedly increased supply of metabolizable Met to dairy cattle. The unresponsiveness of milk protein yield may suggest our model was not optimal for assessing Met supply.

Key words: methionine, dairy, soybean meal

794 Effects of chromium propionate fed through the periparturient period and starch source fed postpartum on productive performance and dry matter intake of Holstein cows. R. J. Rockwell* and M. S. Allen, *Michigan State University, East Lansing.*

Holstein cows (n = 48) entering second or later lactation were used in a randomized block design experiment with a 2 × 2 factorial arrangement of treatments to determine production and dry matter intake (DMI) responses to chromium propionate supplementation throughout the periparturient period and starch source in the postpartum (PP) diet. Treatments were chromium propionate (KemTRACE Chromium Propionate, Kemin Industries, Cr–Pr, 8 mg Cr/cow/d) or control (CONT, ground corn) top–dressed (20 g/d) daily at feeding from 28 ± 3 d before expected parturition until 28 ± 3 d PP, and dry corn (DC) or high moisture corn (HMC) in diets fed from parturition until 28 ± 3 d PP. Cows were fed a common diet from 28 ± 3 to 84 ± 3 d PP. Data was analyzed using a mixed model with repeated measures. No treatment effects were detected for daily DMI from parturition until 28 ± 3 d PP, but an interaction of chromium, corn and days PP was detected ($P = 0.06$) when cows were fed a common diet. An interaction among chromium, starch source, and week was detected for 3.5% fat–corrected milk (FCM, $P = 0.07$) from parturition until 28 ± 3 d PP. The Cr–Pr/HMC and CONT/DC treatments resulted in consistent and higher (54.9 kg/d) and lower (49.3 kg/d) FCM, respectively throughout the period compared with the other treatments in which FCM decreased over time. After treatment ceased, Cr–Pr tended to increase milk yield (55.4 vs. 51.9 kg/d, $P = 0.09$) and FCM (52.0 vs. 48.3 kg/d, $P = 0.108$) from 28 ± 3 to 84 ± 3 d PP. There was also an interaction of starch source by week for FCM ($P < 0.001$) with FCM increasing throughout the period for DC, but decreasing for HMC; yield of FCM was greater for HMC compared with DC at 42 ± 3 d PP (57.0 vs. 48.0 kg/d), but lower at 84 ± 3 d PP (48.3 vs. 49.3 kg/d). No main effects of treatment or interactions with time relative to parturition were observed for body weight or body condition score. Cr–Pr interacted with starch source throughout the periparturient period in PP diets and days PP to affect production responses that were also affected after treatment application ceased.

Key words: peripartum, starch, chromium propionate

Small Ruminant Symposium: Advancements in Genetic Selection of Small Ruminants for Performance and Parasite Resistance

795 Advancements in genetic selection of small ruminants for performance and parasite resistance: Introduction and purpose. K. Andries*, *Kentucky State University, Frankfort.*

Small ruminant production has steadily increased over the past 10 to 15 years. Most of this increase has been in the area of meat goat production and started with the introduction of the Boer breed in the 1990 ′s. This growth has led to an increased need for basic and applied research into meat goat production. There has been an increasing need for information on genetics and breed differences in meat goats and re-evaluation of many sheep breeds due to changes in selection focus and breed types being used. There is a vast amount of genetic information available on cattle; however, little information is available for sheep and little to no information is currently available for goats, especially meat goats. The cattle industry has been able to utilize research in genetics to make tremendous advancements in productivity in the past 30 years. The Sheep Improvement Program has also moved forward using similar information through the calculation of flock expected progeny differences. Dairy goats also have genetic selection information available through the national dairy improvement program. However, meat goats do not have these types of programs readily available today. The use of molecular genetics as seen in the beef industry demonstrates the potential for small ruminants to find major genes for economically important traits. The sheep industry has implemented some of this research already but research in the goat industry is lagging behind. The one trait that seems to be achieving more research than others is parasite resistance. These efforts will play a major role in the future of small ruminant production. The purpose of this symposium is to show some of the history of genetic research and use of the information in other species and in small ruminants today. The hope is that this will help inspire future research and extension efforts in small ruminants to move both sheep and meat goats into more use advanced animal breeding methodology to improve production in these industries.

Key words: small ruminant, genetic

796 Genetic evaluation: Lessons learned in the beef industry. J. K. Bertrand*, *University of Georgia, Athens.*

The goal of the presentation is to provide a history of US beef cattle genetic evaluation programs and the lessons learned from their implementation. Initially, visual appraisal was to sole criteria for selection of beef cattle. In the 1950s and 60s, State Beef Cattle Improvement Associations and Performance Registry International were formed for the collection of objective phenotypic information. In 1968, The Beef Improvement Federation was formed to provide a framework for standardized record collection and systematic genetic evaluation procedures. During the late 1960s, beef breed associations became the "keepers" of phenotypic and pedigree information in the US During the 1970s and 80s, the beef breed associations began partnerships with Land Grant Universities, where the universities supplied the research and development and also conducted the genetic evaluations for the breed associations in return for grant dollars. In the end, this model was not sustainable due to insufficient funding to cover personnel and equipment. The National Beef Cattle Evaluation Consortium was formed in 2001 with a federal special grant that provided funds to the universities involved in servicing beef genetic evaluation programs to help supplement costs over and above those provided by the breed associations. Beginning in 2007, there was movement toward universities divesting themselves from the servicing of genetic evaluations to allow them to concentrate solely on research. Entities have formed or are still forming, usually at a breed association, to conduct genetic evaluations using the software/methodology provided by universities. Based on the experience of the beef industry, a sustainable industry-wide genetic evaluation program is dependent on 1) use of common sires across herds to provided the proper data infrastructure, 2) a system that allows for the collection of on-farm performance records, 3) a centralized system that maintains both phenotypic and pedigree information, and now genomic information, 4)) a national organization that provides leadership for record and procedure standardization, 5) a well funded group of research scientists and servicing personnel.

Key words: genetic evaluation, beef cattle

797 National Sheep Improvement Program's current impact and future potential. D. F. Waldron*, *Texas AgriLife Research, San Angelo.*

Since implementation in 1987 the US National Sheep Improvement Program (NSIP) has evolved to take advantage of developments in technology. The methods used in NSIP make use of all available performance records along with pedigree information to predict genetic merit for economically important traits. Statistical methods employed in NSIP were first developed for, and applied to, dairy cattle and later to beef cattle and other meat-producing livestock. Beef cattle breeders in the US increased adoption rates of the technology through the 1980s and 1990s. The US sheep industry's use of NSIP is expanding. Although NSIP is available to all breeds of sheep, many of the NSIP participants are from a small number of breeds. Targhee, Suffolk, and Polypay are the breeds that have had the most NSIP participation. Estimates of genetic trends are indicators of the impact of using NSIP for selection decisions. The impact of NSIP in the US sheep industry has been limited by low adoption rates. Costs of performance recording, perceived value of genetic evaluation, and lack of a consensus, within a breed, on breeding objectives are all factors that have limited the use of NSIP in the US sheep industry. Adoption of a national genetic improvement program by US sheep breeders has lagged behind that of US beef breeders. An adaptation of NSIP was developed first for Boer goats (Boer Goat Improvement Network) and then for Kiko goats. Participation in NSIP by breeders of meat-producing goats is lower than it is for sheep. As the impact from use of NSIP becomes more evident, participation is expected to increase. Recently implemented NSIP evaluations for fecal egg count as an indicator trait for resistance to parasites may lead to increased participation. Advances in genomic evaluation, as implemented in dairy cattle genetic evaluation, may be feasible to use for small ruminants in the future. However, the substantial numbers of recorded animals required to develop effective genomic evaluations are not currently available. If breeders of small ruminants will realize the potential of genomic evaluation, increased participation in NSIP is necessary, so that the records are available.

Key words: sheep, goats, genetic improvement

798 Advancements in genomics: Application and potential for small ruminant research. P. K. Riggs*, *Texas A&M University, College Station.*

Genome science and genomic tools have led to revolutionary biological breakthroughs that dramatically affect and continue to advance animal agriculture. In a short period of time, costs have fallen while technology has improved to make possible the reality that assembled genome sequences can be produced for any species of interest, particularly agricultural species. Research focused on small ruminant genomes will be able to make rapid progress by leveraging resources, tools, and knowledge gained from bovine and other species' genome projects. The cattle and sheep genome research consortia have recently completed high density gene maps, genome assemblies, haplotype maps, and related analyses. Research in goat genomics can take advantage of comparative genome similarity, as well as lessons learned from bovine and ovine studies, to make progress toward development of caprine-specific genome tools. Currently, several efforts are underway for construction of radiation-hybrid gene maps, SNP discovery, and genome sequence assembly. All of these projects present challenges for production of high quality data, storage and management of data, and bioinformatic analyses, but goat genome research can potentially move quickly as a result of previous findings. The future availability of genomic resources for goat provides great opportunity for application in the goat industry.

Key words: genomics, goat, molecular genetics

799 Sheep and goat genetic resources: Recent findings and potential for future development. H. Blackburn*, *National Animal Germplasm Program, National Center for Genetic Resources Preservation, Agricultural Research Service, Ft. Collins, CO.*

Genetic variability underpins the ability to manipulate sheep and goat populations for increased productivity and profitability. An assessment of the genetic variability of 28 sheep and 5 goat breeds using microsatellite marker panels has been made. The sheep analysis was extended to determine genetic distance and variation for US vs 5 Kazakhstan (KAZ) breeds. For US sheep the average number of alleles per locus and heterozgousity varied (3.7 to 8.2 and 0.42 to 0.65, respectively) suggesting some breeds (Rambouillet, Suffolk, Polypay, Dorper) possess substantial genetic variability for utilization. Nei′s genetic distances (GD) for US and KAZ breeds generally showed small genetic distances among KAZ breeds and moderate to large GD when compared with US breeds. The greatest GD was among US breeds. Analysis of Angora (AG), Spanish (SP), Myotonic, Boer, and LaMancha goat breeds showed high levels of heterozygousity (0.58 – 0.73) and large GD (0.21 – 0.57). The SP and AG breeds have undergone contractions in population sizes but ranked highest for genetic diversity measures. For sheep and goats these results suggest US breeds have substantial neutral genetic variability which might translate into important variability for traits of interest. But, to fully utilize genetic diversity at the genomic level or via quantitative methodology, development of substantial phenotypic databases that contain economically relevant data in addition to pedigree information must be initiated and utilized. Employing such databases will facilitate combining phenotypic and genomic information; which in turn will provide producers across breeds with an opportunity to improve sheep and goat performance and profitability.

Key words: sheep, goats, genetic resources

Teaching/Undergraduate and Graduate Education Symposium: Adapting Our Teaching to Meet Current and Emerging Societal Needs

800 Effecting change in teaching and learning in the agricultural sciences. R. Kirby Barrick*, *University of Florida.*

Two recent reports provide insight regarding how teaching and learning in the agricultural sciences should and must keep pace with changes in society. The National Research Council (NRC) report (2009) on Transforming Agricultural Education for a Changing World and the Academic Programs Section (APS), Board on Agriculture Assembly of APLU report on Human Capacity Development (May 2009) serve as a call to action to meet the challenges of global competitiveness. The NRC report outlines 9 recommendations for change, and the APS publication offers recommendations to achieve 4 strategic goals for preparing the next generation of scientists and the agricultural workforce. Implications for action center on the following major areas: strategic planning, introductory courses, broadening the undergraduate student experience, faculty development, rewarding teaching, partnerships with other colleges and universities, connecting with K-12 education, partnerships with stakeholders, integration of teaching, research and outreach, doctoral education, recruitment and retention of students, and the utilization of technology. This session will attempt to place in context the recommendations of 2 major national studies with the initiatives of agencies such as USDA/NIFA and the National Science Foundation. Implications to consider in reviewing and updating teaching and learning in both undergraduate and graduate education will be shared with participants for further discussion and potential action in departments and colleges throughout the country.

Key words: teaching and learning, undergraduate education, graduate education

801 Perspectives on using values-based communications as a tool for preparing animal science students to address consumer trust issues challenging the animal industry. J. L. Garrett*, *JG Consulting Services LLC, Dowling, MI.*

Consumer choices and perceptions have a profound impact on global food production, supply and policy. Yet, criticism of animal agricultural practices by national and social media continues to erode consumer trust in the animal industry. Preparing Animal Science students to communicate facts, skills and competence is important in minimizing this decline in trust. However, research shows that communications demonstrating values are 5 times more important in building consumer trust than competence alone. The objectives of this presentation are to: 1) discuss current consumer attitudes and trust research specific to food and agriculture, 2) compare values-based communications with traditional approaches, 3) review and discuss values-based communications learning outcomes with dairy and crop farmers over the last 2 years, and 4) share literature and experiential based best practice considerations for incorporating values-based communications into the animal science curricula for better preparing graduates for success in a consumer-driven economy.

Key words: teaching, values-based communications, consumer trust

802 Course and activities based learning teams: A method of enhancing the first-year university experience. M. D. Kenealy*, *Iowa State University.*

In 1995, under the direction of the Center for Excellence in Learning and Teaching (CELT), Iowa State University (ISU) began testing the concept of course-based learning teams (LTM) with the goal of enhancing the first year experience of students, improving academic performance, and increasing retention rate. The Department of Animal Science (AnS) joined the university effort and placed approximately one-third of freshman students in course-linked LTM's. Students were grouped in teams based upon species interest and level of academic achievement during high school. A typical AnS LTM included linking AnS orientation, introductory AnS, introductory biology, and English composition for a group of 13 students. Faculty in the courses exchanged texts and syllabus materials with the linked English lecturer so that students could write about science topics and see the connections in their learning activities, thereby avoiding the silo concept of education. Additionally, each AnS LTM was assigned an upper-class student mentor and an academic advisor to guide additional team activities, such as study sessions, industry visits, and participation in club activities. As a program incentive, competitive grant monies were available from CELT to compensate student mentors and support LTM programming. Animal Science faculty used the programming grant monies to sponsor field trips to industries and organizations to introduce LTM members to potential internships and careers. Over 15 years, average first year to second year retention rate for ISU was 8 percent higher (89 vs 81 percent) for LTM students versus control groups of non-LTM students. Average 6 year graduation rate was 12 percent higher (74 vs 62 percent) for the LTM students. For FY2010, AnS freshman average cumulative grade-points were: linked-course LTM's: 2.96 (4.0 scale); non-course-linked LTM's: 2.91; non-LTM students: 2.52. Comparison group surveys validated that LTM students had higher satisfaction and engagement with their department and ISU at the end of their first year at the university.

Key words: learning teams, graduation rate, student retention

803 Innovative and effective practices for student development—What are the difference makers? D. Mulvaney*, *Auburn University, Auburn, AL.*

Our animal and allied industries are confronted by a complex array of contemporary issues and problems and need a well-prepared workforce ready to address them. Educational programs in tertiary institutions need to persist in preparing students for life after graduation that: 1) enables them to innovatively solve problems that do not yet exist, and 2) present skills that are most highly demanded or coveted by employers. Are we utilizing available student development theory and data to intentionally prepare students for productive adaptive futures in a constantly changing, flat world? Development of the whole, well-rounded student is a complex process. While multiple theories surround evidence-based practices contributing to student development, the academy may not always incorporate programming insights found in a rapidly growing body of literature focused on growth and development of students. Learning and experiential outcomes for Animal Science curricula often transcend the classroom alone and include opportunities for development of life success skills, work experience, project-based experiential learning, leadership development, emotional intelligence, and social skills to name but a few. The National Summit on Higher Education in Agriculture combined with a National Academies Report on: The New Biology for the 21st Century: Ensur-

ing the United States Leads the Coming Biology Revolution, reinforce the importance of reexamining our approaches to student development and clearly identifying the difference makers. Of benefit to faculty, students and decision makers, this careful examination of theory and application of best practices for development of contemporary Animal Science students should lead to recommendations for strengthening learning environments which foster development of leaders and professionals essential for addressing emerging challenges of the day.

Key words: animal sciences, student development, best practices

804 Best practices in designing undergraduate research experiences in animal science curricula. C. Rosenkrans Jr.*, *University of Arkansas, Fayetteville.*

Experiential learning is an excellent method of facilitating student learning and includes a variety of techniques for student discovery of knowledge. Undergraduate research is an experiential learning technique that is well suited for motivated students who are interested in applying or extending a classroom concept. Identifying students that are a good "fit" in the mentor's research program is essential for successful undergraduate research programs. I have found that a personal interview is the most efficient method of determining if mutual research interests exist and if the student and mentor have compatible personalities, i.e., "fit." However, others prefer to assess "fit" by asking the student to write a brief research proposal before accepting the mentee. After a mentor-mentee match has been established it is incumbent on the mentor to: explain the ethics and importance of quality data collection; establish the learning experience and work expectations; design a challenging research project that can be completed by the student in a timely manner; ensure that supervision is encouraging and occurs in a timely manner; and complete the process by assisting the student in disseminating their results. Students at UofA have the opportunity for oral presentations at professional society meetings (ASAS, etc.), and local events sponsored by Gamma Sigma Delta. Publication opportunities include local undergraduate research publications (Discovery and Inquiry), departmental publications, and peer-reviewed journals. Undergraduates who successfully complete research projects have a more thorough understanding of Animal Science, and enhanced skills related to analysis, interpretation, and communication. In addition, students typically graduate with a greater connection to the department. Undergraduate research is an experiential learning technique that enhances the collegiate experience for our students, and integrates the teaching and research missions for a faculty member.

Key words: scholarship, student learning, integrated projects

805 Casting a line—Creating a national Scholarship of Teaching and Learning (SoTL) for animal sciences: Adapting to the gaps through SoTL and networking. M. A. Wattiaux*, *University of Wisconsin-Madison, Madison.*

In college classrooms both teaching and learning are inextricably linked, yet for the most part each continues to reside in different domains. The gap between what students actually learn and what they should learn was addressed when Schillo (1997; J. Anim. Sci. 75:950–953) drew a sharp contrast between indoctrination (claiming knowledge of scientific fact without critical evaluation) and education (ability to think analytically and make independent judgments about scientific claims). Arguably, the gap between what –and how– instructors actually teach and what –and how– they should teach, remains a professional challenge if not an emotionally charged issue that few are willing to raise. Given the realities of academia (funding, time constraints, reward system), the prospect for instructors to engage in scholarly teaching as an integral part of their professional identity remains an elusive proposition because of: a) lack of graduate training, b) departmental, college or university cultural norms, c) expertise and effort involved in pedagogical research, d) lack of reward, or e) unawareness. Studies have revealed that in order not to jeopardize professional progress, a choice is often made not to oppose traditional ways of teaching. However, the lack of negative correlation between research outcomes and teaching effectiveness should serve as a guide to allow for part of the open space that comes with academic freedom to be committed to high impact teaching practices. Although SoTL (the systematic inquiry into the learning environment for the purpose of advancing the practice of teaching within a discipline in making research findings public) is the most demanding form of commitment, small but significant networks are also effective tools to channel creativity and innovation that cultivate continuous improvement of teaching and student learning. At any point in one's career path, documenting the impact either may have on student learning could serve to alleviate some the aforementioned barriers. There is a need to lay the foundation of an integrated framework that aligns clearly opportunities with expectations and rewards for scholarly teaching efforts in the animal sciences.

Key words: SoTL, pedagogy

806 Casting a line—Multi-institutional collaborations to enhance animal science education. D. L. Boggs*, *Kansas State University, Manhattan.*

Comprehensive undergraduate curricula in animal sciences have traditionally consisted of relevant disciplinary courses and courses that applied these disciplines to management of all relevant species within a state or region. Consolidation of many animal industries has decreased the number of students entering animal sciences programs with background in these industries and interest in exploring them as career options. Thus the enrollment in many species based courses has decreased below the threshold of viability. At the same time, budgetary restrictions have decreased the ability of colleges and universities to maintain a critical mass of faculty within some disciplines and species. Therefore, many departments have eliminated faculty positions as well as animal facilities for experiential learning and are no longer able to offer comprehensive curricula. This first manifested itself in poultry, where budget redirections eliminated many departments, farm units and faculty positions. Recognition of the need to still develop professionals for the industry led to the development of the Midwest Poultry Consortium, a collaborative program to educate students for this industry. Collaborations need to expand if we are to comprehensively educate professionals and leaders for animal industries. Distance education technologies provide numerous opportunities for faculty to work across institutional and physical boundaries to provide innovative educational programs. The Institute for Academic Alliances at Kansas State University identifies the following keys to successful collaboration: commitment of faculty and administration to quality programs and e-learning, work with similar organizations, and combine complementary areas of expertise. AG*IDEA is an affiliate of the Great Plains Interactive Distance Education Alliance and provides an infrastructure for faculty and students to participate in educational collaborations. The AG*IDEA Swine Science Online Certificate is an example of a collaboration among several universities and industry. Opportunities exist to enhance educational opportunities via multi-institution collaborations.

Key words: collaboration, AG*IDEA, distance learning

ADSA Production Division Symposium: Current and Future Determinants of Dairy Product Pricing

807 Factors that are important in determining US milk prices. D. S. Brown*, *Food and Agricultural Policy Research Institute, University of Missouri, Columbia.*

The US dairy industry has experienced extreme volatility in milk prices over the past several years. The milk pricing system is often described as one of the most complicated pricing mechanisms in agriculture. In the past few years, the industry has seen milk prices go from record highs to record lows in very short periods of time. This research will provide some answers and insight into the reasons milk prices have become so volatile. Analysis of retail markets for the major dairy products will be included in this research. Retail pricing of all cheeses, butter, nonfat dry milk and whey are important in understanding how the US dairy industry operates. One longstanding component of federal dairy policy is the federal milk marketing order system. Milk orders provide a mechanism to set minimum prices to be paid for milk used in different manufacturing processes based on dairy product prices. Federal orders only provide for minimum pricing and over-order premiums can also be an important component in determining farm-level milk prices in some areas of the United States. The move to end product pricing with the last round of federal order reform has made for some challenges between processors and producers. There are currently four classes of milk in the federal order system. State milk pricing can also be important in determining milk prices with California's milk pricing system being just one example of other pricing methods in use today. Other federal dairy policy can play a role in US milk prices as well. Currently, the industry has a price support program in place for some manufactured dairy products. In periods of low prices, the government stands ready to purchase all products offered at the set purchase prices. This program has had a smaller effect in the past few years given the rise in feed prices. The Milk Income Loss Contract (MILC) program also operates in the dairy industry as a direct payment program in periods of low milk prices and/or high feed costs. This program can also affect the outlook for milk prices. A brief look at potential new dairy policy will be addressed as it relates to milk prices.

808 Issues facing US dairy exports: Regulatory coherence and trade barriers. J. Castaneda*, *U.S. Dairy Export Council, Arlington, VA.*

Lack of regulatory coherence and trade barriers limit the US dairy industry's access to export markets. The crux of the problem is the unjustified use of technical barriers, particularly sanitary and phytosanitary (SPS) measures that US exports face. This issue is one that threatens to grow even larger and more problematic in the future if not immediately addressed. We, collectively as an association and individually as members, are spending more and more time on these issues. In too many cases the problems faced by the dairy industry are growing and trade is being negatively affected. This presentation will focus on some of the problems we and other sectors have encountered with SPS measures, including lack of regulatory coherence among the various US agencies working on SPS issues. I will address (1) promotion of approaches that could improve the situation, including increased transparency, notification, harmonization between nations; (2) how the Administration can use past, current and future trade agreements to provide a vehicle for strengthening international rules and practices, which will help facilitate trade. It is important to note that the World Trade Organization's SPS agreement is essentially the only tool we have to deal effectively with countries that create SPS barriers to block trade. It provides a set of rules and an institutional setting to pressure countries that clearly stray from science-based standards to stop imports. However, as a set of principles agreed to 15 years ago, the SPS agreement is currently insufficient. In many cases there is a need for stronger and more specific rules to address trade barriers. This will be the focus of our attention in the coming years, so that the U.S. Dairy Export Council can assist in keeping international markets open for our products.

809 Producing for a global export market. M. Piper*, *Fonterra (USA) Inc., Rosemont, IL.*

After more than 18 years in the New Zealand dairy industry, with roles ranging from technical and commercial to marketing; living in 3 countries (New Zealand, Japan and now the USA), I have developed a good understanding of the world dairy environment. During my involvement in the global dairy market, there has been an evolution in the way people view quality: from product quality and consistency to supply chain quality. Traditional concerns about price still exist, but they have now been overtaken by concerns about food safety, and attention to issues encompassed by new phrases like "application focus" and "value added." To succeed in today's global environment we need to understand our future customers. The historic dairy markets of Europe and North America still remain the leading consumers of dairy products, but Asia is fast emerging as the new market for growth. Standard dairy products are still required along with development of additional products for these "new" markets, but the focus on application know-how and food safety concerns in Asia differ from what we consider the "norm" in Europe and North America. This presentation will focus on identifying new customers and touching on some of the areas that need to be front-of-mind when supplying these new global customers.

Thursday, July 14, 2011

SYMPOSIA AND ORAL SESSIONS

Animal Health: Dairy II

810 I. Dairy calving management: Dystocia and timing for intervention. G. M. Schuenemann*, I. Nieto, S. Bas, K. N. Galvao, and J. Workman, *Department of Veterinary Preventive Medicine, The Ohio State University, Columbus.*

Dystocia is defined as an abnormal or difficult birth at any stage of labor. The objective of this study was to determine the timing for intervention in dairy cattle [primiparous (PRIM) and multiparous (MULT)] that need assistance during calving. Cows (85) from 1 commercial dairy operation were used in this study. Periparturient dairy cows (PRIM, n = 54; MULT, n = 31) were placed in calving pens and constantly monitored until birth. The calving ease (CE) of cows (1–2 scale; 1 = unassisted or 2 = assistance required), timing from amniotic sac (AS) appearance to birth, and stillbirth (born dead or within 24 h after birth) were recorded. According to farm protocol, assistance was provided to cows without calving progress 80 min after the AS appearance. Data were analyzed using PROC MIXED of SAS. Least squares means (LSM) and 95% CI were reported. For unassisted calving (CE1), the time from AS appearance to birth was not different ($P > 0.05$) for PRIM (51 min; CI: 38.9–63.2) and MULT (46.7 min; CI: 31.4–61.9) cows. For cows that received assistance (CE2), the time from AS appearance to birth was not different ($P > 0.05$) for PRIM (83.6 min; CI: 66.4–100.8) and MULT (79.4 min; CI: 53.5–105.2) cows. However, the overall time from AS appearance to birth differed ($P < 0.05$) for CE1 cows (48.9 min; CI: 39.1–58.6) compared with CE2 cows (81.5 min; CI: 65.9–97). Cows with CE2 had greater incidence of stillbirth (23.2%) compared with CE1 cows (0.8%; $P < 0.05$). Cows with assisted births (dystocia) had longer time period from the AS appearance to birth and increased incidence of stillbirth as opposed to cows with unassisted calving. This study suggested that calving personnel should start assisting cows 60 min after the AS appearance. Recognizing the signs of normal calving such as appearance of the AS and timing to birth is critical to know when to intervene. These findings have important implications for dairy personnel executing the calving tasks.

Key words: calving management, education, dystocia

811 II. Dairy calving management: Effect of perineal hygiene scores on metritis. G. M. Schuenemann*, I. Nieto, S. Bas, K. N. Galvao, and J. Workman, *Department of Veterinary Preventive Medicine, The Ohio State University, Columbus.*

The objective of the present study was to assess the impact of hygiene scores of the perineal region (HSPR; surface around the birth canal) of dairy cows [primiparous (PRIM) and multiparous (MULT)] at the time of calving on the risk of metritis. Cows housed in free-stalls from 2 commercial Ohio dairies were used in this study. Periparturient cows (n = 562) were placed in individual calving pens and monitored until birth. Wheat straw bedding was changed every 2 d. Immediately before calving, the HSPR of cows was recorded using a 1–3 scale (1 = free of dirt-manure and completely dry; 2 = slightly wet dirt-manure in 1–10% of the surface; 3 = moderately covered with wet dirt-manure in 11–30% or greater of the surface) by 1 calving personnel in each farm. Both calving personnel received calving training at the beginning of the study. The average length of stay per cow in the calving pen was 1.9 h. Immediately after calving, cows were moved to a fresh pen. The calving ease (CE; 1–2 scale; 1 = unassisted or 2 = assistance required), stillbirth (born dead or within 24 h after birth), and retained fetal membranes (RFM) were recorded. Lactating cows were screened for metritis within 14 DIM by farm personnel. Metritis was defined as a foul-smelling red-brown watery uterine discharge. Data were analyzed using PROC GLIMMIX of SAS, accounting for the effects of CE, parity, stillbirth, herd, and RFM. Cows with a HSPR of 3 (n = 84) or 2 (n = 177) had greater incidence of metritis (22.4 ± 6% and 18.9 ± 4%, respectively) compared with cows (n = 301) with a HSPR of 1 (10.8 ± 3%; $P < 0.05$). These findings indicate that cleanliness of the perineal region at the time of calving is significantly associated with metritis.

Key words: calving hygiene, education, metritis

812 Dam heat load affects neonatal calves' bacterial levels and innate immunity. D. Pan*[1,2], C. N. Lee[3], M. H. Rostagno[2], and S. D. Eicher[2], *[1]Purdue University, W Lafayette, IN, [2]USDA- ARS, W Lafayette, IN, [3]University of Hawaii, Honolulu.*

Heat stress is known to suppress animal's immunity, making them more susceptible to bacterial infections. Field observations have shown that calves have greater morbidity and mortality when they are born after a heat event. Objectives of this study were to determine effects of heat load on bacterial levels in the calves' environment and on calves' innate immunity. The study was undertaken in March and August, 2010 on 2 commercial dairies (dairy 1 and dairy 2) located in Hawaii. Fifty-three neonatal Holstein calves were used, 27 born in spring (SP) and 26 born in summer (SU). Hide and udder swabs (100 cm^2) from the dams on dairy 1 were taken shortly after calving. Rectal and nasal swabs from calves on the same farm (n = 15 for each SP an SU) were taken 1, 2, and 3 wk after birth. Colony forming units of total aerobes and total coliforms were determined for all samples. Jugular blood samples from calves on dairy 2 (n = 12 and 11 for SP and SU, respectively) were collected wk 1, 2, 3, and 4 after birth to determine blood leukocyte RNA expression of toll-like receptor 4 (TLR4) and tumor necrosis factor-α (TNF-α). All data were transformed and analyzed using the MIXED procedure of SAS with season and time as fixed effects. Hide and udder total coliform counts did not differ between SP and SU cows. However, compared with the SP cows, SU cows had greater hide ($P = 0.0003$) and udder ($P = 0.0002$) total aerobe counts. Rectal coliform counts in SP calves were greater ($P < 0.0001$) than in SU calves throughout the 3-wk study. SP calves also had greater ($P < 0.0001$) nasal coliform counts at wk 2. No difference was found in rectal aerobe counts between SP and SU calves. SU calves had greater ($P < 0.0001$) nasal aerobe counts than SP calves at wk 1 and 3. No difference in TLR4 expression was detected between SP and SU calves. However, TNF-α expression in SU calves was less ($P < 0.01$) at wk 2 compared with SP calves. Our results showed that heat load increased the total aerobes in the calving environment and

decreased TNF-α expression of neonatal calves, thus may increase calf morbidity and mortality.

Key words: heat stress, innate immunity, microbial populations

813 Antisecretory factor counteracts calf diarrhea and increases daily weight gain. B. E. O. Johansson*[1], E. Johansson[2], and S. Lange[2,3], *[1]Lantmännen Lantbruk, Lidköping, Västra Götaland, Sweden, [2]Bacteriological Laboratory, Sahlgrenska University Hospital, Gothenburg, Västra Götaland, Sweden, [3]Institute of Biomedicine, Department of Infectious Diseases, Section of Clinical Bacteriology, University of Gothenburg, Gothenburg, Västra Götaland, Sweden.*

Antisecretory factor (AF) is a protein with potent antisecretory and anti-inflammatory actions and part of the natural, innate defense system. This study investigated whether the AF level in calf blood were correlated with diarrhea. The study was performed in 101 dairy calves raised according to standard Swedish procedures: colostrums/whole milk for 3 d, milk replacer d 4 to 55 with ad lib access to forages and concentrates. No experimental diet was given. Live weight and incidents of diseases were documented during the study period. Blood plasma samples were taken at d 3 after birth and AF activity in the samples was tested by an in house developed enzyme-linked immunosorbent assay (ELISA). The AF activity was compared for calves who either got diarrhea before 55 d or who did not. Live weight at d 55 was compared between calves with or without diarrhea before this age. Both comparisons were made with one-way ANOVA in Minitab 15 and sample means were tested with Student′s *t*-test. Differences were judged significant when the p-value was lower than 0.05. Standard error means are reported directly after the group means. Live weight was recorded for 83 of the 101 calves. Plasma was analyzed from 17 of the 83 calves with live weight records, and from 18 without weight records. In total were 35 plasma samples analyzed and live weight compared on 83 calves. The mean AF activity (net absorbance at 405 nm) in calves suffering from diarrhea was significantly lower than in the healthy calves (0.520 ± 0.049 vs. 1.287 ± 0.164, $P < 0.05$). On d 55, calves who had experienced diarrhea weighed 75 ± 2.15 kg compared with the 81 ± 0.94 kg of healthy calves ($P < 0.05$). The natural level of AF activity in calves has a positive and significant correlation to diarrhea. Thus, calves with low AF activity are subjected to an increased risk of catching a diarrheal disease, which is commonly followed by a diminished growth rate.

Key words: antisecretory factor, calf diarrhea, innate defense system

814 Innate immune function of Holstein calves after commingling. L. E. Hulbert*[1,2], C. J. Cobb[1], L. R. Schwertner[1], and M. A. Ballou[1], *[1]Department of Animal and Food Sciences, Texas Tech University, Lubbock, [2]Department of Animal Sciences, University of California-Davis, Davis.*

Sixty-four Holstein dairy calves were all reared in individual polyethylene calf-hutches (Agri-Plastics) until they were randomly assigned to treatments of Grouped (3 calves/pen, n = 36 calves) or Control (remained in hutch, n = 28 calves). The individual calf hutch design (5.98 m^2 of free space) allowed visual, olfactory and auditory contact but no physical contact with other calves. Grouped calves were moved at 68 ± 2.3 d of age to pens of 3 calves (5.97 m^2/calf of free space). Whole blood was collected via venapuncture from all calves at 68, 71, 75, and 87 d of age. Cortisol and haptoglobin concentrations, total leukocyte and differential counts, neutrophil L-selectin and β_2-integrin expressions, neutrophil phagocytosis and oxidative burst, and tumor necrosis factor-α (TNF-α) secretion from lipopolysaccharide (LPS)-stimulated whole blood were measured. Grouped calves had reduced ADG, DMI, and gain:feed for the 21 d period, and weighed less than Control calves at 87 d of age ($P < 0.01$). Seven d after commingling, Grouped calves had greater cortisol concentrations than Control calves ($P < 0.01$). In addition, Grouped calves tended ($P = 0.06$) to have more total leukocytes than Control calves for the entire period. Grouped calves also had decreased oxidative burst response 3 d after commingling ($P < 0.05$); however, the phagocytic responses were increased on d 3, but were decreased 7 d after Group calves were commingled ($P < 0.01$). On d 87 of age, all calves had increased haptoglobin concentrations and TNF-α secretion ($P < 0.05$), and Grouped calves had increased neutrophil:lymphocyte ratio and neutrophil β_2-integrin expression with a concomitant decreased neutrophil L-selectin expression ($P < 0.05$) compared with Control calves at d 87 of age. Commingling calves decreased innate immune responses and performance during the 21 d observation period.

Key words: calf, grouping, immunity

815 Risk factors and impact of postpartum anovulation in dairy cows. J. Dubuc*[1], T. F. Duffield[2], K. E. Leslie[2], J. S. Walton[3], and S. J. LeBlanc[2], *[1]Faculté de médecine vétérinaire, Université de Montréal, St-Hyacinthe, Québec, Canada, [2]Department of Population Medicine, University of Guelph, Guelph, Ontario, Canada, [3]Department of Animal and Poultry Science, University of Guelph, Guelph, Ontario, Canada.*

The objective of this study was to identify risk factors for and to quantify the impact of postpartum anovulation on reproductive performance in dairy cows. Data from 2178 Holstein cows (6 herds) enrolled in a randomized clinical trial were used. Data on periparturient disease, calving history, and body condition score at calving were collected. Cytological endometritis (CYTO) was defined as ≥6% polymorphonuclear cells in endometrial cytology at wk 5 postpartum. Purulent vaginal discharge was defined as the presence of mucopurulent or purulent vaginal discharge at wk 5 postpartum. Serum BHBA, NEFA, and haptoglobin were measured at wk 1, 2, and 3 postpartum. Serum progesterone (P4) was measured at wk 3, 5, 7, and 9 postpartum. The end of postpartum anovulation period was defined as the first sampling time at which P4 was >1ng/mL. Statistical analyses were performed using logistic regression models and Cox proportional hazard models in SAS, accounting for the effects of treatments in the clinical trial and herd clustering. The prevalence of anovulation was 72, 44, 26, and 17% at wk 3, 5, 7, and 9, respectively. Risk factors for prolonged anovulation (ANOV; no P4 > 1 ng/ml through wk 9) were CYTO (OR = 1.5; $P = 0.02$), and elevated NEFA concentration (≥0.9 mmol/L; OR = 1.5; $P = 0.02$), hyperketonemia (≥1.2 mmol/L; OR = 1.4; $P = 0.03$), and hyperhaptoglobinemia (≥0.8 g/L; OR = 1.6; $P < 0.01$) at wk 1. Parity group (≥3; OR = 1.5; $P < 0.01$) and season (summer and spring; OR = 1.6; $P < 0.01$) were also associated with ANOV. Cows with ANOV had an increased median time to first breeding (ANOV = 77 d; cyclic = 72 d; HR = 0.88; $P < 0.01$) but no difference in first service conception risk (ANOV = 28.9%; cyclic = 30.1%; $P = 0.73$). The impact of ANOV on median time to pregnancy was conditional on parity group; a detrimental impact was present in cows of parity ≥3 (ANOV = 196 d; cyclic = 135 d; HR = 0.56; $P < 0.01$) but there was no impact in cows of parity ≤2 (ANOV = 137 d; cyclic = 128 d; HR = 0.91; $P = 0.54$). Overall, these findings suggest that ANOV was associated with indicators of energy balance and uterine inflammation, and with detrimental impacts on reproductive performance.

Key words: dairy cow, anovulation, risk factor

816 Inflammation and infection of the reproductive tract in dairy cows. T. Osawa*[2], R. C. Neves[1], and S. J. LeBlanc[1], [1]*University of Guelph, Guelph, ON, Canada,* [2]*Iwate University, Morioka, Japan.*

Purulent vaginal discharge (PVD), cytological endometritis (>6% neutrophils; CYTO_U), and cytological cervicitis (>5% neutrophils; CYTO_C) are associated with impaired reproductive performance. Weak agreement between PVD and CYTO_U led to the question of the source of PVD. The objective was to describe relationships among inflammation and bacterial infection in various parts of the reproductive tract of postpartum dairy cows. 102 cows were examined by vaginoscopy, ultrasound (US), and cytobrush cytology of the vagina (V), cervix (C), and uterine body (U) at 3 and 5 weeks postpartum. In a subset of 78 cows, aerobic and anaerobic bacterial cultures were performed from each site. At wk 3 and 5 postpartum the prevalence of PVD was 17 and 13%, of CYTO_U 32 and 18%, of CYTO_C 37 and 14%, and of bacterial contamination of V 65 and 59%, C 68 and 54%, and U 69 and 49%, respectively. There was no association of CYTO_U or CYTO_V or of prior or concurrent gross vaginitis or cervicitis with PVD at wk 5. However, 43% of cows with CYTO_C had PVD vs. 8% among cows without CYTO_C ($P = 0.003$). Infection of V, C, or U with A. pyogenes (prevalence = 8–11%) and fluid in the uterus visible by US (sensitivity = 85%; specificity = 51%) were associated with PVD at wk 5. In a logistic regression model, CYTO_C and uterine A. pyogenes infection were significantly ($P = 0.002$) associated with increased odds of PVD. CYTO_U was associated with gross and cytological cervicitis but not with bacterial infection of any segment of the tract. There was strong association ($P < 0.0001$) and good agreement (Kappa = 0.4) between CYTO_C and CYTO_U, yet 43 to 55% of cows with inflammation in one location did not have it in the other. In a logistic regression model, CYTO_C and swollen cervical folds seen by vaginoscopy were associated with cytological endometritis at wk 5. Leukocyte esterase test strips on uterine swabs provided good to high (85–93%) negative predictive value but moderate to low (66–33%) positive predictive value for cowside diagnosis of CYTO_U using test scores of 3 to 1, respectively. Cervicitis and endometritis are distinct, sometimes overlapping conditions.

Key words: reproductive health, endometritis, cervicitis

817 Physiological and behavioral characteristics related to vitality of newborn dairy calves and the efficiency of absorption of immunoglobulins. C. Murray*[1], D. Viera[2], A. Nadalin[2], V. Bielmann[1], and K. Leslie[1], [1]*Department of Population Medicine, University of Guelph, Guelph, Ontario, Canada,* [2]*Agriculture and Agri-Food Canada, Agassiz, British Columbia, Canada.*

Calving difficulty and stillbirth are formidable issues for the dairy industry. Recent research has identified associations between assisted calving and failure of passive transfer of immunoglobulins. The objective of this research was to examine physiological and behavioral characteristics of newborn Holstein calves with the aim of developing a newborn calf vitality scoring system that would be strongly associated with absorption of colostral immunoglobulins, general health and performance. A total of 48 calving events (n = 51calves) were continuously monitored from the first sight of fetal membranes. All calves were assessed for measures of vitality at the time of first sternal recumbency (SR), and at 2 and 24h, 7 and 14 d of age. Measurements included time to SR and standing, blood gases, oxygen saturation, lactate, glucose, rectal temperature, respiration and heart rates, suckling response, IgG absorption and growth. At 2 h, all calves were separated from their dam and fed 180 g of IgG from a commercial colostrum replacer by esophageal tube feeder. Calves born from a hard pull (n = 10) were more acidotic (mean pH ± SD: 7.20 ± 0.12 vs. 7.28 ± 0.05) and took twice as long to attain SR than those born unassisted (n = 18) (SR ± SD: 5.2 ± 3.0 vs. 10.3 ± 4.4 min). All calves achieved a normal pH (7.4 ± 0.04) within 24 h of birth. A higher proportion of calves born from a hard pull had a weak suckling response at SR and at 2 h compared with unassisted calves (86 vs. 43% and 50 vs. 6%, respectively). No correlation was found between SR, first attempt to stand, to stand for 2.5 and 5 min when compared with IgG concentration at 24 h of age. There was no trend between level of calving difficulty and average apparent efficiency of absorption of IgG. Overall, calves born from a hard pull are weaker and less responsive in the first few hours than calves born unassisted or from an easy pull. Yet, objective and easy to measure physiological or behavioral outcomes that are highly correlated to calf vitality and success of passive transfer remain unclear.

Key words: newborn, calf, vitality

818 The effect of omega-3 supplementation on the immune response of Holstein calves. E. L. Karcher*[1], T. M. Hill[2], N. Vito[1], L. M. Sordillo[1], H. G. Bateman[2], R. L. Schlotterbeck[1], and M. J. VandeHaar[1], [1]*Michigan State University, East Lansing,* [2]*Nurture Research Center, Provimi North America, Lewisburg, OH.*

The ability to reduce incidence of disease in calves and improve early vaccination strategies is of particular interest for dairy producers. Omega-3 fatty acids (FA) were shown to reduce inflammation in human diseases, such as diabetes and cardiovascular disease, but there is limited research in calves. Therefore, the objective of this study was to determine if supplementation with omega-3 FA from fish and flax oils improves immune function in calves. Forty-eight Holstein bull calves from a commercial dairy were randomly assigned to 1 of 3 diets beginning at 4 d old: 1) control milk replacer (MR) with all pork fat, 2) MR with 2% flax oil, and 3) MR with 2% fish oil. All diets were 27% CP, 17% fat on DM basis with all protein from whey sources. Calves were each fed 654 g DM of MR daily for the first 25 d and then 327 g/d for d 26, 27, and 28. On d 28, calves were challenged with a *Pasteurella* vaccine (Presponse HM) and the temperature response to the vaccine was recorded. Milk and feed intake and fecal scores were recorded daily and BW and skeletal measures were recorded weekly. Blood was collected on d 25. One tube of collected blood was incubated with endotoxin (LPS, 2 μg/mL) for 2 h. Quantitative RT-PCR was used to assess the effects of LPS stimulation on TNFα and IL-4 gene expression in leukocytes isolated from whole blood. During the 28 d, calves supplemented with flax oil had a greater gain to feed efficiency than calves supplemented with fish oil (0.522 ± 0.02 vs. 0.477 ± 0.02 g gain/g feed; $P < 0.03$). Both flax and fish oils tended to decrease the expression of TNFα following a 2 h in vitro stimulation with LPS compared with the control ($P < 0.08$). Flax oil, but not fish oil, decreased the expression of the IL-4 ($P < 0.05$). Calves receiving the flax oil treatment tended to have a decreased rise in rectal temperature in response to a *Pasteurella* vaccine ($P < 0.08$). In conclusion, supplementation with omega-3 FA tended to decrease the expression of the pro-inflammatory cytokine TNFα and reduce the temperature increase in response to a *Pasteurella* vaccine. Results indicate that supplementation may affect the ability of the calves to respond to a disease challenge.

Key words: calves, omega-3

819 Impact of intrauterine dextrose therapy on conception of lactating dairy cows with clinical endometritis. T. A. Brick*, S. Bas, J. B. Daniels, C. Pinto, D. M. Rings, and G. M. Schuenemann, *The Ohio State University, Columbus.*

The objective of this study was to determine if lactating dairy cows with clinical endometritis (CE) treated with an intrauterine infusion of 50% dextrose in water (DEX) have similar pregnancy per AI (PAI) compared with parental ceftiofur crystalline free acid (CEF) and untreated cows (CON). Cows (n = 760) from 2 herds were screened using vaginoscopy for CE at 26 ± 3 DIM and scored using a 0–3 scale. Cows scored as 2 or 3 were stratified by parity and randomly allocated into 1 of 3 treatment groups: 1) CON (n = 83), 2) 6.6 mg/kg CEF sq (n = 75), or 3) 200 mL DEX (n = 79). Fourteen days post-therapy (at 40 ± 3 DIM), treated cows were re-examined to assess treatment responses. All cows were presynchronized with 2 injections of PGF given 14 d apart (starting at 26 ± 3 DIM) followed by Ovsynch (OV; GnRH-7 d-PGF-56 h-GnRH 16 h-timed-AI; TAI) 12 d later. Cows displaying standing estrous any time during the protocol received AI, while the remaining cows were subjected to TAI-16 h after second GnRH of OV. Body condition scores (BCS) were recorded at calving, 26 ± 3 and 40 ± 3 DIM. Pregnancy diagnosis was performed via ultrasonography at 39 ± 3 d post-AI. DIM to first service (DIMFS) and pregnancy per AI (PAI) were evaluated. DIMFS, milk yield at first service, BCS at treatment, rectal temperature at treatment were not different among the treatment groups. Mortality within 10 d post-treatment and culling rate at 250 DIM were not different for cows with or without CE. Cows with CE had greater cervical diameters at the time of treatment compared with cows without CE. Mean vaginoscopy scores were reduced for DEX cows compared with CON and CEF cows ($P = 0.05$). PAI in DEX (29.8 ± 4%) tended to differ from cows in CON (21.1 ± 4%) and CEF groups (19.7 ± 4%; $P = 0.1$). However, PAI in DEX cows was not different from cows without CE (39.1 ± 2%). Based on these findings, the use of intrauterine DEX alone or as an adjunct of antibiotic therapy for the treatment of cows diagnosed with CE needs further investigation.

Key words: dairy cow, dextrose, endometritis

820 Effect of propylene glycol in fresh cows diagnosed with subclinical ketosis on milk yield and resolution of ketosis. J. A. A. McArt*[1], D. V. Nydam[1], P. A. Ospina[2], and G. R. Oetzel[3], *[1]Cornell University, Department of Population Medicine and Diagnostic Science, Ithaca, NY, [2]Cornell University, Department of Animal Science, Ithaca, NY, [3]School of Veterinary Medicine, University of Wisconsin, Madison.*

The purpose of this study was to determine the effect of oral propylene glycol (PG) administration on ketosis resolution and milk yield in cows diagnosed with subclinical ketosis (SCK) using the Precision Xtra meter (Abbott Laboratories, Abbott Park, IL). Cows from 4 freestall dairy herds in NY and WI were each tested 6 times for SCK from 3 to 16 d in milk. SCK was defined as a β-hydroxybutyrate (BHBA) reading of 1.2–2.9 m*M*; clinical ketosis was defined as ≥ 3.0 m*M*. Cows with SCK were randomized to treatment group (oral PG) or control group (no PG); treatment cows were drenched with 300 mL PG once daily from the day they tested 1.2–2.9 m*M* until the day they tested < 1.2 m*M*. Outcomes evaluated for all farms included time from SCK until BHBA test < 1.2 m*M* or until BHBA test ≥ 3.0 m*M*; individual milk weights for the first 30 d in milk were evaluated for 3 farms. Semiparametric proportional hazards models were used to evaluate time to event outcomes; repeated measures ANOVA was used to assess milk weights which were stratified by herd after a significant treatment by herd interaction was found. A total of 741 of 1,777 (41.7%) eligible enrolled cows had at least one BHBA test of 1.2–2.9 m*M*. Of these, 372 were assigned to the treatment group and 369 to the control group. Based on hazard ratios, PG treated cows were 1.50 (95% confidence interval (CI) = 1.26 to 1.79) times more likely ($P < 0.0001$) to resolve their SCK and 0.56 (95% CI = 0.35 to 0.88) times less likely ($P = 0.013$) to develop clinical ketosis than control cows. Treated cows produced more milk per milking on Farm A (0.98 kg, $P = 0.0002$) and Farm B (1.16 kg, $P < 0.0001$) in the first 30 d of lactation than control cows, for a total difference of 2.94 kg and 3.49 kg per day, respectively; there was no difference in milk (0.055 kg, $P = 0.70$) between the 2 groups on Farm D. These results show the positive effects of oral PG administration in fresh cows with SCK by both helping resolve SCK as well as prevent clinical ketosis. In addition, oral PG significantly improves milk yield during early lactation in some herds.

Key words: ketosis, propylene glycol, milk yield

821 Association between serum metabolite concentrations in the transition period and milk production in dairy cows. N. Chapinal*[1,2], M. E. Carson[1], S. L. Leblanc[1], K. E. Leslie[1], S. Godden[3], M. Capel[4], J. E. P. Santos[5], M. W. Overton[6], and T. F. Duffield[1], *[1]Department of Population Medicine, University of Guelph, Guelph, ON, Canada, [2]Animal Welfare Program, University of British Columbia, Vancouver, BC, Canada, [3]Department of Veterinary Population Medicine, University of Minnesota, St. Paul, [4]Perry Veterinary Clinic, Perry, NY, [5]Department of Animal Science, University of Florida, Gainesville, [6]Department of Population Health, University of Georgia, Athens.*

The objective was to study the association of the serum concentrations of nonesterified fatty acids (NEFA), β-hydroxybutyrate (BHBA) and calcium with milk yield across the first 4 Dairy Herd Improvement (DHI) tests. Serum from 1919 Holstein cows in 45 herds was collected weekly from 1 wk before through 2 wk after calving. The herds were located in California, southeast (Georgia, Florida, Virginia, South and North Carolina), northeast (New York and Ontario, Canada) and Midwest (Wisconsin and Minnesota) North America. Repeated measures ANOVA was conducted including parity, clinical disease, precalving body condition score, and region as covariates, and the random effect of herd. Serum concentrations were dichotomized at various cut-points to identify the thresholds of metabolites with the strongest associations with milk loss. Precalving NEFA ≥ 0.5 mEq/L (in multiparous cows only; 25% of the cows), BHBA ≥ 600 μmol/L (26% of the cows) and calcium ≤ 2.1 (5% of the cows) were associated with milk loss of 1.6 ± 0.5, 1.7 ± 0.4, and 3.3 ± 0.8 kg/d, respectively, across the first 4 DHI tests. In wk 1 after calving, NEFA ≥ 0.7 mEq/L (in multiparous cows only; 41% of the cows), BHBA ≥ 1,400 μmol/L (12% of the cows) and calcium ≤ 2.1 (23% of the cows) were associated with milk loss of 1.9 ± 0.6, 2.5 ± 0.6, and 2.6 ± 0.5 kg/d, respectively, at the first DHI test. In wk 2 after calving, NEFA ≥ 1.0 mEq/L (12% of the cows), BHBA ≥ 1,200 μmol/L (20% of the cows) and calcium ≤ 2.1 (8% of the cows) were associated with milk loss of 1.7 ± 0.8, 1.4 ± 0.6, and 4.8 ± 1.0 kg/d, respectively, at the first DHI test. Increased serum concentrations of NEFA and BHBA and decreased concentrations of calcium around calving are associated with milk loss in early lactation.

Key words: transition cow, nonesterified fatty acids, ketones

822 Whey protein nanoparticles prepared by desolvation: Encapsulation capacity and interfacial activity. I. Gülseren* and M. Corredig, *University of Guelph, Dept. of Food Science, Guelph, Ontario, Canada.*

Whey protein nanoparticles were prepared using a desolvation method, using ethanol as solvent. Physical characterization including particle size characteristics, encapsulation capacity for a model hydrophilic molecule (Brilliant Blue FCF), and interfacial activity at the oil-water interface were carried out, after diluting the samples in acidic conditions (pH 3). The particle size distribution was determined using dynamic light scattering technique, and particle diameter was between a few nm up to about 100 nm. Solvent composition was highly influential on the average particle size and its distribution. The release of the Brilliant Blue from the nanoparticles with storage was quantified using UV-Visible spectrophotometry, after separation of the whey protein particles by centrifugation. Both unloaded and loaded nanoparticles were stable at room temperature after one month of storage, and little release of the encapsulated dye molecules was observed. The interfacial properties of the unloaded nanoparticles were also tested using drop tensiometry, and it was shown that nanoparticle formation only slightly affected the interfacial activity.

Key words: whey protein nanoparticles, desolvation, encapsulation

823 Comparative proteomic analysis of whey proteins between healthy and subclinical mastitic cows. J. Bian, Q.-Z. Li*, and X.-J. Gao, *Key Laboratory of Dairy Science of Ministry of Education, Northeast Agricultural University, P.R. China.*

This study was to investigate different whey protein contents between healthy dairy cows and subclinical mastitical dairy cows, and to explore the mechanism of pathogenesis. This study presented changes of the whey proteins from healthy dairy cows and subclinical mastitical dairy cows by using 2-DE. After the protein stained with coomassie blue G-250, 21 differential expression protein spots were detected by ImageMaster 2D Platinum 6.0 software, then 10 protein spots were analyzed by using the MALDI-TOF/MS. Meanwhile. Proteins were identified by using the Mascot software to search the NCBInr database and the swiss-port database.8 proteins were identified successfully. In cows with subclinical mastitis, 3 proteins were downregulated: Alpha-S1 casein precursor, Chain D of bovine β-Lactoglobulin A and Chain B of the bovine β 1,4 galactosyltransferase catalytic domain ; 5 proteins were upregulated:Serotransferrin precursor, α-1-acid glycoprotein, β 2- microglobulin, Complement C3 precursor and Cytokeratin 9, these proteins were involved in signal transduction, binding and transportion and immune defense activity. The α-1-acid glycoprotein expression in whey of cows with subclinical mastitis was 2.55-fold higher than the healthy dairy cows confirmed by ELISA protocol. The results provided valuable information for the investigation on mechanism of the subclinical mammitis of dairy cows and potential protein targets for treatment.

Key words: subclinical mastitis, whey protein, comparative proteome

824 Controlling whey proteins spontaneous self assembly. T. Croguennec*[1], D. Salvatore[2], T. Nicolai[3], V. Forge[2], and S. Bouhallab[1], *[1]UMR 1253, INRA- Agrocampus Ouest, Science et Technologie du Lait et de l'Oeuf, Rennes, France, [2]Laboratoire de Chimie et Biologie des Métaux, CEA-Grenoble, Grenoble, France, [3]UMR CNRS-Université du Maine, Polymères, Colloides, Interfaces, Le Mans, France.*

Sustainability in food manufacture involves a profound reasoning of the way food are produced. Reducing energy input during food processing and optimizing ingredient formulation to meet both sensorial acceptance and nutritional benefit through a controlled release of macro- and micro-nutriments constitute great challenges for food industries. Controlled self-assembly of molecules into biomaterials throughout bottom-up approach is a promising way to achieve these goals. Because of their omnipresence in food systems, whey proteins are the focus of many attempts for their use as building blocks for such biomaterials. For instance, the apo form of α-lactalbumin (α-LA) and β-lactoglobulin are able to self-assemble into well-defined microspheres in the presence of an oppositely charged protein such as lysozyme (LYS). Formation and destabilization of microspheres are inducible by changing the physicochemical conditions. Because of this reversibility, such microspheres could be used to trap, protect during processing and storage, carry and deliver bioactives. However, to complete this challenge, a perfect understanding of protein assembly and disassembly mechanisms are necessary. In this communication we address the mechanism of formation of microspheres of α-LA and LYS from the molecular scale to the microspheres. One of the first events in the mechanism of formation of microspheres is a specific interaction between α-LA and LYS leading to a heterodimer. Probably throughout charge screening, α-LA/LYS heterodimers rapidly self-assembled into nanometer-sized aggregates. These small entities further aggregate into clusters following a diffusion limited mechanism (DLCA) and fuse upon physical contact into spherical microspheres. The driving force for the reorganization of the clusters into microspheres is suggested to be the decrease of the total surface free energy. However, the reorganization of the clusters was only inducible when the temperature was increased above 30°C, temperature above which α-LA adopt a molten globule structure. We put forward that the higher flexibility of α-LA above 30°C may facilitate clusters–microspheres transition.

Key words: self assembly, α-lactalbumin, microsphere

825 Study of the combined acidification and rennet gelation behavior of casein micelles using single *Streptococcus thermophilus* strains, with high or very low exopolysaccharide production. Z. Miao*, E. Kristo, and M. Corredig, *University of Guelph, Guelph, Ontario, Canada.*

The effect of the presence of exopolysaccharide (EPS) produced by lactic acid bacteria on the gelation properties of caseins is still largely unknown. Objective of this work was to study the gelation behavior of caseins during renneting, after controlled fermentation with high-EPS producing or very low-EPS producing *S. thermophilus* cultures. Fresh skim milk was fermented with either a high ropy exopolysaccharide-producing strain (CHCC-5086, Chr. Hansen); or a very low EPS producing strain (CHCC-742, Chr. Hansen), as control. The inoculated skim milk was incubated at 40°C and rennet was added when a pH of 6.2 was reached. The gelation behavior was followed using rheology, diffusing wave spectroscopy (DWS) and confocal microscopy. Milk containing the high-EPS producing strain showed a significantly higher viscosity than the control during fermentation up to pH 6.2. After addition of rennet, the gelation point occurred earlier (at significantly higher pH values) in milk fermented with high-EPS producing strain compared with milk fermented with control strain. Confocal

microscopy also showed differences in the microstructure between the gels, with larger pores in the presence of EPS. These results further our fundamental understanding of the effect of EPS on the beginning stages of the rennet-induced gelation.

Key words: exopolysaccharides, casein, gelation

826 In situ structural investigations of the milk fat globule membrane revealing heterogeneities and sphingomyelin-rich domains. C. Lopez*, *INRA-STLO, Rennes, France.*

In recent years, the milk fat globule membrane (MFGM) has attracted the attention of scientists and industrials because of its interesting functional, nutritional and health properties. These properties of the MFGM result from its chemical composition, but they may also be influenced by the capacity of the MFGM components to be specifically structured. Various models of the MFGM have been proposed, all of them presenting polar lipids as a homogenous 2D solvent for membrane proteins (Singer & Nicholson fluid mosaic model). However, the structure of the MFGM still remains the least understood aspect of milk. The objective of this work was to investigate the organization of the MFGM in situ in milk, using confocal laser scanning microscopy and adapted fluorescent dyes (exogenous polar lipid, lectins). For the first time, our work revealed i) the lateral segregation of sphingomyelin (SM; 20 to 25% of milk polar lipids) in rigid liquid-ordered domains surrounded by the fluid matrix of the glycerophospholipids (PC, PE, PI, PS), ii) that the SM-rich domains are of micronic size with a circular shape for bovine milk, iii) that the SM-rich domains diffuse in the plane of the outer bilayer of the MFGM as a function of time, iv) that the SM-rich domains are devoid of proteins. These SM-rich domains have been characterized whatever the size of milk fat globules and in milks from various species. As a conclusion, we showed that the MFGM is a heterogeneous and highly dynamic biophysical system. Moreover, on the basis of our experimental results, we proposed a new model for the organization of the MFGM. These original results raised the question of the role played by these SM-rich domains on the functional and nutritional properties of milk fat globules. Directions for future research studies will be discussed.

Key words: milk fat globule membrane, sphingomyelin, confocal microscopy

827 Fractionation of glycomacropeptide and beta lactoglobulin using positively charged ultrafiltration membranes in staged configurations. S. Gemili* and M. R. Etzel, *University of Wisconsin-Madison, Madison.*

Membrane ultrafiltration is a commonly used method for the concentration and diafiltration of protein solutions. For fractionation of proteins, ultrafiltration is not commonly used, because it lacks the separation capability of chromatographic methods. The selectivity of membrane ultrafiltration is increased dramatically when a charge is added to the membrane surface. Configuring the membranes in stages also increases the selectivity of the separation. Using membrane ultrafiltration instead of chromatography for protein fractionation has advantages for the dairy industry of a lower cost of manufacture resulting from decreased buffer consumption and the use of existing installed membrane equipment. In this study, positively charged cross-flow ultrafiltration membranes having a 300 or 30 kDa molecular weight cut off were used to fractionate glycomacropeptide (GMP) and β lactoglobulin (BLG). Sieving coefficients of GMP and BLG were determined experimentally by ultrafiltration of binary protein mixtures. These sieving coefficients were used to calculate purity and yield of GMP products from one-stage and 2-stage membrane configurations using mass balance models. Flow configurations that allowed for recycle of by-product streams were compared with cases without recycle. Different volume concentration factors (ratio of permeate to feed solution) ranging from 0.01% to 80% were also included in the evaluation. A ratio of 80% gave the highest GMP purity (97%) using a 300 kDa membrane in the first stage and a 30 kDa membrane in the second. However, this configuration gave the lowest GMP yield (21%) in the permeate stream. In contrast, a one-stage configuration using a 300 kDa membrane gave a 60% yield of GMP in the permeate stream at a purity of 74%. In conclusion, GMP fractionation can be accomplished using positively charged ultrafiltration membranes. Different flow configurations and membranes having different molecular weight cut offs can be used to balance yield and purity.

Key words: ultrafiltration, fractionation, glycomacropeptide

828 Antimicrobial role of serum amyloid A3 in goat milk. A. Domènech*[1], J. G. Raynes[2], A. Arís[1], A. Bach[1,3], and A. Serrano[1], *[1]Department of Ruminant Production, IRTA, Caldes de Montbui, Spain, [2]Immunology Unit, Department of Infectious and Tropical Diseases, London School of Hygiene and Tropical Medicine, London, United Kingdom, [3]ICREA, Barcelona, Spain.*

Milk is an important source of antimicrobial compounds. Serum Amyloid A3 (SAA3) is an acute phase protein which level is particularly high in colostrum and milk during mastitis, suggesting a potential protective role against infections. The aim of this study was the recombinant production of the milk goat SAA3 (gM-SAA3) and to evaluate 2 possible mechanisms of antimicrobial activity, directly preventing bacterial gastrointestinal adhesion and indirectly participating in macrophage-phagocytosis activation. Previous studies have explored some of these roles using either just fragments of the bovine milk-derived protein or the human plasma circulating form (SAA1). The recombinant gM-SAA3 was cloned from goat milk through RNA isolation, retrotranscription and specific amplification. Recombinant expression was achieved using the pET101 TOPO-cloning. For gastrointestinal assays, differentiated intestinal Caco-2 cells were incubated in 6-duplicates during 1h with 30 µg/mL of gM-SAA3 prior 2 h infection with 10^6 cfu/well of enteropathogenic *Escherichia coli* (EPEC). Phosphate buffer saline (PBS) and 10^8 cfu/well of *Lactobacillus rhamnosus* were used as negative and positive controls. Bacterial adhesion was quantified by viable cell counts. Human blood and goat milk macrophages were isolated using histopaque gradient density or conventional centrifugation. Macrophages were incubated for 1 h with 3 and 30 µg/mL gM-SAA3, PBS or human serum along with fluorescent labeled *E. coli* BL21-GFP+. Phagocytosis was evaluated using confocal microscopy and quantified as the association index (AI): number of fluorescent bacteria per 100 macrophages. Soluble gM-SAA3 was successfully expressed at 0.5 mg/ml. In gastrointestinal assays, a 70% decrease ($P < 0.001$) in EPEC binding was observed after incubation with gM-SAA3. Also, gM-SAA3 increased ($P < 0.05$) the AI in both human (62 ± 11%) and goat (72 ± 17%) macrophages, compared with PBS (9.8 ± 8% and 18 ± 15% respectively). These results confirm that the whole gM-SAA3 protein may play an active role in the newborn's defense via milk intake and it could participate in the clearance of bacteria through macrophage activation.

Key words: SAA, antibacterial, phagocytosis

Lactation Biology 2

829 Effects of short- and long-chain fatty acids on expression of lipogenic genes in bovine mammary epithelial cells. A. A. A. Jacobs*[1], J. S. Liesman[2], M. J. VandeHaar[2], J. Dijkstra[1], A. M. van Vuuren[1], and J. van Baal[1], *[1]Wageningen University, Wageningen, the Netherlands, [2]Michigan State University, East Lansing.*

Several long-chain polyunsaturated fatty acids can exert an inhibitory effect on the expression of lipogenic genes, including acetyl-CoA carboxylase (ACC), fatty acid synthase (FAS) and stearoyl-CoA desaturase 1 (SCD1), in the bovine mammary gland. Nevertheless, the effect of the short-chain fatty acids acetate (Ac) and β-hydroxybutyrate (BHBA), which are the main precursors for de novo fatty acid synthesis, on expression of these lipogenic genes remains unclear. To examine these effects, we used a bovine mammary epithelial cell line (MAC-T) incubated in fatty acid-free media (CON) and added either 5 m*M* Ac, 5 m*M* BHBA or a combination of 5 m*M* Ac + 5 m*M* BHBA. Furthermore, MAC-T cells were treated with either 100 μ*M* palmitic acid (PA), 100 μ*M* stearic acid (SA), 100 μ*M* oleic acid (OA), 100 μ*M* trans-vaccenic acid (TVA), 100 μ*M* linoleic acid (LA) or 100 μ*M* α-linolenic acid (ALA), which were complexed with BSA. Cells were grown to confluence in DMEM-F12 with 10% serum and all treatments were performed in triplicate. Fatty acids were added to the cells in serum-free DMEM-F12 including the hormones insulin, prolactin, apo-transferrin, progesterone and hydrocortisone. After 12 h of incubation, total RNA was extracted from the cells and mRNA expression of ACC, FAS and SCD1 was analyzed by real-time PCR. In comparison with CON, expression of ACC was increased by Ac (+44%) and was reduced by LA (−48%) and ALA (−49%). Expression of SCD1 was increased by Ac (+61%) and was reduced by OA (−61%), LA (−84%) and ALA (−88%). The treatments did not significantly affect expression of FAS compared with CON. Our results demonstrate that Ac upregulates the expression of ACC and SCD1 in MAC-T cells, which indicates that Ac may increase de novo synthesis and desaturation of fatty acids in the bovine mammary gland.

Key words: mammary epithelial cells, short-chain fatty acids, lipogenic gene expression

830 Effect of timing of feed intake on circadian pattern of milk synthesis. L. W. Rottman*, Y. Ying, and K. J. Harvatine, *The Pennsylvania State University, University Park.*

The rate of feed intake varies over the day and is expected to create a daily rhythm of nutrient absorption. The objective of this study was to characterize the effect of timing of feed intake on the pattern of milk synthesis. Twenty Holstein cows were used in a crossover design with 21d periods. Cows were milked every 6 h on d 14 to 21 of each period. Milk samples were collected at each milking on d 18 through 21, and 6 blood samples were collected on d 20 to 21. Treatments were feeding a TMR once daily (1x fed) or in 4 equal meals every 6 h (4x fed). All cows were fed ad libitum at 110% of daily DMI. Data were analyzed as a repeated measures design, and the model included the random effect of period, sequence, and cow nested within sequence, and the fixed effect of treatment, time, and the interaction of treatment and time. Treatment did not affect daily milk yield, and there was no treatment by time interaction. Milk yield was different by time ($P < 0.001$) with peak yield at 0200 h and 2000 h and a nadir at 1400 h. There was a treatment by time interaction for milk fat percent, but 4x fed resulted in higher milk fat percent at all time points compared with 1x fed (0.22 to 0.45% higher; $P < 0.05$). Daily milk fat yield was increased 0.13 kg/d by 4x feeding ($P < 0.001$). However, milk protein percent and daily yield were higher in 1x fed (0.1% and 0.05kg/d; $P < 0.001$). Plasma nonesterified fatty acids had a daily pattern with a predominant peak at 0700 h and a second, smaller peak at 1800 h (Time, $P < 0.0001$). Interactions were detected between treatment and time for plasma glucose, insulin, and blood urea nitrogen. Plasma glucose nadirs occurred at 0200 h, 1400 h, and 2200 h for 4x fed whereas 1x fed showed a single, higher nadir at 1000 h ($P < 0.01$). More peaks were observed, and the daily range of plasma insulin was greater in 1x fed (21.56 vs. 11.43 μIU/mg). Blood urea nitrogen peaked at 1400 h in 4x fed compared with 1000 h in 1x fed, but had similar daily ranges and nadirs. In conclusion, dairy cows have a circadian pattern of milk synthesis that is responsive to the timing of feed intake.

Key words: circadian, dairy cow

831 Long term effect of feeding rumen protected fish oil or microalgae on mammary gene expression in Holstein cows managed under pasture or confinement systems. P. Vahmani*[1], K. Glover[2], L. A. MacLaren[2], J. Green-Johnson[3], and A. Fredeen[2], *[1]Dalhousie University, Halifax, NS, Canada, [2]Nova Scotia Agricultural College, Truro, NS, Canada, [3]University of Ontario Institute of Technology, Oshawa, ON, Canada.*

The objective of this study was to examine how milk fat percent and yield, and the expression of mammary lipogenic genes were affected by the source of dietary marine oil (fish oil vs. microalgae) in grazing or confined dairy cows. Forty 8 Holstein cows were deployed across 2 feeding systems: either grazing pasture (n = 23) from Apr08 to Sep08, or receiving a TMR in confinement (n = 25) from Oct 08 to Feb09. Cows within each feeding system were blocked by calving date and assigned randomly within block to a control (no supplement) or one of 2 isolipidic supplements: rumen protected fish oil (RPF) or rumen protected microalgae (RPM) for 125 ± 5 d beginning 30 d pre-calving. The RPM supplement provided ~50 g/d of DHA, whereas the RPF supplement provided ~25 g/d each of EPA and DHA. Milk samples were taken at 90 ± 5 DIM for compositional analysis. Four cows from each treatment within each feeding system were slaughtered at 95 ± 5 DIM and mammary parenchymal tissue was sampled. Expressions of mammary genes involved in de novo fatty acid synthesis (ACACA, FASN), desaturation (delta5-, delta6- and delta-9 desaturases), fatty acid uptake (LPL), transcriptional regulation (SREBP1, ChREBP, INSIG1, SCAP, THRSP) and nuclear receptor signaling (PPARα, PPARγ) were determined using qPCR. Milk fat percent was higher ($P = 0.02$) for control (3.52 ± 0.18) compared with RPM (3.02 ± 0.19), but was not different ($P = 0.23$) from RPF (3.28 ± 0.19). However, milk fat yield was not affected ($P = 0.25$) by the lipid supplements (1.34 ± 0.07, 1.25 ± 0.08 and 1.22 ± 0.09 kg/d for control, RPF and RPM, respectively). Expression of SREBP1, the main transcriptional regulator of milk fat synthesis, was reduced ($P < 0.05$) by 26% with RPM or RPF compared with the control, but the rest of measured genes were not altered by the treatments. The lipid supplements did not affect the regulation of the mammary lipogenic complex except for a reduced expression of SREBP1. This effect was apparently insufficient to alter the expression of lipogenic genes and milk fat yield.

Key words: fish oil, microalgae, mammary gene expression

832 Reduced milking frequency increases the concentration of host-defense proteins in milk. K. Stelwagen*[1], M. K. Broadhurst[2], K. Kim[2], A. J. Molenaar[2], D. P. Harris[2], and T. T. Wheeler[2], *[1]Agri-Search Ltd., Hamilton, New Zealand, [2]AgResearch Ltd., Hamilton, New Zealand.*

Milk is a very complex fluid and while its main components, fat, lactose, caseins and major whey proteins, have been reasonably well studied, increasingly its minor components are being elucidated. Many of these minor components have known bioactive properties, including those related to innate immune function, and may have potential to add economic value to the dairy industry. We have previously shown that once-daily milking (ODM), compared with twice daily (TDM), can be used as an on-farm tool to increases the content and yield of the host-defense protein lactoferrin in milk. In the present study we show the effect of ODM on the level of several additional host-defense proteins in milk. Lactating (128 ± 15 DIM) New Zealand Friesian dairy cows (n = 10), grazed on pasture, were continued on normal TDM for the first 3 d of the experiment and then switched to ODM for a further 9 d. At each milking samples were collected for analysis of gross milk composition, SCC, and the abundance of the host-defense proteins lactoferrin, serum amyloid A3 (SAA3), angiogenin/RNase5 and RNase4. The level (μg/mL) of all 4 proteins was increased ($P < 0.05$) during ODM (TDM vs. ODM: lactoferrin, 81%, 110.1 vs. 199.8 ± 38.7 ; SAA3, 82%, 0.09 vs. 0.16 ± 0.02; angiogenin/RNase5, 12%, 8.63 vs. 9.63 ± 0.27; RNase4, 38%, 1.77 vs. 2.39 ± 0.11). The moderate increase of angiogenin/RNase5 is likely to be a consequence of the corresponding decrease in milk yield of 8% due to ODM, as the total yield of angiogenin/RNas5 did not differ significantly between TDM and ODM. Based on indirect indicators of mammary tight junction permeability and a small but significant increase in SCC (TDM vs. ODM: 30 vs. 42 ± × 1000/mL; $P < 0.05$), the increase in milk of host-defense proteins is likely to be due to a mild sterile intramammary inflammatory response accompanying the transition from TDM to ODM. This study shows that ODM may be used as a management tool to increase the level of valuable immune-related minor proteins in milk.

Key words: milk bioactive, milking frequency, host-defense

833 Effect of milking frequency early post-partum on energy metabolism in grazing dairy cows. C. V. C. Phyn[1], T. M. Grala[2], J. K. Kay[1], A. G. Rius[1], S. R. Morgan[1], and J. R. Roche*[1], *[1]DairyNZ Ltd., Hamilton, New Zealand, [2]DairyNZ Ltd., C/- ViaLactia Biosciences (NZ) Ltd., Auckland, New Zealand.*

In grazing dairy cows, short-term once-daily (1X) milking immediately post-calving results in long-term decreases in milk, fat and protein yields, and improves BCS, whereas thrice-daily (3X) milking does not increase energy-corrected milk yields. This study investigates the immediate and long-term effects of post-calving milking frequency (MF) on energy metabolism. Multiparous Holstein-Friesians (n = 150) were randomly assigned to one of 5 groups following calving: milked 1X for 3 or 6 wks and twice daily (2X) thereafter; milked 2X for the entire lactation (control); or milked 3X for 3 or 6 wks and 2X thereafter. Weekly blood samples (wks 1 to 12 post-calving) were analyzed for plasma NEFA, glucose, and aspartate aminotransferase (AST). Liver and adipose tissue was collected at 3, 6 and 9 wks post-calving (n = 12 cows/trt), and gene expression measured using RT-qPCR. Data were analyzed using mixed models fitted with REML in GenStat including: treatment and contrasts to test MF, duration and their interaction as fixed effects, and cow as a random effect. Gene expression of growth hormone receptor (GHR)-total and GHR1A was reduced ($P < 0.05$) and insulin receptor-B increased ($P < 0.01$) at 3 wks post-calving in the liver of cows milked 3X. Cows milked 1X had greater insulin-like growth factor (IGF)-I expression at 3 wks compared with cows milked 2X or 3X. Expression of lipogenic genes (SCD, LPL, THRSP) in adipose tissue was greater ($P < 0.05$) in cows milked 1X at 3 and 6 wks. In contrast, at 9 wks post-calving, cows milked 3X for 6 wks had decreased lipogenic (SCD, THRSP), lipolytic (hormone sensitive lipase) and GHR-total expression. Plasma glucose was greater ($P < 0.001$) and NEFA was lower ($P < 0.001$) during wks 1 to 6 in cows milked 1X. Cows milked 1X for 6 wks also had greater glucose post-treatment (wks 7 to 12). During wks 1 to 3, cows milked 3X had lower glucose and greater NEFA, while AST was greater ($P < 0.05$) throughout (wks 1 to 12). Results indicate that grazing cows milked 1X post-calving maintained a better energy balance and greater lipogenesis than cows milked 2X, whereas 3X milking induced a more severe negative energy balance.

Key words: milking frequency, dairy cow, energy metabolism

834 Regulation of STAT and IGF signaling during reversible and irreversible involution of the bovine mammary gland. K. Singh*[1], J. Dobson[1], K. Oden[1], A. Molenaar[1], R. Murney[1], K. Swanson[1], and K. Stelwagen[2], *[1]AgResearch Ltd., Ruakura Research Centre, Hamilton, New Zealand, [2]Agri-Search Ltd., Hamilton, New Zealand.*

STAT and IGF signaling play a major role at the onset of rodent mammary involution. The aim of this study was to investigate the reversibility of mammary STAT5/3 and IGF signaling following involution induced by not milking, and subsequent re-milking in dairy cows. Mammary alveolar tissue was obtained from non-pregnant cows (n = 5/group) slaughtered at mid-lactation 6h post-milking (control), cows not milked for either 7 or 28d, and cows that were re-milked for 7d following both non-milked periods. Western blot analyses showed that pSTAT5 (activated) protein levels following 7 and 28d involution were lower ($P < 0.001$; 8.5- and 9.5-fold, respectively), compared with lactating controls and cows returned to lactating levels when re-milked following both non-milked periods. In contrast, apoptosis marker pSTAT3 levels were much greater ($P < 0.001$; 40- and 16-fold, respectively) following both 7 and 28d of involution, compared with lactating controls and remained greater ($P < 0.01$; 5-fold) following re-milking after a 28d involution. Similar results were observed for other indicators of apoptosis, lactoferrin and αBax. In contrast to rodent involution, IGF-I was increased in 7 ($P < 0.1$; 2-fold) and 28d ($P < 0.01$; 3.5-fold) non-milked cows and only returned to lactation levels when cows were re-milked after the 7d non-milked period. IGF-II and IGF-BP5 mRNA levels were similar between all groups ($P < 0.1$). Average expression of the major milk proteins αS1-, β-, and κ-CN, α-LA and β-LG declined (RT-PCR; $P < 0.05$) following 7 and 28d of involution (3.5 to over 200-fold) compared with lactating controls. Levels returned to those of lactating controls re-milked after 7d of involution. When re-milked after 28d non-milking, all but κ-CN returned to lactating levels. The variability in milk protein gene expression in response to involution and re-milking between animals was supported by histological analyses demonstrating differences in response rates between cows. These data suggest that STAT3 and IGF-I play a role in the irreversible phase of involution.

Key words: STAT5/3, IGF, bovine mammary involution

835 Variations in the mammary uptake of nutrients throughout an extended milking interval in dairy cows. J. Guinard-Fla-

ment*, C. Hurtaud, and S. Lemosquet, *UMR Production du Lait, INRA/Agrocampus Ouest, Saint-Gilles, France.*

The rate of milk secretion remains steady until 16 h after milking. However, little is known about milk synthesis and the way the udder adapts its nutrient uptake in relation to variations in arterial nutrient flow to sustain its metabolic activity. A trial was carried out to describe variations in mammary blood flow, and in arterial concentrations, mammary arteriovenous differences (AVD), extraction rates (ER), and uptake of nutrients in the course of milk accumulation in the udder over a 36-h period. The trial was performed twice on 2 consecutive wk with 3 dairy cows (34 kg/d of milk). Cows were fed and milked twice daily at the same time, except over the 2 36-h intervals. During milk accumulation, 20 blood samples were collected using 1- to 3-h intervals between samplings. Uptakes of glucose, acetate, BHBA, glycerol, O2, and release of CO2 were reduced by 27–38% on the last 12 h compared with the first 12 h of milk accumulation ($P < 0.05$). But patterns of variations in the course of time between feed distributions were preserved. The mammary uptake of glucose and glycerol did not vary or only slightly between feed distributions (1.4-fold variation; $P < 0.05$). In contrast, acetate and BHBA showed larger variations to a maximum of 50 to 100% ($P < 0.05$ except for BHBA on the last 12 h of milk accumulation). Uptakes of acetate and BHBA were maximal 3 h after feed distribution and were correlated to their arterial concentrations and AVD (r = 0.73 and 0.88 for acetate and r = 0.63 and 0.83 for BHBA, respectively) whereas those of glucose and glycerol were correlated to ER (r = 0.80 and 0.90, respectively). Maximal uptakes of acetate and BHBA were also associated with greater uptakes of glucose, glycerol, O2 and maximal releases of NEFA and CO2 ($P < 0.05$). These results suggest that the de novo synthesis of milk fatty acids could vary throughout the day according to the arterial concentration of acetate or BHBA or both. In contrast, the uptake of glucose and glycerol would depend on the metabolic activity of the mammary gland, the udder modifying its efficiency of extraction from blood according to its metabolic needs.

Key words: milk synthesis, udder uptake, dairy cow

836 Effect of heat stress during the dry period on insulin sensitivity of multiparous dairy cows. S. Tao*, I. M. Thompson, A. P. Monteiro, M. J. Hayen, and G. E. Dahl, *University of Florida, Gainesville.*

Heat stress during the dry period affects hepatic gene expression and adipose tissue mobilization during the transition period. One of the possible outcomes may be altered insulin action on peripheral tissues. Our objective was to evaluate the effect of heat stress during the dry period on insulin sensitivity in the transition period. Cows were dried off 46 d before expected calving and assigned to 1 of 2 treatments: heat stress (HT, n = 16) or cooling (CL, n = 16). During the dry period, the average THI was 78, but CL cows were cooled with sprinklers and fans and HT cows were not. After calving, all the cows were housed together in the same barn and cooled. Rectal temperatures (RT) were measured twice daily (0730 and 1430h) and respiration rate (RR) recorded thrice weekly during the dry period. DMI was recorded daily from dry-off to 42 d relative to calving (RTC). BW and BCS were measured weekly from dry-off to 42 DIM. Milk yield and composition were recorded daily to 126 DIM. Glucose and insulin tolerance tests were performed at dry-off, −14, 7 and 28 d RTC from a subset of cows (HT, n = 8; CL, n = 8). Relative to HT, CL cows had lower RT in the afternoon (39.3 vs. 39.0 0C; $P < 0.01$) and lower RR (69 vs. 48 breaths/min; $P < 0.01$). CL cows consumed more feed than HT cows prepartum (11.4 vs. 10.2 kg/d; $P = 0.05$), but not postpartum ($P = 0.25$). Compared with HT, CL cows gained more weight before calving ($P = 0.01$) but lost more weight in the early lactation ($P = 0.02$). Treatment did not affect BCS. CL cows produced more milk than HT cows (40.4 vs. 32.7 kg/d; $P < 0.01$), but prepartum cooling did not affect milk composition. Preliminary data from the glucose tolerance test indicate that CL cows had similar glucose disposal rates ($P = 0.3$) relative to HT cows 2 weeks before calving. Regardless of treatment, cows had increased glucose disposal rate at −14 d RTC compared with dry-off. We conclude that heat stress during the dry period compromises lactation performance but does not affect insulin sensitivity late in the dry period.

Key words: heat stress, insulin sensitivity, dairy cow

837 Dry period seasonal effects on the subsequent lactation. I. M. Thompson*, A. P. Monteiro, and G. E. Dahl, *University of Florida, Gainesville.*

Photoperiod and heat stress during the dry period influence subsequent lactational performance, and health. To determine the effects of heat stress abatement during the dry period on subsequent lactation under commercial conditions in north central Florida, cows were dried off approximately 45d before expected calving and randomly assigned to 2 treatments, heat stress (HT; n = 77) and cooling (CL; n = 56). Cool cows were kept outside and provided with sprinklers, fans and shade, whereas HT cows were outside under shade. Relative to HT, CL cows had greater milk production (45.62 vs. 43.21; $P = 0.02$) through 120 DIM. Having confirmed significant production effects of heat stress during the dry period, we analyzed records of 2,614 multiparous cows under commercial conditions in Florida over 3 years to determine seasonal effects during the dry period on subsequent lactation performance, reproduction and occurrence of health disorders during the first 60 DIM. Seasons were Cool (Dec, Jan and Feb) and HOT (June, July and Aug). Traits analyzed were lactation number, 305d milk production, calving interval, number of breedings, days open and occurrence of postpartum health disorders such as digestive problems, mastitis, metritis, retained fetal membranes, and respiratory problems. Cows dried during HOT months had lower milk yield in the subsequent lactation relative to COOL cows (10,351 vs. 10,902 kg; $P < 0.01$). Additionally, HOT cows had a higher incidence of mastitis ($P < 0.01$) and respiratory problems ($P < 0.01$) compared with COOL cows. Moreover, cows exposed to heat tended to have a higher incidence of retained fetal membrane ($P < 0.07$) compared with cows cooled while dry. Of interest, COOL cows had a higher incidence of postpartum digestive problems ($P < 0.01$). Therefore, environmental management strategies during the dry period may be needed to attain optimal lactation performance.

Key words: dry period, season, milk production

Meat Science and Muscle Biology: Extracellular Matrix in Skeletal Muscle Development and Meat Quality

838 Stem cell niche and postnatal muscle growth. S. Kuang*, *Purdue University, West Lafayette, IN.*

Stem cell niche plays critical roles in regulating the function of adult stem cells that underlie tissue growth, maintenance and regeneration. In the skeletal muscle, stem cells called satellite cells contribute to postnatal muscle growth and hypertrophy, thus meat production in animal agriculture. Satellite cells are located adjacent to mature muscle fibers underneath a basal lamina sheath. Microenvironmental signals from extracellular matrix mediated by the basal lamina and from the adjacent muscle fiber both impinging on satellite cells to regulate their activity. This talk focuses on how such signals acting together to affect stem cell fate in the niche, and use Dlk1 as an example to elucidate how extracellular cues dynamically regulate satellite cell function during muscle growth and regeneration. Ongoing research in my lab takes advantage of this knowledge to engineer bioactive scaffolds that mimic the key physical and chemical properties of satellite cell niche, and explore the potential of using engineered stem cell niche to enhance tissue regeneration in vivo.

Key words: stem cell niche, skeletal muscle, satellite cell

839 Extracellular matrix regulation of skeletal muscle formation and growth. S. Velleman*, *The Ohio State University/OARDC, Wooster.*

Skeletal muscle growth and development is a highly organized process regulated by interactions between muscle cells and their extracellular environment. Communication between the extracellular matrix (ECM) and cells plays a pivotal role in the regulation of muscle cell proliferation and differentiation. The ECM is a dynamic network of molecules secreted by the cells and includes collagens, proteoglycans, and noncollagenous glycoproteins. The ECM was viewed to be merely a component that the cells were embedded in and provided a structural framework for the cells. In skeletal muscle, the ECM is a major component of the intramuscular connective tissue. In recent years, the ECM has been shown to be an integral part of the cellular communication network regulating cell shape and gene expression. Proteoglycans are a diverse family containing a central core protein and at least one covalently attached glycosaminoglycan (GAG) chain. Proteoglycans are involved in tissue hydration, regulation of gene expression, cell proliferation and differentiation, migration, and adhesion which are all essential for the muscle development process. Two major groups of membrane-associated heparan sulfate proteoglycans, the syndecans and glypicans, are found in skeletal muscle. Both are capable of regulating fibroblast growth factor 2 (FGF2) signal transduction. Syndecan-4 and glypican-1 differentially affect muscle cell proliferation and differentiation and the cellular response to FGF2. Differential regulation of muscle growth by these proteoglycans results, in part, from different signal transduction pathways, such as mitogen activated protein kinase and protein kinase C α, being activated. Understanding the effect of these proteoglycans on these pathways is necessary to develop a comprehensive insight into the mechanisms of proteoglycan-mediated modulation of muscle development and growth. Recent research findings on syndecan-4 and glypican-1 regulation of muscle development will be discussed.

Key words: extracellular matrix, muscle, proteoglycans

840 The influence of extracellular matrix on intramuscular and extramuscular adipogenesis. G. J. Hausman*, *USDA ARS, Athens, GA.*

The extracellular matrix (ECM) and specific ECM components can have a major influence on cell growth, development and phenotype. The influence of the ECM and ECM components on adipogenesis in vivo and in vitro will be reviewed. Engelbreth-Holm-Swarm (EHS) substratum and laminin per se markedly increased attachment, spreading, and hypertrophy of preadipocytes in serum free primary cultures of adipose tissue stromal-vascular (SV) cells while antagonizing spreading of non-preadipocytes. In addition, adipocyte number increased on these substrata resulting in a greater proportion of preadipocytes. Furthermore, immunocytochemistry in primary cultures of adipose tissue S-V cells showed that preadipocytes express ECM components after preadipocyte recruitment and the ECM may be critical for morphological development of adipocytes. Preadipocytes on ECM substrata accumulated lipid but were "flat" and did not express ECM components, regardless of insulin or DEX treatment. The influence of ECM was examined in "marbling" adipocytes by developing a protocol to culture semitendinosus muscle stromal-vascular (SV) cells. The co-development of myotubes and preadipocytes was evident only on laminin substrata when compared with other ECM components following seeding and plating with fetal bovine serum (FBS) with or without DEX. In vivo studies of fetal adipose tissue staining for galactose binding lectins, type IV collagen and laminin will also be reviewed. Adipocyte reactivity for laminin was strong throughout development and was similar for developing adipocytes and vasculature. Staining for lectins and type IV collagen was greater for blood vessels than for adipocytes. The differentiation of the extracellular matrix of blood vessels and adipocytes is clearly distinct throughout development. Therefore, these studies indicated that the ECM and in particular laminin may play a critical role in morphological aspects of preadipocyte development.

Key words: adipogenesis, extracellular matrix, differentiation

841 Connective tissue turnover and meat quality. P. P. Purslow*, *Department of Food Science, University of Guelph, Guelph, ON, Canada.*

Intramuscular connective tissue (IM-ECM) is necessary for patterning muscle development and its turnover is also necessary during muscle growth. The amount and state of maturity of IM-ECM are strong contributors to cooked meat toughness. Amounts of IM-ECM in each muscle appear to be dictated by functional requirements, but its maturity may be reduced by increasing its turnover, as newly deposited IM-ECM has immature crosslinks. IM-ECM degradation is principally by the matrix metalloproteinases (MMPs), and synthesis is by intramuscular fibroblasts. Studies in our laboratory have shown: (1) Fibroblasts from 3 bovine muscles have different proliferation rates and different levels of MMP expression, with fibroblasts in the Semitendinosus being most active. (2) Reactive oxidative species depress new collagen synthesis and increase MMPs expression by intramuscular fibroblasts moderately. When vitamins E or C (or both) are added, both MMP expression and collagen synthesis are elevated. (3) IM-ECM degradative activity is located at the periphery of muscle fibers and fascicles in adult skeletal muscle, and is mostly MMP-related. The major-

ity of MMP expression is in fact from muscle cells, and the levels may vary with muscle fiber size or type. (4) The activity of collagenases expressed by myoblasts is comparable to fibroblasts in cell culture, and responds more to mechanical stimulation. Mechanical stimuli (exercise) are known factors for muscle adaptation and hypertrophy. (5) The stress hormone epinephrine increases the extracellular activity of MMP-2 from fibroblasts, but more so from myoblasts at physiological levels. The β-agonist ractopamine increases both MMP but especially the MMP inhibitor TIMP-1 expressed by myoblasts. These studies suggest that there is good capacity to manipulate IM-ECM turnover by several pathways, including dietary manipulations, by altering the rates of degradation by MMPs and synthesis of new collagen, with less heat-stable crosslinks. However, phenotypic differences between muscles may mean that different muscles may react quite differently to a given treatment applied to the whole animal.

Key words: extracellular matrix, meat quality, proteolysis

Nonruminant Nutrition: Energy and Dietary Fat

842 Determining the energy digestibility of mold-damaged corn selected for low mycotoxin content in finishing pigs. C. M. Pilcher*, A. Greco, C. R. Hurburgh, G. P. Munkvold, C. K. Jones, and J. F. Patience, *Iowa State University, Ames.*

There is very limited information on the impact of mold damage on the digestibility of nutrients in corn. The objective of this study was to determine the DE content of mold damaged corn samples selected for low mycotoxin content. Corn samples with visible mold damage were collected from 14 Midwestern sites and corn samples with no visible mold damage were selected from 4 Midwestern sites. All samples were screened for mycotoxin content and only samples with low mycotoxin content (i.e., < 1.0 ppm deoxynivalenol; < 20 ppb aflatoxin; < 10 ppm fumonisin; < 3 ppm zearalenone) were selected for use in the trial. A single control sample was created by blending 3 samples with no visible mold damage, and 7 mold damaged samples were selected. Corn samples were inspected by an official US grain inspection agency. Mold damaged samples varied in test weight (58 to 72 kg/hL; mean = 67 ± 5.2 kg/hL), total damaged kernels (9.4 to 65.8%; mean = 33.8 ± 21.70%) and moisture (13.9 to 16.5; mean = 14.9 ± 0.84%). Experimental diets were comprised of 96.9% corn from the control or one of the 7 mold damaged sources supplemented with vitamins and minerals. Barrows (initial BW = 99.0 ± 4.98 kg, n = 16) were allotted to an 8 × 3 Youden square design with the 8 diets and 3 replicate periods. Periods included 6 d of adaptation to treatment diets followed by a 2 d fecal collection period. Pigs received a fully balanced finishing diet for 4 d between replicates. Gross energy of diets and feces was determined by bomb calorimetry. There was a considerable range among the mold damaged corn samples for DM digestibility (85.2 to 87.3%; $P < 0.01$), energy digestibility (83.2 to 85.7%; $P < 0.01$) and DE (3,436 to 3,611 kcal/kg DM; $P < 0.0001$). DM digestibility (86.8 vs. 89.2%; $P < 0.01$), energy digestibility (85.0 vs. 87.8%; $P < 0.01$), and DE (3,558 vs. 3,714 kcal/kg DM; $P < 0.001$) were lower for mold damaged corn compared with the control corn. The current practice of blending mold damaged corn with good quality corn presents risks of lowering nutrient availability.

Key words: corn, mold, swine

843 Effects of dietary energy density on performance and lean deposition of growing-finishing pigs raised in a commercial environment. L. C. Chu*, C. J. Cai, G. J. Zhang, S. Y. Qiao, and D. F. Li, *China Agricultural University, Beijing, China.*

Three experiments were conducted to determine the effects of digestible energy (DE) density on performance and lean deposition in growing-finishing pigs (Yorkshire × Landrace × Duroc) during 3 separate phases when housed in a commercial environment. A completely randomized block design within sex was used involving 480 pigs (20.8 to 55.9 kg) in Exp. 1, 420 pigs in Exp. 2 (57.0 to 76.6 kg) and 240 pigs (78.6 to 105.8 kg) in Exp. 3. Pigs were allotted to one of 5 treatments containing 13.62, 13.87, 14.12, 14.37 and 14.62 MJ DE/kg. Pig body weight and feed consumption were determined every 2 weeks and carcass composition was evaluated at the start and end of the experiments to evaluate lean deposition. ANOVA, linear and quadratic contrasts and the broken-line regression model was used to analyze the experimental data. In Exp. 1, energy density had no significant effect ($P > 0.05$) on weight gain or feed efficiency. Meanwhile, carcass fat-free lean gain decreased (linear, $P = 0.02$; quadratic, $P = 0.02$) and fat-free lean index decreased quadratically (quadratic, $P = 0.05$) with increasing dietary energy density. The optimum level of dietary DE to maximize lean deposition was 13.81 MJ DE/kg. In Exp. 2, both weight gain ($P = 0.01$) and feed efficiency ($P = 0.06$) increased linearly with increasing DE density, while carcass fat-free lean gain ($P = 0.05$) and fat-free lean index decreased significantly ($P < 0.01$). The optimum level of dietary DE to maximize lean deposition was 13.76 MJ DE/kg. In Exp. 3, weight gain ($P = 0.09$) and feed efficiency ($P = 0.05$) also showed an increasing trend. The decreasing trend of carcass fat-free lean gain ($P = 0.05$) and fat-free lean index ($P < 0.01$) suggest the optimum level of dietary DE to maximize lean deposition was 13.82 MJ DE/kg. The results of the present study demonstrate that pigs reared in a commercial environment require different dietary energy levels for lean deposition compared with performance. Therefore, diets may be formulated with different energy levels depending on the overall goal of a swine producer.

Key words: digestible energy, growing-finishing pigs, lean deposition

844 Effect of feeding soy and sunflower based reconstituted fat or monoestearate as fat sources in piglet diets. J. J. Mallo[1], J. Alcañiz*[1], M. I. Gracia[2], and C. Millán[2], *[1]Norel, S.A., Madrid, Spain, [2]Imasde Agroalimentaria, S.L., Madrid, Spain.*

A total of 216 weaned piglets (Large White x Landrace*Large White) were allocated at random to 4 experimental treatments (T1: basal diet, 4% soy oil; T2: 4% Soy+Sunflower oil fatty acids esterified with glycerol (reconstituted fat, RE); T3: 4% Soy+Sunflower oil monoestearate (ME); and T4: 2% soy oil + 2% ME), including 6 replicates of 9 piglets per treatment (half male and half female). Mash feeds and water were offered ad libitum with no added growth promoter or veterinary antibiotics. A common prestarter diet was offered from weaning at 26 d during a week. Experimental treatments were applied in the starter diets from 33 to 63 d of age. After consuming the experimental diets for 9 d, fecal samples were taken to calculate nutrient digestibility. Observations included body weight (BW), growth (ADG), feed intake (ADFI), feed conversion ratio (FCR) and apparent fecal digestibility of dry matter, organic matter, ether extract and gross energy of the diets. Data were analyzed as a completely randomized design by GLM of SAS. No significant differences were observed between fat sources in any of the performance parameters studied (374, 368, 375, 357 g/d and 1.28, 1.34, 1.32, 1.35 g feed/g gain for growth and feed conversion at 33–63 d of age, for T1 to T4, respectively; $P > 0.10$). Significant differences were observed in digestibility between the 4 treatments. Apparent fecal digestibility of dry matter was improved with RE, ME and the combination when compared with the basal diet (68.8^{b}, 75.0^{a}, 78.1^{a}, 76.6^{a} %, $P = 0.0288$, for T1-T4, respectively). Apparent fecal digestibility of gross energy (DCGE) and organic matter (DCOM) were improved when ME or the combination were used, presenting RE intermediate results (DCGE: 68.7^{b}, 73.5^{ab}, 77.8^{a}, 76.3^{a} %, $P = 0.0334$; and DCOM: 73.8^{b}, 78.2^{ab}, 81.5^{a}, 80.9^{a} %, $P = 0.0246$, for T1-T4, respectively). It is concluded that soy and sunflower oil reconstituted fat or monoestearate improve digestibility of piglet diets and can be used as an alternative to soya oil for weaned piglets.

Key words: monoestearate, vegetable reconstituted fat, piglets

845 Impact of fat source on nutrient digestibility and performance in nursery pigs. S. M. Mendoza* and E. van Heugten, *North Carolina State University, Raleigh.*

This study was designed to evaluate the impact of fat saturation (iodine value, IV) and FFA concentration of fat on nursery pig performance and digestibility of fat and gross energy. Pigs (n = 189; BW = 9.32 ± 0.11 kg) were weaned at 21 d and fed a common diet for 14 d. Pigs were housed 3 pigs per pen using a total of 63 pens and assigned within weight blocks to one of 7 dietary treatments. Diets were corn-soybean meal based (3.76% SID lysine/Mcal ME) and consisted of a negative control diet without added fat and a basal diet with 6% added fat from a combination of 4 fat sources to create 6 diets with 2 levels of FFA (0.4 or 54.0%) and 3 degrees of fat saturation (IV = 77, 100, or 123) in a 2 × 3 factorial arrangement. Fat sources were: soybean oil (SO, 0.3% FFA, IV = 129.4), soybean-refined cottonseed acid oil (SAO, 70.5% FFA, IV = 112.9), choice white grease (CWG, 0.6% FFA, IV = 74.8), and choice white acid grease (CWAG, 56.0% FFA, IV = 79.0). Fat sources were included in diets at the following proportions: diet 1, 100% CWG; diet 2, 95% CWAG and 5% CWG; diet 3, 50% SO and50% CWG; diet 4, 38% SAO, 12% SO, 48% CWAG, and 2% CWG; diet 5, 100% SO; and diet 6, 76% SOA and 24% SO. Fat supplementation decreased ADFI (812 vs. 873 g/d; $P = 0.02$) and improved G:F (715 vs. 646 g/kg; $P < 0.001$) compared with the negative control diet. Diets with high FFA tended ($P = 0.08$) to improve BW (21.69 vs. 21.13 kg) and ADG (592 vs. 566 g/d). Apparent digestibility of fat was higher in fat supplemented diets than control diets (63.3 vs. 28.1%, $P < 0.001$). Fat digestibility was higher in diets with low FFA (65.6% vs. 60.9%, $P < 0.001$) and decreased linearly with increasing IV (72.6, 65.5, and 58.9%) when FFA concentration was low, but was unaffected by IV when FFA concentration was high (60.6, 61.3, and 60.9%). Digestibility of GE was higher in diets with low FFA (83.1% vs. 80.9%; $P < 0.001$). In conclusion, G:F was improved when fat was supplemented to pigs. Digestibility of fat and GE was reduced for fats high in FFA. However, nursery pig performance tended to be improved with high FFA, indicating that SAO and CWAG could be economic alternatives to more expensive fats.

Key words: pigs, fat, digestibility

846 Effect of altering the dietary omega-6 to omega-3 fatty acid profile of sow diets on the immune responses of their offspring when challenged with *E. coli* lipopolysaccharide. L. Eastwood*[1,2], A. D. Beaulieu[1,2], and P. Leterme[3], *[1]Prairie Swine Centre Inc, Saskatoon, SK, Canada, [2]Animal and Poultry Science, University of Saskatchewan, Saskatoon, SK, Canada, [3]Cargill - R & D Centre Europe, Havenstraat, Vilvoorde, Belgium.*

The objective of this experiment was to determine the effects of altering the omega-6 (n6) to omega-3 (n3) fatty acid (FA) ratio in sow diets on the immune responses of their offspring. Sows consumed one of 5 treatment diets for 2 reproductive cycles. Treatments were a control (tallow based) or plant based diets with n6:n3 ratios of 10:1, 5:1, 1:1, or a fish based 5:1 ratio. Piglets weaned from the 2nd cycle (d28 of lactation) were used in the immune challenge study. On d 6 post-weaning, weanling pigs (n = 100), 20 from each diet group, were randomized to a challenge control group (saline) or to an *E. coli* lipopolysaccharide (15 µg/kg BW; LPS) injected group (n = 10/challenge/diet). Rectal temperatures were recorded at 0, 1, 2, 3, 4, 5, 6, 12 and 24 h post injection and blood samples were collected at 0, 2, 6 and 12 h post injection for cytokine analysis (IL-1β, IL-6, IL-8, TNFα). Treatments were arranged as a 5 × 2 factorial (diet x immune challenge) and analyzed with time of sampling as a repeated measure. The sow′s milk had n6:n3 ratios of 7.5:1, 4.5:1, 1.5:1 and 3:1 for the 10:1, 5:1, 1:1 and 5:1 fish diets respectively. For all parameters except IL-6, an effect of challenge, time and the challenge by time interaction were observed ($P < 0.05$), indicating the LPS elicited an immune response. Piglets from the 1:1 dietary treatment group had the highest body temperature ($P = 0.0004$). The diet by immune challenge interaction tended to be different for body temperature ($P = 0.12$) and IL-8 ($P = 0.18$). Piglets from the 1:1 and 5:1 fish groups had a greater IL-8 response to the immune challenge relative to piglets from the other diets. A greater febrile response to the LPS challenge was seen in piglets originating from sows consuming the 1:1 diet. Weanling pigs produced from sows consuming different n6:n3 FA ratios respond differently to a LPS induced immune response. This implies that the fatty acid profile of a sow′s diet may affect the response of her offspring to immune challenges that occur regularly at the time of weaning.

Key words: cytokine, omega-3, swine

847 Impact of dietary fat on milk composition, milk output and apparent digestibility is fat source dependent in lactating sows. D. S. Rosero*[1], E. van Heughten[1], J. Odle[1], V. Fellner[1], and R. D. Boyd[2], *[1]Department of Animal Sciences, North Carolina State University, Raleigh, [2]Hanor Company Inc., Franklin, KY.*

This study investigated the impact of 2 sources of supplemental fat on milk composition and apparent digestibility of fat during lactation. In Exp. 1, milk samples were collected from 30 sows (PIC Camborough) during d 4, 11 and 18 of lactation. Sows were assigned to a control diet without added fat and 2 diets supplemented with 6% fat consisting of either animal-vegetable blend (AV; 14.5% FFA, IV = 89) or choice white grease (CWG; 3.7% FFA, IV = 62). In Exp. 2, fecal samples were collected from 56 sows to calculate fat digestibility using TiO2 as a marker. Sows were assigned to a 2 × 3 factorial arrangement and a control diet without fat. Factors included: 1) fat sources (AV and CWG); and 2) fat level (2, 4 and 6%). For the 2 studies, sows were balanced for parity 1, and 3 to 5 (P3+). Diets were corn-soybean meal based with 8% DDGS and 6% wheat middlings, and contained 3.56 g standardized ileal digestible Lys/Mcal ME. Piglet growth rate in Exp. 1 was improved by CWG ($P < 0.05$; 197.7 g/d) but not with AV (169.9) compared with the control (169.2). Calculated milk production (2.5 x ADG + 80 x initial BW + 7) was greater for CWG ($P < 0.01$; 646 $g \bullet pig^{-1} \bullet d^{-1}$) than AV and the control diet (564 and 569, respectively). CWG, but not AV increased ($P < 0.05$; 7.35%) fat content in the milk (6.30, 6.70, for control and AV, respectively). Milk protein decreased ($P < 0.001$; 5.2, 4.6 and 4.7% for d 4, 11 and 18, respectively), lactose increased ($P < 0.001$; 5.2, 5.7 and 5.7) and Ca increased ($P = 0.003$; 0.16, 0.17 and 0.18) during lactation. Linoleic (C18:2) and linolenic acid (C18:3) were higher ($P < 0.001$) in milk fat from sows fed AV (23.2 and 1.4%, respectively) than CWG (18.9 and 1.0) and control (17.4 and 0.7). Milk fat IV was higher ($P < 0.001$) for AV (75.9) than CWG (72.5) and control (68.4). Apparent digestibility of fat increased with each increment (Linear, $P < 0.001$), but CWG was more digestible than A-V (Fat x Level, $P < 0.05$). In conclusion, digestibility of fat was improved with increasing levels of fat and was higher for CWG than AV, affecting positively composition and production of milk, consequently improving piglet growth rate.

Key words: sow, fat, milk

Production, Management and the Environment: Environmental Quality

848 Ammonia emissions from a commercial feedyard measured using passive samplers and a box model. N. A. Cole*[1], R. W. Todd[1], D. B. Parker[2], M. Rhoades[3], and A. Mason[1], *[1]USDA-ARS, Conservation & Production Research Lab, Bushland, TX, [2]USDA-ARS-MARC, Clay Center, NE, [3]West Texas A&M University, Canyon.*

Animal feeding operations are a major source of ammonia gas emitted to the atmosphere. Ammonia emissions can potentially affect air quality and sensitive ecosystems, but because measuring ammonia emissions from open lots is difficult, few studies have investigated ammonia losses from beef cattle feedyards. Our objective was to measure ammonia emissions from a 77-ha, 45,000-head beef cattle feedyard on the southern High Plains. Profiles of ammonia concentration, wind speed, and air temperature were measured downwind (5 d in summer) or in the middle (6 d in winter) of the feedyard. In addition, ammonia concentrations were measured at 7 locations downwind (summer) or in the middle (winter) of the yard using a combination of active and passive samplers. Ammonia flux was estimated using a box model. Samples of rations, fresh feces, pen manure, and compost were obtained for chemical analyses (DM, N, P). Dietary N concentrations averaged 2.14% during the summer and 2.51% during the winter. Hourly ammonia-N flux averaged 365 ± 49 mg/m^2 in the summer and 212 ± 92 mg/m^2 in the winter. Ammonia-N emission rates averaged 5,453 ± 741 kg/d in the summer (63% of N intake), and 3,170 ± 1,383 kg/d in the winter (31% of N intake), with an annualized average of 4,311 ± 1,612 kg/d (47% of N intake). Nitrogen volatilization losses, estimated from the changes in the N:P ratio of rations and dry pen manure, averaged 42% of N intake. The annualized emission factor was 15.4 ± 2.2 kg ammonia-N/head fed. Nitrogen volatilization losses from the compost windrows, estimated from changes in the N:P ratio of manure and compost, averaged 3.4 ± 1.4% of N placed in the windrows during winter and 13.3 ± 1.3% in summer. Ammonia-N volatilization losses from the retention pond, estimated using an empirical model, averaged 5.5 ± 4.4 kg/ha daily or 166 ± 130 kg/d. These values agree well with emissions estimated using an inverse dispersion model and demonstrate that the pen surface is the primary source of feedlot ammonia, and that emissions are greater in summer than winter. This research was partially supported by grant #TS2006–06009 from the USDA-CSREES.

Key words: beef cattle, ammonia, emissions

849 Effects of feeding birdsfoot-trefoil on greenhouse gases emissions from fresh and land incorporated dairy manure. Q. Wang*, R. Franco, Y. Zhao, Y. Pan, and F. Mitloehner, *University of California, Davis, Davis.*

Birdsfoot-trefoil, a legume containing condensed tannins, may improve N utilization efficiency and shift urine N to fecal N. This shift might affect greenhouse gas (GHG) emissions because fecal N versus urine N is less utilizable by denitrifying bacteria that produce GHG from manure. The present study investigated the effects of feeding birdsfoot-trefoil (BFT) on GHG emissions from fresh and land-incorporated dairy manure (LIDM). Eighteen lactating Holstein cows were randomly assigned to 1 of the 2 treatments: 1) alfalfa (ALF) based ration, and 2) BFT based ration. Within each treatment, 9 cows were randomly assigned to 3 groups (n = 3). Animals were fed the respective diets for 8 d and then moved into an environmentally controlled chamber for 12 h to allow for GHG monitoring. Blood samples for blood urea N analysis were collected before cows left the chamber. The fresh manure was left on the chamber floor for 12 h to measure GHG emissions with INNOVA 1412 gas analyzer. CO_2, CH_4 and N_2O emissions from the fresh manure of ALF and BFT fed cows are 5.29, 0.05, 0.01 ppm and 4.71, 0.10, 0.01 ppm, respectively. Then the aged manure was collected and incorporated into loamy soil to simulate LIDM. Flux chambers were connected to the INNOVA 1412 gas analyzer to measure GHG emissions from LIDM over a 10 d period. CO_2 and N_2O emissions from the LIDM of ALF and BFT fed cows are 102.70, 0.02 ppm and 78.15, 0.02 ppm, respectively. Blood urea N was lower in BFT versus ALF fed animals ($P < 0.05$). However, GHG emissions were similar between BFT and ALF fed cow manure. In the present study, BFT did not affect the GHG emissions from dairy manure. A follow-up study, will investigate the effects of BFT on N partitioning over time.

Key words: alfalfa, birdsfoot-trefoil, greenhouse gas

850 Prediction of individual methane emission by dairy cattle from milk mid-infrared spectra. A. Vanlierde*[1], C. Delfosse[1], F. Dehareng[1], E. Froidmont[2], H. Soyeurt[3,4], M. Hammida[1], J.-M. Romnee[1], and P. Dardenne[1], *[1]Walloon Agricultural Research Centre, Quality Department, Gembloux, Belgium, [2]Walloon Agricultural Research Centre, Department of Production and Sectors, Gembloux, Belgium, [3]University of Liège Gembloux Agro-Bio Tech, Animal Science Unit, Gembloux, Belgium, [4]National Fund for Scientific Research, Brussels, Belgium.*

Methane produced by ruminants contributes to global warming. Different experiments were conducted on Holstein cows to predict their individual methane production. The objective was to obtain a wide variation in methane emissions to establish predictive equations. For this, the cows were selected according to their stage and number of lactation and received different types of diet known to promote or not the production of methane during rumen fermentation. Individual methane emission was daily measured by a sulfur hexafluoride tracer during a week. In the same time, a sample of individual milk was analyzed by mid-infrared (MIR) spectrometry. The daily methane data was then related to an average of daily milk spectrum (AMS). Five different calculations were used because of the delay between the generation of fermentation products and their use in the milk components. The methane emissions were compared with AMS at d 0, 0.5, 1, 1.5, and 2. Equations were built with partial last square regression and showed that the AMS at d 1.5 gave the best prediction of the CH4 emission with a cross validation R^2 of 0.79. It indicates that there is more than one day between the formation of feed fermentation products and their "detection" in milk analysis. There is also a close correlation between fatty acid (FA) profile and methane emission at d 1.5. However, results show that applying directly the developed methane equation gives a better prediction than the use of correlation between FA and methane. These observations suggest the feasibility of methane prediction from MIR spectra. Now, it is important to increase the reliability of prediction and make a validation to predict continuously the individual methane emissions in small and large scales and also to identify low methane emitted cows.

Key words: methane, mid–infrared, milk

851 Effects of biotechnology on greenhouse gases, volatile organic compounds, and ammonia from feedlot cattle. K. R. Stack-

house*, M. S. Calvo, S. E. Place, T. L. Armitage, Y. Pan, Y. Zhao, and F. M. Mitloehner, *University of California, Davis.*

The feedlot industry uses biotechnologies such as antibiotics, growth implants, and β_2-adrenergic agonists to improve health and growth performance of cattle. These biotechnologies alter microbes in the rumen and nitrogen retention in the animal, which may lead to changes in greenhouse gas (GHG), volatile organic compound (VOC), and ammonia emissions from feedlots. The present study investigated GHG, VOC, and ammonia emissions from 160 Black Angus steers. Steers were blocked by weight and randomly assigned to 16 pens of 10 animals each. Treatments applied were: (1) control (no biotechnology application, CON), (2) Rumensin and Tylosin (RUM), (3) Rumensin, Tylosin, and Revalor-s (IMP), and (4) Rumensin, Tylosin, Revalor-s, and Zilpaterol hydrochloride (BAA). Cattle were on feed for an average of 107 d and performance and blood urea nitrogen (BUN) measured. Gaseous emissions were measured during the last 10 d of the feeding period when animals were housed in 4 totally enclosed identical cattle pen enclosures. The control was compared with 3 treatment groups using a 4 by 4 Latin square design (n = 4). Nitrous oxide, carbon dioxide, methanol, ethanol, and ammonia were measured using the INNOVA 1412 gas analyzer. Methane was measured using the TEI 55C analyzer. Emissions are reported in g^{-1} kg HCW^{-1} d. All measurements were analyzed using Proc Mixed in SAS. Treatment with IMP and BAA increased ($P < 0.05$) ADG and final BW. BAA vs. other treatments increased HCW ($P < 0.05$) and reduced ($P < 0.05$) methane and ammonia emissions as well as BUN. The present study will provide a better understanding of how antibiotics and growth enhancement application used in feedlot cattle affect atmospheric emissions of GHGs, VOCs, and ammonia per kg of product.

Key words: beef cattle, greenhouse gas, ammonia

852 Life cycle assessment of greenhouse gas emissions from beef production systems in California. K. R. Stackhouse*[1], C. A. Rotz[2], and F. M. Mitloehner[1], *[1]University of California, Davis, [2]USDA/Agriculture Research Service, Pasture Systems and Watershed Management Research Unit, University Park, PA.*

Beef production is recognized as a source of GHG emissions; however, little information exists on the net emission from production systems. A life cycle assessment (LCA) was conducted using the Integrated Farm System Model (IFSM) to estimate whole-farm GHG emissions from representative beef production systems in California. The IFSM is a process-level farm model that simulates crop production, feed production and use, animal production, and the return of manure nutrients back to the land to predict the environmental impacts and economics of production systems. The carbon footprint of major production systems was determined as the net exchange of all GHG in carbon dioxide (CO_2) equivalent units per unit of HCW produced. The calculation of net emissions determined the relative contributions of the cow-calf, stocker, and feedlot phases of beef production to the overall carbon footprint of the consumable product. The IFSM was used to predict all important sources and sinks of methane, nitrous oxide, and carbon dioxide from primary and secondary sources. Primary emission sources included enteric fermentation, manure, cropland used in feed production, and fuel combustion in handling manure and producing feed. Secondary emissions were those produced during the production of resources used on the farm, which included fuel, electricity, machinery, fertilizer, pesticides, and replacement animals. Simulated beef production systems included the cow-calf, stocker, and feedlot phases for the traditional British beef breeds and calf ranch and feedlot phases for Holstein steers. An evaluation of differing production management strategies produced carbon footprint values ranging from 5.4 to 19.3 kg CO_2 equivalent / kg of HCW produced. Within the British beef production cycle, the cow-calf phase was responsible for approximately 70% of total GHG emissions with 12% from feedlot sources. Holstein steers that entered the beef production system as a by-product of milk production had the lowest carbon footprint because the emissions associated with their mothers were attributed to milk rather than meat production.

Key words: beef cattle, carbon footprint, greenhouse gas

853 Effects of calf hutch flooring on air quality and exposure. M. S. Calvo*[1], M. van der Voort[2], J. A. McGarvey[3], J. P. Reynolds[4], T. L. Armitage[1], E. A. M. Bokkers[2], and F. M. Mitloehner[1], *[1]Department of Animal Science, University of California, Davis, [2]Department of Animal Sciences, Wageningen University, Wageningen, the Netherlands, [3]USDA Agriculture Research Service, Plant Mycotoxin Research Unit, Albany, CA, [4]Veterinary Medicine Teaching & Research Center, University of California, Davis, Tulare.*

Respiratory diseases in calves are associated with the exposure of airborne pathogenic microorganisms and dust, as well as gases that can compromise the defense mechanisms of the respiratory system. Calf bedding provided inside hutches may increase the exposure of animals to ammonia, particulate matter (PM), and airborne microorganisms. The present study quantified concentrations of these compounds in calf hutches supplied with or without bedding. In addition, the effectiveness of applying sodium bisulfate (SBS), an acidifier, to calf bedding was tested to determine if a reduction in pH could reduce these air compounds. Holstein bull calves (n = 63) were randomly assigned to one of the 3 treatments at 1 d of age: 1) elevated hutches with conventional wooden slatted floor and no bedding (CON); 2) hutches with dirt floor and bedding provided (BED); 3) hutches with dirt floor and bedding treated with SBS provided (SBED). Ammonia, PM, and airborne bacteria were measured weekly inside calf hutches using an INNOVA 1412 multigas analyzer, cyclone and open-face cassette samplers, and Andersen biological cascade impactors, respectively. Ammonia differed ($P < 0.001$) across treatments, with CON yielding the highest (0.57 ± 0.03 ppm) and SBED the lowest (0.35 ± 0.03 ppm) concentrations. The PM concentrations were similar ($P > 0.05$) across treatments for both fine (diameter ≤ 2.5 μm) and coarse (diameter ≥ 2.5 μm) particles. Bacteria concentrations were lower ($P < 0.0001$) for CON ($1{,}163 \pm 696$ cfu/m^3) versus BED ($3{,}233 \pm 731$ cfu/m^3) and SBED ($2{,}705 \pm 919$ cfu/m^3), which were similar ($P > 0.05$). Overall, the results improve the understanding of air quality inside wooden hutches housing newborn calves. The management of calf bedding may affect certain air compounds known to affect respiratory health.

Key words: ammonia, bacteria, calf

854 Feeding saponins to reduce air emissions from steers. W. Li* and W. J. Powers, *Department of Animal Science, Michigan State University, East Lansing.*

A series of experiments (Exp) were conducted to quantify the effect of saponin extracts from *Quillaja saponaria* (Q), *Yucca schidigera* (Y) and *Camellia sinensis* (T) on gaseous emissions from steers. Exp1 compared a control diet (C; corn-corn silage basal diet), Y (0.64% DM) and Q (1.5% DM); 4 replicates per treatment. Exp 2 evaluated the effect of T (0.25% DM) and C. Products inclusion level was established to provide the same saponin concentration across Exp. Exp 3

compared C, Q (1.5% DM), Y (1.5% DM) and T (0.5% DM). Holstein steers (n = 12) at initial BW of 353 ± 18 kg (Exp1), 428 ± 23 kg (Exp 2) and 391 ± 22kg (Exp 3) were housed, individually, in environmental rooms for 22 d per study. Emissions of methane (CH_4), ammonia (NH_3), hydrogen sulfide (H_2S), nitrous oxide (N_2O) and non-methane total hydrocarbons (NMTHC) were monitored in room exhaust air. In Exp 1, DMI (7.54 ± 0.09 kg) and ADG (1.11 ± 0.18 kg) were not affected by diet ($P > 0.05$). DMI was improved in Exp 2 by adding TS into the diet (8.94 kg in TS vs. 8.53 in C; $P < 0.05$), while ADG was not affected by diet. During Exp 3 steers fed the T diet ate less (6.43 kg/d) and gained less (0.39 kg/d) compared with the average DMI (8.69 kg) and ADG (1.37 kg) of the other 3 treatments ($P < 0.05$). Across Exp, saponin inclusion did not alter daily CH_4 emission when reported on a DMI basis (13.25, 11.08 and 12.65 g/kg DMI, for Exp 1, 2, and 3, respectively). Daily NH_3 emission was not affected by diet in Exp 1 (17.3 g/d). Feeding TS in Exp 2 reduced NH_3 emissions per unit of N intake (131.0 vs. 186.5 mg/g N intake; $P < 0.05$). Feeding Q in Exp 3 resulted in greater mass of NH_3 emitted compared with the other treatments (18.9 g/d vs. 14.1 g/d; $P > 0.05$). Average daily H_2S, N_2O and NMTHC emissions were 84.59, 2963.78 and 1436.06 mg, respectively, across all Exp with no diet effects observed within Exp ($P > 0.05$). Results show that 0.5% DM of T in diet reduced CH_4 emission at the expense of DMI and ADG. Inclusion of Q and Y demonstrated the potential to increase NH_3 emissions.

Key words: *Quillaja saponaria*, *Yucca schidigera*, *Camellia sinensis*

855 Supplementary concentrate type affects nitrogen balance in early lactation dairy cows offered grazed pasture. S. J. Whelan*, K. M. Pierce, J. J. Callan, B. Flynn, and F. J. Mulligan, *School of Agriculture, Food Science and Veterinary Medicine, University College Dublin, Belfield, Dublin 4, Ireland.*

Nitrogen (N) losses from dairy cow production systems have a detrimental effect on the environment. Dietary strategies to improve N balance in dairy cows may help alleviate these effects. This experiment evaluates the effect of supplementary concentrate type on N balance in early lactation dairy cows offered a perennial ryegrass pasture. A total of 48 were assigned to 1 of 4 dietary treatments in a randomized block design (n = 12). All cows received a perennial ryegrass pasture plus one of the following concentrate types: Hi-Pro (18% CP), Lo-Pro (14% CP), Lo-Pro Meth (14% CP, with added methionine) and Lo-Pro Maize (14% CP). Hi-Pro, Lo-Pro and Lo-Pro Meth contained rolled barley, whereas Lo-Pro Maize contained stone ground maize as the starch source. Concentrates were isoenergetic (1.11UFL/kg DM) and offered at 3kg twice daily. On wk 6 and 10 post calving N balance studies were conducted. Data was analyzed using Proc Mixed of the SAS institute. Feed N intake was greater ($P < 0.05$) for Hi-Pro vs. all other dietary treatments; Lo-Pro, Lo-Pro Meth and Lo-Pro Maize were not different ($P > 0.05$). Feces N recovery (N out ÷ N in) was lower ($P < 0.05$) for Hi-Pro vs. all other dietary treatments; Lo-Pro, Lo-Pro Meth and Lo-Pro Maize were not different ($P > 0.05$). Recovery of N in the urine was greater ($P < 0.05$) for Hi-Pro vs. Lo-Pro Meth and Lo-Pro Maize; Lo-Pro was not different ($P > 0.05$) from other treatments. Recovery of N in the milk was lower ($P < 0.05$) for Hi-Pro vs. Lo-Pro Meth and Lo-Pro Maize; Lo-Pro was lower ($P < 0.05$) vs. Lo-Pro Maize but not Hi-Pro or Lo-Pro Meth. Improved milk N recovery with Lo-Pro Maize and Lo-Pro Meth allows for a reduction in urinary N portion.

Table 1. Effect of supplementary concentrate type on nitrogen (N) balance

Concentrate Type	Hi-Pro	Lo-Pro	Lo-Pro Meth	Lo-Pro Maize	SEM
Feed N ($kg \cdot d^{-1}$)	0.511^{a}	0.462^{b}	0.456^{b}	0.445^{b}	0.0160
Proportion of ingested N excreted in feces, urine and milk					
Feces	0.376^{b}	0.440^{a}	0.432^{a}	0.418^{a}	0.0107
Urine	0.374^{a}	0.320^{ab}	0.277^{b}	0.291^{b}	0.0257
Milk	0.250^{c}	0.251^{bc}	0.284^{ab}	0.298^{a}	0.0166

^{abc}Rows with different superscripts differ ($P < 0.05$).

Key words: nitrogen balance, grazed grass, concentrate type

856 Development of a user-friendly online system to quantitatively measure metabolic gas fluxes from ruminants. P. Zimmerman*[1], S. Zimmerman[1], S. Utsumi[2], and D. Beede[2], *[1]C-Lock Inc., Rapid City, SD, [2]Michigan State University, East Lansing.*

We developed and tested a new internet-interfaced system to quantitatively measure methane, carbon dioxide and other metabolic emissions from individual animals and to track changes in emissions over time. Methane is not only a powerful greenhouse gas, but emissions also represent significant losses of energy and feed efficiency. Changes in fluxes are also sensitive indicators of changes in diet, behavior, and health. The system has been tested in robotic dairies, tie-stalls, and pastures. The system includes the following elements: a headstall unit to restrict and control atmospheric mixing; a radio-frequency identification (RFID) of each animal; a feed or water dispenser so that the animal voluntarily keeps its head in the correct position to obtain quantitative, representative metabolic gas measurements; sensors to detect animal head position; a gas intake manifold with mixing and flow conditioning elements; a fan unit to capture expired and eructated gases along with a sensor to measure air flow-rate through the headstall manifold; a tracer gas sampling system; a controlled tracer gas release to calibrate the capture rate of metabolic gases and to corroborate air flow rates; sensors, including methane, carbon dioxide, water vapor, molecular hydrogen, hydrogen sulfide, and air flow rate; a data acquisition and control system; a remote data link to transmit data to a specified secure location; and, a centralized computer for automated data processing. To date, millions of data points have been collected from many individual animals. For beef cattle on pasture, methane emissions averaged 200 g/animal per d; for a herd of lactating dairy cows average methane emissions were 408 g/animal per d over a 7-mo period. A 2-fold difference in methane emissions between high and low emitting animals also was measured. Changes in feeding patterns and health conditions also were reflected in metabolic gas fluxes. For example, carbon dioxide emissions increased significantly with little change in methane fluxes when dairy cattle were moved to a fresh pasture. The system is user-friendly and relatively easy to maintain and operate.

Key words: methane, ruminant, measurement

857 Effects of oxygenated drinking water on gaseous emissions, rumen microorganisms and milk production in dairy cattle. C. J. Neumeier*[1], J. A. McGarvey[2], Y. Pan[1], Y. Zhao[1], and F. M. Mit-

loehner[1], [1]*Department of Animal Science, University of California-Davis, Davis,* [2]*United States Department of Agriculture, Agricultural Research Service, Albany, CA.*

Dairy cattle production systems contribute to greenhouse gas emissions, predominantly in the form of methane. Enteric methane is formed by methanogenic archaea (methanogens) that require anaerobic conditions to thrive. A water treatment system (Oxion, Hugoton, KS) increases the dissolved oxygen concentration in drinking water. We hypothesize that by increasing the dissolved oxygen concentration of the rumen through intake of oxygenated drinking water, one creates an environment detrimental to the proliferation of methanogens. The present study evaluated carbonaceous and nitrogenous gaseous emissions in addition to performance parameters. A total of 36 lactating Holstein dairy cows were used in a completely randomized design. The cows were assigned to 2 treatment groups: control water and oxygenated drinking water (CON and OXI, respectively). The cows were housed in 3 groups of 6 animals within each treatment (n = 3). Dry matter intake (DMI), water intake and milk yield were recorded daily. Rumen fluid samples were extracted via an orogastric tube and quantified for bacteria, methanogens and protozoa. Cows were placed inside an environmental chamber to measure carbon dioxide, nitrous oxide and ammonia using the Innova 1412 photoacoustic field gas monitor (California Analytical Instruments, Orange, CA) and methane using the TEI 55C direct methane analyzer (Thermo Environmental Instruments, Franklin, MA). All measurements were analyzed using Proc Mixed in SAS. The DMI, water intake and energy corrected milk yield were similar but OXI vs. CON treated cattle showed decreased milk yield ($P < 0.01$). Bacteria, methanogen and protozoa quantification yielded no significant differences. While methane production was similar ammonia emission increased for OXI vs. CON treated cattle ($P < 0.05$). Introduction of excess oxygen to the rumen via drinking water did not produce the anticipated effect on methane reduction but instead seems to cause changes in nitrogen cycling of the animal which deserves further investigation.

Key words: greenhouse gas, methane, water treatment

Ruminant Nutrition: Beef: Supplements

858 Effects of residual feed intake classification and breed type on carcass characteristics, tenderness and value in feedlot heifers. J. W. Behrens*[1], R. K. Miller[1], J. C. Bailey[1], J. T. Walter[1], A. N. Hafla[1], E. D. Mendes[1], D. S. Hale[1], T. Machado[2], L. O. Tedeschi[1], and G. E. Carstens[1], *[1]Texas A&M University, College Station, [2]Texas A&M University at Kingsville, Kingsville.*

The objectives were to determine the effects of residual feed intake (RFI) classification and breed type on carcass characteristics, tenderness and value in Angus (AN; n = 184), Brangus (BN; n = 266), Simbrah (SI; n = 196), and Braford (BO; n = 241) heifers obtained over 3 years from Deseret Ranch. Each year, heifers were received in 2 groups; fall and spring (initial age and BW of heifers = 337 vs. 501 ± 86 d and 278 vs. 324 ± 48 kg, respectively). Heifers were fed a high-grain diet (ME = 3.08 Mcal/kg DM), and feed intakes measured using a GrowSafe system for 70 d. Thereafter, heifers were fed in group pens and harvested at an average backfat thickness of 1.2 cm in 2 groups. Within trial, RFI was computed as the difference between actual and expected DMI from the linear regression of DMI on mid-test BW $^{0.75}$ and ADG. Heifers were categorized into low, medium and high RFI groups based on ± 0.50 SD from the mean. Heifers were commercially harvested and USDA Yield and Quality grade characteristics obtained. Warner-Bratzler (WBSF) and Slice shear force (SSF) values were measured on top loin steaks after 1, 7 and 14 d of vacuum-packaged storage at 2°C. The model included fixed effects of RFI, breed, age and interaction terms and random effects of trial and pen. Low and medium RFI carcasses had lower adjusted fat thickness (AFT; $P = 0.001$) and lower yield grades (YG; $P = 0.004$) than high RFI heifers (1.19 and 1.22 vs. 1.30 ± 0.51 cm, respectively; 2.77 and 2.77 vs. 2.89 ± 0.10, respectively). RFI classification did not affect ($P > 0.05$) HCW, KPH, REA, marbling score or WBSF and SSF values. BO heifers had lighter HCW, smaller REA and higher ($P < 0.001$) YG than SI heifers, with AN and BN heifers being intermediate. Marbling scores were lower ($P < 0.001$) and d 1 WBSF was higher ($P < 0.001$) for BO and SI heifers compared with AN and BN heifers. In this study, breed type had more influence on carcass-quality traits than RFI classification. Heifers with low and medium RFI had lower YG than high RFI heifers, but RFI classification did not affect carcass marbling or tenderness traits.

Key words: breed, residual feed intake, tenderness

859 Effects of residual feed intake classification and breed type on feed efficiency and feeding behavior traits in heifers fed a high-grain diet. J. C. Bailey*, G. E. Carstens, J. T. Walter, A. N. Hafla, E. D. Mendes, L. O. Tedeschi, and R. K. Miller, *Texas A&M University, College Station.*

Objectives of this study were to evaluate the effects of residual feed intake (RFI) classification and breed on feed efficiency and feeding behavior traits in heifers fed a high-grain diet (ME = 3.08 Mcal/kg DM). Six trials were conducted over 3 yr with Angus (AN; n = 185), Braford (BO; n = 241), Brangus (BN; n = 266) and Simbrah (SI; n = 196) heifers from the Deseret Ranch; with 2 trials conducted each yr during the fall (n = 415) and spring (n = 473). Initial ages were 337 vs. 501 ± 86 d for heifers used in the fall (younger) and spring (older) trials. DMI and feeding behavior traits were measured for 70 d using a GrowSafe system. Within trial, RFI was calculated as the difference between actual and expected DMI from linear regression of DMI on ADG and mid-test BW$^{0.75}$, and heifers classified into RFI groups based on ± 0.5 SD from the mean. Low RFI heifers consumed less ($P < 0.0001$) DM (8.91 vs. 10.97 ± 1.04 kg/d), had lower ($P < 0.0001$) F:G (6.71 vs. 8.47 ± 1.81), but had similar initial BW (315.2 ± 48 kg) and ADG (1.38 ± 0.34 kg/d) compared with high-RFI heifers. Younger heifers with low RFI consumed 18.2% less DM than high-RFI heifers, whereas, older low-RFI heifers consumed 19.3% less DM than high-RFI heifers (RFI x age interaction; $P < 0.05$). Bunk visit frequency (48.5 vs. 63.4 ± 4.2 events/d) and duration (55.1 vs. 64.0 ± 3.6 min/d) were less ($P < 0.0001$) in heifers with low compared with high RFI. Likewise, low-RFI heifers had lower ($P < 0.005$) meal frequency (6.27 vs. 6.81 ± 0.80 events/d) and duration (139 vs. 157 ± 8.6 min/d) than high-RFI heifers. BO heifers had lower ($P < 0.001$) ADG (1.26, 1.45, 1.40 and 1.41 ± 0.07 kg/d) and DMI (9.50, 10.36, 10.13, 9.83 ± 0.43 kg/d) than AN, BN and SI heifers, respectively. F:G tended ($P < 0.13$) to be lower in SI compared with BO heifers (7.37 vs. 7.78), with AN and BN heifers (7.65 and 7.62 ± 1.8) being intermediate. In contrast, breed type did not affect RFI. Independent of breed, heifers with low RFI consumed 18.8% less DM and had fewer feeding behavioral activities than high-RFI heifers.

Key words: feeding behavior, residual feed intake

860 Analysis of the ruminant microbial ecosystem in cattle divergent for residual feed intake using next generation sequencing technology. C. A. Carberry*[1,2], D. A. Kenny[1], C. J. Creevey[1], and S. M. Waters[1], *[1]Animal and Bioscience Department, Animal and Grassland Research and Innovation Centre, Teagasc, Grange, Dunsany, Co. Meath, Ireland, [2]School of Agriculture, Food Science and Veterinary Medicine, University College Dublin, Belfield, Dublin 4, Ireland.*

As feed is one of the main input costs in beef production, improvements in feed efficiency are paramount to maintaining and increasing the profitability of the enterprise. There is now general agreement that the concept of residual feed intake (RFI) is the most appropriate approach for the selection of more energetically efficient beef cattle without compromising animal growth or performance. However, although suggested as having a putative role in determining the feed efficiency phenotype of an animal, little is known on whether the rumen microbial ecosystem differs between animals of different RFI phenotypes. The objective of this research was to analyze the rumen microflora in cattle divergent for RFI using 454 pyrosequencing technology. Beef heifers (n = 86), initially selected on the basis of sire EBV for RFI, were ranked on the basis of phenotypic RFI over an 80 d finishing period while consuming a 30:70 maize silage to concentrate diet. The 7 highest (HRFI; least efficient) and 7 lowest (LRFI; most efficient) ranking animals were selected for use in this study. Both groups had similar mean bodyweight and ADG at ranking but HRFI had, on average, 20% higher DMI. Following ranking on RFI all animals were offered a grass silage diet ad libitum for a 6 week period. Ruminal fluid was sampled at the end of this period using a specialized trans-esophageal sampling device. Total microbial DNA was isolated from the ruminal fluid and amplified using fusion primers including adaptors for titanium 454 sequencing and a region complementary to the bacterial 16s V3 region. Analysis of this data revealed many shared bacterial populations between the HRFI and LRFI animals, predominantly from the bacteriodales and clostridia clades. Most interestingly however, a significantly higher number of bacterial clusters were found to be unique to the rumen of HRFI compared with the LRFI animals. This suggests a correlation between microbial diversity and

feed efficiency in cattle and a mechanism through which differences in inherent ruminal microbial populations may influence feed efficiency in cattle.

Key words: residual feed intake, rumen bacteria, pyrosequencing

861 Association of myostatin with weight and carcass traits in crossbred heifers adjusted to different endpoints. S. K. Pruitt*, K. M. Rolfe, B. L. Nuttelman, W. A. Griffin, G. E. Erickson, and M. L. Spangler, *University of Nebraska-Lincoln, Lincoln.*

The objective of this study was to investigate a potential association of an inactive myostatin allele with performance and carcass traits using 60 individually fed crossbred heifers (395 ± 27 kg) genotyped for 0, 1, or 2 copies of the inactive myostatin (IM) (n = 25 homozygous active myostatin, n = 26 heterozygous, and n = 9 homozygous inactive myostatin, respectively). Heifers were fed a finishing diet that consisted of 52% corn, 35% wet distillers grains plus solubles, 8% hay and 5% supplement (DM basis) for 114 d. Ultrasound measurements of rump fat (RUMF), rib fat (RIBF), LM area (uLMA) and intramuscular fat percentage (IMF) were taken at 28 d intervals over the feeding period. Initial BW, final BW, DMI, and ADG decreased linearly ($P < 0.01$) with increasing copy number of IM. A linear decrease ($P = 0.03$) in G:F was observed as IM copy number increased. A quadratic decrease ($P < 0.05$) was observed in HCW, LM area, and marbling as well as a linear decrease ($P < 0.01$) in fat depth as IM copy number increased. Final ultrasonically measured traits, BW, and age were adjusted to common endpoints (BW, age, RIBF and RUMF) using regression estimates pooled within genotype class. Common endpoints were determined by the average value of each endpoint across genotype classes. Best-fit endpoints were determined by comparing Akaike′s Information Criterion (AIC) values. Given the strong correlation between RIBF and RUMF, BW was chosen for adjustment and was ranked second for AIC. Adjusted data were 4.69, 4.06, 2.35% for IMF (adjusted for RIBF); 90.3, 94.8, 110.3 cm^2 for uLMA (adjusted for age); 506, 485, and 453 kg for BW (adjusted for age); and 1.04, 0.74, and 0.46 cm for RIBF (adjusted to BW) for homozygous active, heterozygous, and homozygous inactive animals, respectively. Age adjusted to a constant BW and RIBF suggests that homozygous IM animals would require 26 and 84 more d on feed as compared with homozygous active animals to reach the same harvest BW and RIBF, respectively. This suggests that inactive myostatin genotype decreases IMF, G:F, RIBF, and final BW, while increasing uLMA.

Key words: beef cattle, compositional endpoints, myostatin

862 Effects of varying forage levels in diets containing whole flint corn and benefits of steam flaking the corn on finishing Nellore bulls performance, carcass characteristics, and liver abscesses. R. S. Marques[1], J. R. R. Dórea[1], A. M. Pedroso[2], A. W. Bispo[1], C. G. Martins[1], W. F. Angolini[1], and F. A. P. Santos*[1], *[1]University of Sao Paulo, Piracicaba, SP, Brazil, [2]Embrapa Cattle Southeast, Sao Carlos SP, Brazil.*

The objective of the present study was to determine the effect of increasing levels of sugar cane bagasse (0, 3, and 6% of diet DM) in finishing diets with whole flint corn and also the effect of processing flint corn as steam flaking on performance and carcass characteristics of zebu cattle. One hundred sixteen Nellore bulls with an initial BW of 373 kg were used in an 86-d randomized complete block design feeding trial. Animals were blocked by initial BW and randomly assigned to 20 pens. Animals were raised on pasture and were adapted to the feedlot diets during a 21 d pre-trial period. The final diets contained sugar cane bagasse, corn, urea, vegetable protein (soybean meal) and mineral and vitamin mix with monensin. Treatments were: 1) W0 (whole corn and no forage); 2) WC3 (whole corn with 3% sugar cane bagasse); 3) WC6 (whole corn with 6% sugar cane bagasse); 4) WC6-Opt (W6 with extra nitrogen from slow release urea - Optigen); 5) SFC6 (steam flaked corn with 6% sugar cane bagasse). Data were analyzed using the Mixed procedure of SAS (1999) with pen as experimental unit. There was a quadratic effect ($P < 0.01$) of forage level in whole corn diets for DMI, ADG, final BW and hot carcass weight. Compared with whole corn, steam flaked corn decreased DMI ($P < 0.01$), had no effect on ADG ($P > 0.05$) and improved feed efficiency (ADG/DMI) ($P < 0.01$). Carcass characteristics were not affected by treatments ($P > 0.05$) and liver abscesses incidence was negligible.

Table 1. Effects of roughage levels and corn processing

	WC0-	WC3	WC6	WC6-Opt	SFC6	Forage level[1]	SFC6 × WC[2]	SEM
DMI, kg	8.42	10.51	10.16	10.15	8.44	0.0001	0.0001	0.3
ADG, kg	1.19	1.58	1.55	1.50	1.55	0.0027	0.311	0.11
ADG/DMI	0.143	0.152	0.153	0.149	0.184	0.3272	0.001	0.014
HCW, kg	273.9	290.1	293.8	288.0	289.7	0.0048	0.514	6.64
Dressing, %	57.5	57.1	58.3	57.4	57.5	0.8209	0.901	0.67
REA, cm^2	77.5	79.6	79.5	79.5	79.4	0.283	0.817	1.47
FT, mm	4.45	5.29	4.81	5.04	5.1	0.2318	0.640	0.39

[1]Forage level: quadratic effect.

[2]Contrast SFC × WC diets.

Key words: corn, processing, feedlot

863 Evaluation of two complete-feed receiving diets. C. J. Schneider*[1], B. L. Nuttelman[1], K. M. Rolfe[1], W. A. Griffin[1], T. J. Klopfenstein[1], R. A. Stock[2], and G. E. Erickson[1], *[1]University of Nebraska, Lincoln, [2]Cargill Inc., Blair, NE.*

A receiving trial was conducted to evaluate effects of feeding 2 complete feeds on cattle performance during the receiving period. Crossbred steers (n = 965; BW = 261.1 ± 6.6 kg) were received over a 2-d period and processed within 12 h of arrival. Steers were blocked by arrival date and randomly allocated to pens within block based on processing order, resulting in 15 and 20 cattle per pen for blocks 1 and 2, respectively, with 17 pens per treatment. Treatments included a control receiving diet (35% alfalfa hay, 30% Sweet Bran, 30% dry rolled corn, and 5% supplement; 16.7% CP, 36.7% NDF) and 2 complete feeds. RAMP (21.9% CP, 41.9% NDF) and Test Starter (23.4% CP, 43.5% NDF) contained a high level of Sweet Bran with a minimal amount of forage and were formulated and provided by Cargill Inc., Blair, NE. All diets contained 27.6 mg/kg monensin and 26.5 mg/kg thiamine. Cattle were offered ad libitum access to treatment diets for 30 or 31 d and limit-fed a common diet (47.5% Sweet Bran, 23.75% grass hay, 23.75 alfalfa hay, and 5% supplement) for 5 d before collecting final BW to minimize variation in gut fill. Initial and final BW were averages of 2-d weights and a 4% pencil shrink was subtracted from final BW. Feeding RAMP increased ($P = 0.03$; Table 1) ADG when compared with the control diet. ADG for cattle fed Test Starter was not different ($P > 0.11$) from cattle fed control or RAMP. Final BW, DMI, and G:F were similar ($P > 0.14$) for all treatments. Starting cattle on RAMP is a viable alternative to starting cattle on a mixture of grain and forage.

Table 1. Performance of cattle fed RAMP, Test Starter, or a control receiving diet

Item	Treatment			SEM	*P*-value
	Control	RAMP	Test Starter		
Initial BW, kg	261	262	260	6.6	0.89
Final BW, kg	293	298	293	9.2	0.36
DMI, kg/d	6.08	6.30	6.26	0.11	0.14
ADG, kg	0.90[a]	1.03[b]	0.93[ab]	0.10	0.08
G:F	0.148	0.165	0.148	0.019	0.18

[a,b]Means within a row without a common superscript are different, $P = 0.03$.

Key words: beef cattle, feedlot, receiving

864 Rumen degradable protein supply effects microbial efficiency in continuous culture and growth in crossbred Angus steers. M. A. Brooks*[1,2], R. M. Harvey[2], N. F. Johnson[2], and M. S. Kerley[2], *[1]North Carolina State University, Raleigh, [2]University of Missouri - Columbia, Columbia.*

We hypothesized microbial efficiency (MOEFF) and output from ruminal fermentation was optimized when rumen degradable peptide (RDPep) supply was balanced with RDPep requirement. This study was conducted to measure response of varying RDPep supply on ruminal fermentation characteristics and steer growth. A continuous culture experiment was conducted with diets formulated to achieve a predicted RDPep balance (RDPep supplied/ RDPep required) of 0.0, 0.6, 1.8, and 3.0% DM and rumen degradable nitrogen (RDN) balance (RDN supplied/ RDN required) of −0.2% DM. Two additional treatments had RDPep balances of 0.0 and 1.8% CP with −0.5% DM RDN balance. Twenty-four single-flow fermenters (n = 6) were inoculated with rumen fluid and maintained anaerobically at 39°C with a 0.06 h^{-1} dilution rate. Inadequate RDN (0.5% RDN balance) decreased OM digestion and microbial N and increased rumen undegradable nitrogen ($P < 0.01$). MOEFF was also poorer in diets with 0.5% RDN balance and greatest when RDPep balance ranged from 0 to 1.83% ($P < 0.01$). Total VFA concentration decreased with 0.5% RDN balance while increasing levels of lactate were measured ($P < 0.01$). The second experiment was a growth study consisting of 4 diets varying in RDPep balance (0.52, −0.13, −0.48, −0.97% DM) but with similar and adequate RDN (~−0.7% RDN balance). Forty-nine yearling crossbred Angus steers (initial body weight ~370 kg) were assigned by weight into treatment groups (n = 12, with an extra steer in −0.48% RDPep treatment). Each treatment was divided into 3 pens with 4 animals per pen. Animals were maintained on treatment for 70 d with pen intake recorded daily and animal weights taken on d 0, 1, 21, 42, 70 and 71. Final body weight (average of d 70 and 71 weight) decreased linearly with decreasing RDPep ($P = 0.05$). DM intake did not differ among treatments (7.77 to 8.51 kg/hd/d; $P = 0.09$). Gain efficiency (G:F) and ADG displayed a quadratic effect with greater values occurring at the higher RDPep level ($P = 0.02$). We concluded balancing RDPep supply to requirement improved fermentation efficiency and output, which in turn improved animal performance.

Key words: peptide, microbial efficiency, nitrogen

865 Beef cow performance when fed cotton co-product and distillers grain blocks as a hay replacement. G. M. Hill*, A. N. Franklin, G. W. Stone, and B. G. Mullinix, *University of Georgia, Tifton.*

A compressed 250 kg block product (CPM; A. G. Daniel Co., Eastman, GA) containing cotton gin trash (59%), distillers dried grains with solubles (15%), wheat middlings (15%), a molasses product and minerals (11%), was evaluated as a hay replacement for cows. Angus cows (n = 52; AOD 5.9 ± 1.9 yr; initial BW 667.0 ± 53.67 kg) were ranked by BW, and randomly assigned to replicated treatments for 42 d. Initial and final cow BW were 2-d full BW means. A preliminary steer CPM intake study suggested that cow CPM intake might be elevated. Therefore, treatments included: free-choice Hay (HFC); 1 CPM block/6 cows every 4 d with hay (CPM4D); 1 CPM block/6 cows every 3 d with hay (CPM3D); free-choice CPM (CPMFC). The DM, CP, ADF, NDF (% DM basis) of 10 bermudagrass hay samples, were: 89.3, 9.4, 37.3, 77.2; and of 10 CPM samples, were: 89.8, 17.5, 37.3, 46.3. The TDN, K, S (% DM basis), NE_m and NE_g (Mcal/kg), in CPM were: 49.4, 2.4, 0.46, 0.91, 0.36. Cows were fed CPM blocks in bunks in a barn, and round-baled hay was weighed and fed free-choice in hay rings. The experiment began October 26, 2010, and the days pregnant at palpation on July 13, 2010, respectively, by treatment, were: 78.8, 87.7, 81.9, 78.7, SE 3.47, ($P < 0.27$). Cow ADG was greatest for CPM4D and CPMFC, intermediate for CPM3D, and lowest for HFC cows (Table; $P < 0.01$). Cow BCS tended to increase ($P < 0.97$) for cows fed CPM compared with HFC. The DMI of CPM in CPMFC was increased compared with CPM4D and CPM3D, and total DMI of CPMFC was 65% greater than HFC. All CPM treatments substantially increased cow BW gain in late pregnancy, while cost of providing CPM free-choice may be prohibitive.

Table 1

Item	HFC	CPM4D	CPM3D	CPMFC	SE
No. Cows	14	12	12	14	
Initial BW, kg	674.4	659.9	662.1	669.8	14.87
42-d ADG, kg[d]	0.39[c]	1.15[a]	0.88[b]	0.99[ab]	0.08
Initial BCS (Scale 1 to 9) [d]	5.34	5.51	5.39	5.46	0.18
42-d BCS Change[d]	0.13	0.18	0.26	0.24	0.22
CPM DMI, kg/d	0.00	9.52	11.91	22.31	
Hay DMI, kg/d	13.49	8.29	7.22	0.00	
Total DMI, kg/d	13.49	17.80	19.13	22.31	
Gain/feed	0.029	0.065	0.046	0.44	

[abc]Means with different superscripts differ ($P < 0.01$).

[d]Initial BW covariate effect ($P < 0.01$).

Key words: cotton, co-product, cow

866 Effects of energy supplementation frequency and forage quality on performance of replacement beef heifers. P. Moriel*[2], R. F. Cooke[1], F. N. T. Cooke[1], E. Alves[2], L. Custodio[2], D. W. Bohnert[1], J. M. B. Vendramini[2], and J. D. Arthington[2], *[1]Oregon State University–Eastern Oregon Agricultural Research Center, Burns, [2]University of Florida–Range Cattle Research and Education Center, Ona.*

The objective was to compare performance of beef heifers consuming forages differing in nutritional quality and offered an energy-based supplement at 2 different frequencies. Forty-eight Brahman × British heifers were ranked by initial BW and age and allocated to 16 drylot pens (3 heifers/pen). Pens were assigned to receive, in a 2 × 2 factorial arrangement, 1 of the 4 treatment combinations: 1) low-quality hay (LF; *Cynodon nlemfuensis* with 8% CP, DM basis) and daily supplementation (S7), 2) LF and supplementation 3x/wk (S3), 3) medium-quality hay (MF; *C. dactylon* with 12% CP, DM basis) and S7, 4) MF

and S3. Forages were offered ad libitum to heifers throughout the experimental period (d 0 to 120). Supplement was based on soybean hulls and offered at a daily rate of 2.2 (1.0% of initial BW) and 1.1 (0.5% of initial BW) kg of DM to LF and MF heifers, respectively. Heifer shrunk BW was obtained at the beginning and end of the experiment. Forage and total DMI were evaluated daily, from d 20 to 26, d 33 to 39, and d 46 to 52. Mean BW gain was greater ($P < 0.01$) for LF vs. MF heifers (0.34 vs. 0.19 kg/d, respectively). Mean forage DMI was greater ($P < 0.01$) for MF vs. LF heifers (3.6 vs. 2.6 kg/heifer/d) and for S7 vs. S3 heifers (3.4 vs. 2.9 kg/heifer/d). Total DMI was greater ($P < 0.01$) for S7 vs. S3 heifers (5.1 vs. 4.6 kg/heifer/d). Mean NE_m and NE_g intakes were greater ($P < 0.01$) for LF vs. MF heifers (5.8 vs. 5.0 and 3.0 vs. 2.4 Mcal/heifer/d of NE_m and NE_g, respectively) and for S7 vs. S3 heifers (5.6 vs. 5.2 and 2.8 vs. 2.6 Mcal/heifer/d of NE_m and NE_g, respectively). Mean CP intake was greater ($P < 0.01$) for MF vs. LF heifers (0.64 vs. 0.59 kg/heifer/d) and for S7 vs. S3 heifers (0.64 vs. 0.59 kg/heifer/d). In summary, independently of forage quality, replacement beef heifers offered an energy-based supplement daily had greater nutrient intake but similar BW gain compared with cohorts supplemented 3x/wk. Heifers consuming low-quality forage and supplemented at 1.0% of BW had similar DMI, reduced CP intake, but greater energy intake and BW gain compared with cohorts consuming medium-quality forage and supplemented at 0.5% of BW.

Key words: supplementation, forage, heifer

867 Impact of rumen digesta inoculation on feeding value of urea-molasses treated wheat straw. M. Sarwar*, M. A. Shahzad, and M. Nisa, *Institute of Animal Nutrition and Feed Technology, University of Agriculture, Faisalabad, Punjab, Pakistan.*

The study was conducted to examine the chemical composition of urea–molasses treated wheat straw (WS) fermented with bovine rumen digesta (RD). The WS treated with varying levels of urea (0, 2 and 4%) and molasses (0, 2 and 4%) was ensiled with 10% rumen digesta (on dry matter basis) for different fermentation periods (20, 30 and 40 d). Data were analyzed using completely randomized design with 3 × 3 × 3 factorial arrangement of levels of urea, molasses and fermentation time, respectively and means were separated by Duncan's multiple range test using general linear model procedure of SPSS. Fermented wheat straw (FWS), after each fermentation period, was analyzed for pH, dry matter (DM), crude protein (CP), true protein (TP), ammonia nitrogen (NH3-N), neutral detergent fiber (NDF) and acid detergent fiber (ADF). High ($P < 0.05$) pH, CP, TP, NH3-N and low ($P < 0.05$) NDF contents were observed with increase in urea level, however, DM and ADF contents remained unaltered. Increasing molasses level resulted in high ($P < 0.05$) CP, TP, NH3-N and low ($P < 0.05$) NDF contents were observed while increase in fermentation period resulted in high ($P < 0.05$) CP, TP and minimum ($P < 0.05$) NH3-N, NDF contents. The pH, DM, CP, TP, NH3-N and NDF contents were affected ($P < 0.05$) by urea × molasses interaction and urea × fermentation days interaction. The CP, TP, NH3-N and NDF contents were also influenced ($P < 0.05$) by molasses × fermentation days interaction, however, pH, DM and ADF contents remained unaffected. Similar trend was observed in urea × molasses × fermentation days interaction. The 4% urea and 4% molasses after 40 d of fermentation period indicated increase in CP and TP contents and decrease in NDF content of WS. The study found 4% urea and 4% molasses for 40 d fermentation period best combination for large-scale production of FWS to evaluate its feeding value for ruminants.

Key words: nutritive value, rumen digesta, wheat straw

868 Effect of sorghum grain supplementation on glucose metabolism 1: Bovine. M. Aguerre*[1], M. Carriquiry[2], A. L. Astessiano[2], C. Cajarville[3], and J. L. Repetto[1], *[1]Departamento de Bovinos, Facultad de Veterinaria, Universidad de la República, Montevideo, Uruguay, [2]Departamento de Producción Animal y Pasturas, Facultad de Agronomía, Universidad de la República, Montevideo, Uruguay, [3]Departamento de Nutrición Animal, Facultad de Veterinaria, Universidad de la República, Montevideo, Uruguay.*

Crossbred heifers (n = 12; 210 ± 42.5 kg), blocked by BW, were used to evaluate the effects of sorghum grain supplementation (0 vs. 1.5% BW, S0 vs. S1.5, respectively) on plasma glucose, insulin and glucagon concentrations and on hepatic expression of genes related to glucose metabolism. Heifers were fed ad libitum fresh *Lotus corniculatus* (31.8% DM, 12.4% CP, 41.8% NDF). At the end of treatments (31 d) blood samples were taken every 2 h from 0 to 6 h post-supplementation, to determine glucose by colorimetry and insulin and glucagon by RIA. Liver biopsies were collected to quantify abundance of pyruvate carboxylase (PC), phosphoenolpyruvate carboxykinase (PCK-1) and insulin receptor (IR) mRNA by SYBR-Green real-time PCR, using hypoxanthine-guanidine phosphoribosyltransferase as endogenous control. Data were analyzed with MIXED procedure (SAS). Glucose were greater in S1.5 than S0 (74.3 vs. 63.5 ± 9.88 mg/dL, $P = 0.004$) and the shape of the curves was similar over the 6 h post-supplementation. Insulin levels tended to be greater in S1.5 than S0 (12.2 vs. 8.33 ± 2.18 μUI/mL; $P = 0.084$), recording a 2-fold increase from 0 to 2h only in S1.5 group (6.96 vs. 15.0 ± 2.70 μUI/mL, $P = 0.050$). Glucagon concentrations were lower in S1.5 than S0 (58.0 vs. 66.9 ± 4.52, $P = 0.020$) but while glucagon decreased 4 h post-supplementation (77.6 vs. 56.9 ± 5.75 μUI/mL, $P = 0.002$) in the S0 group, glucagon increased in the first 2 h post-supplementation in the S1.5 (48.5 vs. 61.8 ± 6.16 μUI/mL, $P = 0.057$). The insulin/glucagon ratio tended to be greater in S1.5 than S0 (0.20 vs. 0.13 ± 0.03, $P = 0.084$). Plasma insulin and glucagon were correlated with each other (r = 0.60, $P = 0.032$) and insulin was correlated with OM intake (r = 0.67, $P = 0.013$). The IR and PC mRNA did not differ between treatments (14.2 vs. 12.1 ± 1.86 and 60.2 vs. 40.7 ± 7.44, for S0 and S1.5 respectively), but PCK-1 mRNA was lower in S.15 than S0 (15.4 vs. 28.4 ± 3.42, $P = 0.020$). The expression of PCK-1 was negatively correlated with plasma insulin (r = –0.86, $P = 0.001$). Sorghum supplementation increased glucose and insulin concentration and reduced glucagon and PCK-1 mRNA abundance. This would indicate an increased anabolism in supplemented animals.

Key words: hormones, liver mRNA, grazing cattle

869 Response to increased sorghum grain supplementation levels: Comparison between cattle and sheep. M. Aguerre*[1], C. Cajarville[2], and J. L. Repetto[1], *[1]Departamento de Bovinos, Facultad de Veterinaria, Universidad de la República, Montevideo, Uruguay, [2]Departamento de Nutrición Animal, Facultad de Veterinaria, Universidad de la República, Montevideo, Uruguay.*

Crossbreed heifers (n = 24; 210 ± 42.5 kg), and lambs (n = 24; 45.6 ± 6.2 kg), blocked by BW, were used to compare the response on OM intake and digestibility (OMI and OMD), ruminal pH, N–NH_3 and microbial protein synthesis (MPS) to increased levels of sorghum grain supplementation (0, 0.5, 1.0 and 1.5% BW). Heifers and lambs were fed ad libitum fresh *Lotus corniculatus* (31.8% DM, 12.4% CP, 41.8% NDF). After 21d, OMI was measured for 10d and all feces and urine were collected for 5d. The MPS was calculated from total urinary excretion of purine derivatives. Ruminal liquor samples were taken every 1h from 0 to 6h post-supplementation, to determine pH

and N-NH_3. Mean data values and linear regressions were compared among species with the MIXED procedure (SAS). Mean OMD did not differ between cattle and sheep (71.4 vs. 72.1 ± 0.98%; $P = 0.635$), but mean ruminal pH, N-NH_3 and MPSE were different between species (6.38 vs. 6.05 ± 0.10, $P = 0.056$; 21.8 vs. 37.1 ± 1.58 mg/dL, $P < 0.01$; 16.5 vs. 11.8 ± 0.68 g of MN/kg of DOMI, $P < 0.01$, for cattle and sheep respectively). No differences were detected on OMD, ruminal pH, N-NH_3 and MPS efficiency (MPSE) response to the increasing sorghum supplementation levels between species (Table 1). In contrast, OMI and MPS were differently affected in both species ($P < 0.01$). While in heifers OMI and MPS increased as sorghum supplementation increased, in lambs OMI and MPS decreased as the level of supplementation increased. Increasing levels of supplementation affected differently cattle and sheep. Therefore, both species should not be used as similar models for ruminant nutrition research.

Table 1

Item	Cattle	Sheep	P^1
OMI (% $BW^{0.75}$)	Y = 10.3 + 2.00X; $R^2 = 0.50$, $P < 0.01$	Y = 9.65 – 1.32X; $R^2 = 0.23$, $P = 0.02$	<0.01
OMD (%)	Y = 68.7 + 3.64X; $R^2 = 0.21$, $P = 0.03$	Y = 68.7 + 4.65X; $R^2 = 0.23$, $P = 0.02$	0.674
Ruminal pH	Y = 6.73 – 0.46X; $R^2 = 0.22$, $P < 0.01$	Y = 6.46 – 0.55X; $R^2 = 0.34$, $P < 0.01$	0.477
MPS (g MN/d)	Y = 71.6 + 10.2X; $R^2 = 0.26$, $P = 0.02$	Y = 16.5 – 4.43X; $R^2 = 0.28$, $P < 0.01$	<0.01
MPSE (g MN/kg DOMI)	Y = 18.4 – 2.70X; $R^2 = 0.20$, $P = 0.05$	Y = 13.9 – 2.80X; $R^2 = 0.21$, $P = 0.02$	0.954

[1]*P*-value of compared regression.

Key words: bovine, ovine, fresh pasture

870 A ring test of in vitro neutral detergent fiber digestibility: analytical variability and sample ranking. M. B. Hall* and D. R. Mertens, *U. S. Dairy Forage Research Center, USDA-ARS, Madison, WI.*

In vitro neutral detergent fiber (NDF) digestibility (NDFD) is an empirical measurement used to describe fermentability of NDF by rumen microbes. Variability is inherent in assays and affects the precision that can be expected for replicated samples. The study objective was to evaluate variability within and among laboratories (labs) of 30 h NDFD values measured in repeated runs. Subsamples of alfalfa (n = 4), corn silage (n = 5), and grass (n = 5) ground to pass a 6 mm screen were sent to 10 labs on 3 occasions over a 12 mo period. Subsamples passed a test for homogeneity. Labs ground the samples and ran 2 or 3 replicates of each sample within run, and analyzed 2 or 3 sets of samples. A lab that did not provide in-run replicate data was not included in evaluation of standard deviations (SD). Mean and SD for sample within run within lab were calculated. Factors in the statistical model were lab, run within lab, sample, and lab by sample. All factors affected NDFD ($P < 0.01$ for all) and within-run SD of NDFD ($P < 0.03$ for all). The lab by sample effect suggests against a simple lab bias. Labs used 2 NDFD procedures: 8 labs used a procedure similar to Goering and Van Soest, 1970 (GVS) using fermentation vessels or filter bags, and 2 used a procedure with pre-incubated inoculum (PInc.). Among GVS labs, NDFD results were affected by all factors ($P < 0.01$ for all; mean 48.5%, range 42.7 to 53.2%, SED = 0.98). For PInc., mean NDFD was 30.7% (range: 31.8 to 29.6%); GVS and PInc. NDFD differed ($P < 0.01$, SED = 0.95). Mean within-run SD were 1.9% (range: 0.5 to 3.4%) for GVS and 2.6% (range 1.8 to 3.4%) for PInc. The mean SD for all labs of 2.0% indicates that 95% of results for a sample within a run would be within a range of 8.0% NDFD. Labs ranked samples similarly within forage type. Spearman correlation coefficients between average rankings and those reported by labs were 0.83 for alfalfa, 0.70 for corn silage, and 0.90 for grass ($P < 0.01$ for all). It is concluded that across all labs an average precision of 8% NDFD can be expected for a single analysis within run. Differences between GVS and PInc. suggest using results in contexts appropriate to each procedure.

Key words: NDF, digestibility

871 Effects of supplemental Smartamine or MetaSmart in moderate-energy close-up diets on peripartal liver tissue composition and blood metabolites. J. S. Osorio*, P. Ji, J. K. Drackley, and J. J. Loor, *University of Illinois, Urbana.*

Twenty-eight multiparous Holstein cows were fed a control diet (ME, n = 11; 1.49 Mcal/kg DM prepartum and 1.67 Mcal/kg DM postpartum), ME plus MetaSmart (MS, n = 9; Adisseo France S.A.S.), or ME plus Smartamine (SA, n = 8; Adisseo France S.A.S.). All cows received a common diet (1.30 Mcal/kg DM) during the far-off period [-50 to −21 d in milk (DIM)]. Treatments started at −21 DIM and continued through 30 DIM. MetaSmart (0.19% of DM prepartum and 0.18% of DM postpartum) and SA (0.07% of DM prepartum and postpartum) were top-dressed on the ME diet. Blood samples were collected at −17, −10, 7, 14, and 21 DIM. Whole blood phagocytosis (Phagotest) was assessed at d −10, 3, and 21. Total liver lipid and triglyceride content (Biopsy) were evaluated at −10, 7, and 21 DIM. Data were analyzed using the MIXED procedure of SAS with the preplanned contrasts ME vs. SA+MS and SA vs. MS. Treatments did not affect total lipid and triglyceride concentrations in liver. In contrast to MS and SA, however, the slope of total lipid % between d 7 and 21 for ME was significant ($P = 0.04$) suggesting that supplemental Met prevented increased lipid accumulation during that time-frame. Serum NEFA (0.511 mEq/L) and glucose (54.0 mg/dL) concentrations did not differ due to treatment. Although slopes of NEFA concentrations were negative for all treatments between 7 and 21 DIM, only those of Met-supplemented cows were significant ($P = 0.02$) suggesting that Met decreased NEFA more rapidly after calving. Analysis of whole blood phagocytosis after calving revealed an increase (treatment × time $P = 0.005$) due to MS and SA vs. ME. Energy corrected milk (ECM) was greater ($P = 0.05$) for MS+SA vs. ME (46.4 vs. 42.8 kg/d). Close-up and postpartal DMI did not differ. Enhanced ECM due to MS or SA was associated with a faster decline in serum NEFA and lack of additional lipid accumulation between 7 and 21 DIM. The overall effect of Met supplementation to peripartal cows is encouraging but more conclusive evidence would require increased sample size.

Key words: transition cows, methionine, immune function

872 Effect of supplemental Smartamine or MetaSmart in moderate-energy close-up diets on peripartal cow performance. J. S. Osorio*, P. Ji, J. K. Drackley, and J. J. Loor, *University of Illinois, Urbana.*

Peripartal cows are in negative methionine (M) balance due to increased requirements of tissues for methylated compounds and M for milk protein production. Decreased dry matter intake (DMI) during early lactation aggravates the supply of nutrients such as M. Therefore, supplementation of rumen-protected M during the peripartal period may improve yield of milk and protein. Forty multiparous Holstein cows were fed a controlled-energy diet (1.30 Mcal/kg DM) during the far-off dry period [-50 to −21 d in milk (DIM)]. During the close-up dry period (−21 to 0 DIM), cows were fed a higher-energy diet (1.49 Mcal/kg DM) without (ME, n = 14) or with 0.07% of DM Smartamine (SA, Adisseo France S.A.S.; n = 15) or 0.19% of DM MetaSmart (MS, Adisseo France S.A.S.; n = 11). Supplementation of M continued until 30 DIM. Body weight (BW), body condition score (BCS), DMI, milk yield and composition, and energy corrected milk (ECM) were recorded during the study. Data were analyzed using the MIXED procedure of SAS with the preplanned contrasts ME vs. SA+MS and SA vs. MS. No differences in close-up DMI were observed (average of 12 kg/d). When comparing SA+MS vs. ME, DMI through the first 30 DIM was significantly greater ($P = 0.04$) for M-supplemented cows (14.7 kg/d vs. 12.2 kg/d). Milk yield with SA+MS (41.5 kg/d) was greater ($P = 0.06$) compared with ME (37.7 kg/d). Although milk protein % during wk 2 through 4 did not differ between SA+MS vs. ME, supplemental MS resulted in greater ($P = 0.05$) milk fat % than SA (4.68% vs. 4.09%). There was a tendency ($P = 0.11$) for greater ECM when feeding SA+MS vs. ME (46.0 kg/d vs. 42.8 kg/d). The positive response to MS or SA on milk production seemed to be associated with greater (treatment × time $P = 0.02$) ECM/DMI, at least during the first wk postpartum. The present results suggest that increasing the availability of Methionine in moderate-energy close-up feeding systems may improve lactational performance and DMI.

Key words: methionine, transition cow, amino acid

873 Determining the effectiveness of proteases on production variables in lactating Holstein cows. E. Sucu*[1,2], A. Nayeri[1], M. V. Sanz-Fernandez[1], N. C. Upah[1], S. C. Pearce[1], and L. H. Baumgard[1], *[1]Department of Animal Science, Iowa State University, Ames, [2]Department of Animal Science, Uludag University, Bursa, Turkey.*

Ninety-six multiparous lactating Holstein dairy cows (2.7 ± 1.6 parity, 153.8 ± 103.7 DIM, 40.3 ± 5.9 kg milk/d, 624 ± 62 kg BW) housed in a free stall barn were blocked by parity, days in milk and previous milk production and randomly assigned to a control TMR or a TMR containing a blend of supplemental protease enzymes (4 g/cow/d; Rumagentin, Feed Sources LLC, Alta Loma CA). The TMR consisted primarily of corn silage, alfalfa hay, dried distiller grains, and concentrate and did not contain supplemental by-pass protein. Cows were housed 24 to a pen (4 pens total) and thus pen was the experimental unit in a crossover design with 2 21 d experimental periods. Two pens received the supplement during period 1 and the other 2 pens received the control. Pens then switched treatments during period 2 and there was a 7 d washout between periods. The 7 d immediately before period 1 were used as a covariate in the statistical analysis (repeated measures in the Proc Mixed procedure of SAS). Daily pen milk yield and DMI were recorded and milk composition from all cows was determined on d 15, 17, 19 and 21 of each period. All data was condensed into weekly means. There was no treatment effect on milk yield (37.6 kg/d), but supplemental enzyme-fed cows had less DMI (0.93 kg/d; $P < 0.05$) compared with controls and therefore tended ($P = 0.08$) to have improved (13%) feed efficiency (solids corrected milk/DMI). Protease treatment had no effect on milk fat (3.53%) or milk protein (3.24%), but tended ($P = 0.08$) to increase milk lactose (4.73 vs. 4.76%). Feeding supplemental enzymes tended ($P = 0.10$) to decrease milk urea nitrogen levels (15.1 vs. 14.6 mg/dl) but had no effect on milk SCC. In conclusion, supplementing a proprietary blend of protease enzymes improves feed efficiency and may enhance feed nitrogen utilization in lactating dairy cows.

Key words: protease enzymes, feed efficiency, feed intake

874 Effects of supplementing a mixture of plant extracts to lactating dairy cows on milk and methane production. G. F. Schroeder*[1], D. Bravo[2], M. Jerred[1], and B. D. Strang[1], *[1]Cargill Animal Nutrition, Innovation Campus, Elk River, MN, [2]Pancosma S.A., Geneva, Switzerland.*

The goal of this study was to determine the effects of supplementing a mixture of plant extracts containing cinnamaldehyde, eugenol, and garlic on milk production and composition, DMI, and methane production in lactating dairy cows. Six rumen-cannulated Holstein cows (100 DIM) were used in a replicated 3 × 3 Latin square design with 3 25-d periods (18 d for adaptation and 7 for data collection). Cows were housed in individual tie-stalls and received the same diet (46.2% DM, 18.7% CP, 31.1% NDF, 3.8% EE, and 37.3% NFC) twice daily. Treatments consisted in the supplementation (top-dress) with: none (Control), 300 mg/d monensin (MON), or 300 mg/d of plant extract mixture (PEM). Milk production and DMI was measured daily and milk composition was determined twice during the last 7 d of each period. Methane production was measured using the SF6 tracer technique during the last 4 d of each period. Although milk yield and DMI were not statistically different among treatments, supplementing with PEM increased feed efficiency respect to the Control. Both monensin and PEM reduced milk fat concentration and PEM also reduced milk protein concentration, but total production of those components was not affected. Methane production was not significantly affected but either additive. Total VFA concentration (99.4 mM), acetate to propionate ratio (2.43) and rumen pH (5.9) were similar among treatments. Results of this study indicate that the mixture of plant extracts evaluated can be a valid alternative to increase feed efficiency in lactating dairy cows. Further research is needed to better determine the optimal dose of PEM.

Table 1

	Control	Mon	PEM	SEM	*P* =
Milk, kg/d	37.7	39.0	39.6	2.34	0.57
DMI, kg/d	25.0	24.9	24.1	0.79	0.37
Efficiency, kg/kg	1.50[b]	1.57[ab]	1.65 [a]	0.06	0.06
Milk fat, %	3.29[a]	3.09[b]	3.06 [b]	0.15	0.10
Milk fat, kg/d	1.22	1.19	1.21	0.10	0.84
Milk protein, %	2.89[a]	2.86 [a]	2.72 [b]	0.07	0.08
Milk protein, kg/d	1.07	1.11	1.07	0.06	0.58
CH4, g/d	411.1	408.6	382.3	25.6	0.72
CH4, g/kg milk	10.9	10.5	9.67	0.42	0.95

Key words: plant extracts, methane, efficiency

875 Effects of feeding hay and baleage on growth and rumen parameters in prepubertal Holstein heifers. T. S. Dennis*, J. E. Tower, and T. D. Nennich, *Purdue University, West Lafayette, IN.*

Although ensiled forages are commonly included in diets of growing dairy heifers, little research has been conducted to evaluate feeding baleage as a primary forage source. The objectives of this study were to evaluate the effects of feeding dry hay or baleage to prepubertal dairy heifers on growth, feed efficiency, and rumen parameters. Thirty-six Holstein heifers (age = 189.3 ± 9.3 d; BW = 185.3 ± 1.3 kg) were randomly assigned to 1 of 12 pens and fed a 60:40 forage-to-concentrate diet (DM basis) containing either dry hay (H) or baleage (B) as the only forage source. Heifers were weighed biweekly and hip and withers heights, heart girth circumference (HGC), and body condition scores (BCS) were measured monthly. Blood was collected monthly for plasma urea nitrogen and glucose analysis. Rumen fluid was collected from 24 heifers at the start and end of the study via esophageal tube and measured for pH and rumen ammonia. Rumen fluid was also collected to evaluate in vitro cellulose digestion and total gas production. Data were analyzed as repeated measures using the MIXED procedure of SAS with pen as the experimental unit. Heifers fed H were 6.7 kg heavier ($P < 0.01$) than heifers fed B at the conclusion of the study. Heifers fed H also gained 0.63 kg/d compared with 0.56 kg/d for heifers fed B ($P < 0.05$). Overall, heifers fed H consumed 0.30 kg more DM/d than B ($P < 0.01$), resulting in a tendency ($P < 0.10$) for a 5.4% improvement in gain to feed ratios for H compared with B. Hip and withers heights, HGC, and BCS were similar ($P > 0.10$) between treatments. Plasma urea nitrogen and glucose concentrations were similar between treatments ($P > 0.10$), as was rumen pH ($P > 0.10$). Cellulose disappearance tended to be 9.4% greater for H compared with B ($P < 0.10$); however, total in vitro gas production was similar between treatments. Rumen ammonia concentrations were similar between H and B ($P > 0.10$), though ammonia concentrations declined significantly from 16.3 to 13.2 mg/dL over the entire study ($P < 0.05$). In summary, feeding baleage decreased BW gain, but did not alter skeletal growth or rumen parameters in prepubertal dairy heifers.

Key words: dairy heifer, baleage, hay

876 Direct enumeration of metabolically active yeast from the rumens of lactating dairy cows. H. C. Bruns*[1], A. R. Hippen[1], M. Witt[2], and J. M. Tricarico[2], *[1]South Dakota State University, Brookings, [2]Alltech, Lexington, KY.*

Four ruminally cannulated Holstein cows were used to evaluate the potential for direct enumeration of metabolically active yeast from rumens. A diet devoid of supplemental yeast was individually fed once daily at 1000 h. The diet contained 54% forage and 46% concentrate mix. All ruminal liquid samples were collected directly under the fibrous mat, strained into a thermos and immediately transported to the laboratory. Samples were diluted in 1% Bacto Peptone NaCl solution ranging from 10^{-2} to 10^{-4} and plated onto Dichloran Rose Bengal Chloramphenicol agar. Yeast colonies were enumerated after incubation at 30°C for 48 h. A logarithmic transformation (base 10) was applied on yeast counts before analysis. No yeast was recovered from cows consuming the basal diet or 24 h after dosing with supplemental yeast. A second study examined if the daily pattern of yeast recovery varied between cows. All cows were dosed intraruminally with 25×10^9 colony forming units (cfu) of *Saccharomyces cerevisiae* (Yea-Sacc, Alltech Inc., Nicholasville, KY). Samples were collected at 0.5, 1, 2, 4, and 6 h after dosing on 3 d. Average yeast counts were: 5.17, 5.33, 4.85, 4.34, and 3.95 log cfu per g of rumen contents at 0.5, 1, 2, 4, and 6 h after dosing, respectively. The fractional rate of yeast disappearance from the rumen was similar between cows and averaged 0.052^{h-1}. Lastly, a 4 × 4 Latin square was used to examine the quantitative recovery 1 h after dosing with increasing supplemental yeast (0, 5, 25, or 125×10^9 cfu). Polynomial contrasts were used to examine linear and nonlinear trends. Yeast counts from rumen fluid increased linearly with dose (0, 4.22, 4.89, and 5.83 log cfu per g, respectively; $P < 0.01$). Percent yeast recovery also increased linearly with dose (43.5, 47.0, and 52.6%, for 5, 25, and 125×10^9 cfu, respectively). Assuming metabolically active yeast can be enumerated with this culture-based procedure, we estimate that 25×10^9 cfu of supplemental metabolically active yeast will no longer be detectable 12 h after dosing (limit of detection 10^2 cfu/g) and will no longer be present in rumen fluid of lactating dairy cows 19 h after dosing.

Key words: dairy cows, enumeration, yeast

877 Evaluation of dry hay and baleage for transitioning post-weaned, prepubertal dairy heifers to higher forage diets. L. N. Pereira*, T. S. Dennis, J. E. Tower, and T. D. Nennich, *Purdue University, West Lafayette, IN.*

Dairy heifers often undergo rapid diet changes as they transition from the post-weaned phase to the growing period. Feeding strategies during this transition period have the potential to improve feed efficiency and growth performance of dairy heifers. The objective of this study was to determine whether feeding dry or ensiled forages during the transition period improved heifer performance and rumen parameters. Sixty Holstein heifers (141.9 ± 1.2 kg BW) were randomly assigned to 1 of 12 pens for a 4 wk period. Individual pens were assigned to 1 of 2 treatments: dry hay (H) or baleage (B) and were fed diets containing 40% hay or baleage (on a DM basis). Heifers were weighed weekly, with hip heights, withers heights, heart girth circumference (HGC), and body condition score (BCS) measured every 2 wk. Blood was collected every 2 wk and analyzed for plasma urea nitrogen (PUN), amylase and glucose. During this same collection time, rumen fluid was collected via an esophageal tube from 2 heifers in each pen and analyzed for pH, rumen ammonia, and cellulose disappearance. Data were analyzed as repeated measures using the Proc Mixed procedure of SAS. Average daily gain (ADG) was greater ($P = 0.04$) for H than for B (1.01 and 0.89 kg/d, respectively), though final BW were similar ($P = 0.26$). Heifers fed H had gain to feed ratios of 0.071 compared with 0.037 kg/kg for B during wk 4 ($P = 0.03$), and DMI were similar between treatments over the study ($P = 0.44$). Hip height, withers height, HGC, and BCS were similar between treatments. Rumen pH was greater for B than for H at wk 2 (6.85 and 6.58, respectively; $P = 0.01$), and rumen ammonia ($P < 0.01$) levels were greater for H at wk 2 with levels of 15.5 and 11.7 mg/dl for H and B, respectively. Cellulose disappearance was similar between treatments ($P = 0.25$). Plasma urea nitrogen was greater for H at both wk 2 and 4 ($P = 0.02$). Blood amylase was similar between treatments, but there was a trend ($P < 0.10$) for blood glucose levels to be greater in H at wk 2. Diets containing dry hay resulted in greater ADG than heifers fed ensiled forage during the transition period.

Key words: baleage, dairy heifer, transition

878 Rumen fill score was not related to feed intake response of fresh cows to a less filling diet. K. A. Kurtz, S. E. Stocks*, and M. S. Allen, *Michigan State University, East Lansing.*

Feed intake is likely controlled by mechanisms unrelated to ruminal distention for cows immediately postpartum but as lactation advances, control of feed intake likely begins to be dominated by ruminal distention. We conducted a switchback design experiment with 31 multiparous lactating cows to determine if a visual scoring system for rumen distention (1 = least, 5 = greatest) can be used to predict response in DMI to a less filling diet. We hypothesized that DMI of cows with a higher rumen fill score when fed a higher fill diet (HF, 34% NDF) would respond more positively to a lower fill diet (LF, 29% NDF). Cows ranged between 7 and 27 d postpartum and were blocked by calving date. Treatment diets were fed for 3 d each in the sequence HF-LF-HF for a total of 9 d per block. Cows were fed once and milked twice per day. Feed intake, milk yield, and milk components were measured daily throughout the experiment. Rumen fill score was observed 30 min before feeding (RS-BF) and 8 h later (RS-AF) each day in period 1. Rumen fill score ranged from 1.3 to 3.5 for RS-BF and from 1.6 to 4.3 for RS-AF among cows, was 0.73 units higher after feeding compared with before feeding, and RS-BF and RS-AF were highly correlated ($r = 0.8$, $P < 0.0001$). Response to diet was determined as the response for LF (period 2) minus the mean response for HF (periods 1 and 3) and ranged from −4.9 to 5.1 kg/d for DMI and −11.6 to 9.1 kg/d for milk yield. Response was greatest for the first day following the diet switch with 1.8 kg higher DMI for LF compared with HF, which decreased to 0.20 kg/d for d 2 and −0.30 kg/d for d 3. DMI response was not related to RS-BF, RS-AF, or their difference ($P > 0.71$) nor was it related to days in milk, BW, BCS, or DMI in period 1 ($P > 0.33$). Although response to diet was highly variable among cows for both DMI and milk yield, responses for DMI and milk yield were not related ($P = 0.73$). Further research is needed to assess the usefulness of rumen fill score for moving cows from the fresh diet to the high-group diet.

Key words: intake control, grouping cows, transition period

879 Effects of abomasal dosing of ferrous or ferric sulfate on short-term iron status of lactating dairy cows. O. N. Genther*, J. A. Zyskowski, T. H. Herdt, and D. K. Beede, *Michigan State University, East Lansing.*

The majority of Fe in feeds is in the ferric (Fe^{3+}) state, and poorly absorbed by ruminants. We hypothesize that the majority of Fe naturally occurring in drinking water is in the more bioavailable ferrous (Fe^{2+}) state. Therefore, Fe from drinking water, though present in lower concentrations, could have a greater impact on Fe status and potential toxicity than feed Fe. Our objective was to evaluate the difference in short-term effects of Fe^{2+} and Fe^{3+} when administered at concentrations to simulate total daily Fe intake from high-Fe drinking water. Six mid-lactation Holstein cows were assigned in a replicated 3 × 3 Latin Square balanced for treatment sequences. There were 7 d between experimental periods. Treatments were: 1) 0 mg Fe; 2) 1.5 mg Fe from ferrous sulfate/kg BW; and, 3) 1.5 mg Fe from ferric sulfate/kg BW. Treatments were iso-sulfate. The Fe^{2+} treatment approximated total Fe intake from water containing 9 ppm Fe, and the Fe^{3+} treatment provided the same Fe concentration. Treatments were infused in ~1 min directly into the abomasum via the ruminal fistula in 1.5 L of deionized water to avoid ruminal effects on Fe valence. Six hourly blood samples were taken before dosing; and, post-dosing hourly for 12 h each period. Liver biopsies were 0 (before dosing), 18 and 36 h of each period. Mean of pre-dosing blood samples was used as a covariate for each dependent variable in statistical analysis. There were no treatment by time interactions ($P > 0.10$) for serum Fe, unsaturated iron-binding capacity (UIBC), total iron-binding capacity (TIBC), percent Fe saturation, Zn, and for liver Fe, Cu and Zn. There was no main effect of treatment for any response variables. There was an effect of hour pooled across all treatments for serum Fe ($P = 0.014$), TIBC ($P = 0.043$), Fe saturation ($P < 0.0001$) and Cu ($P = 0.033$). There was a treatment by time interaction for serum α-tocopherol ($P = 0.016$) and Cu concentration ($P = 0.091$). Results indicate that dosing of amounts of Fe used in this study do not impact short-term Fe status of lactating dairy cows.

Key words: iron, lactating dairy cows, iron status

880 Evaluation of total mixed rations fractions retained on the Penn State Particle Separator as additional variables to influence milk production and composition. A meta-analysis. I. Schadt*[1], M. Caccamo[1], G. Azzaro[1], and G. Licitra[1,2], *[1]CoRFiLaC, Regione Siciliana, Ragusa, Italy, [2]DISPA, Catania University, Catania, Italy.*

Determination of forage and total mixed ration (TMR) fractions retained on the Penn State Particle Separator (PSPS) has become a widely used application on dairy farms and in research. The objective of this study was to evaluate the following variables on milk yield and percentage fat and protein: PSPS TMR fractions (% of total); chemical composition of TMR, [dry matter (DM % of as-fed), crude protein, neutral detergent fiber], and forage content (all as % of DM); average days in milk and average dry matter intake. A data file containing 109 treatment means was generated from 28 published research papers and one unpublished study conducted at the CoRFiLaC dairy research center. The variables, squared variables and possible interactions were tested, using the backward-forward elimination, stepwise selection option in PROC REG, multi-regression procedure using SAS statistical software. Models were calculated both ways, excluding and including PSPS fractions as variables and interactions where PSPS fractions were involved. A total of 150 or 108 variables were allowed to determine either predicting models including or excluding PSPS variables. Corrected R^2 values for the prediction models of milk yield were 0.95 and 0.91 when PSPS fractions were either admitted or not, involving 34 and 32 model terms, respectively. The models for milk fat prediction contained 32 and 26 possible terms, and corrected R^2s were 0.86 and 0.75 when PSPS variables were either included or not. Models to predict milk protein selected 18 and 17 terms either including or excluding PSPS variables, and respective R^2s were 0.79 and 0.58. These results suggest that for adequate formulation of dairy rations we might be able to eliminate some of the chemical analysis of feeds, which are currently recommended by some nutrition models. The consistent improvement in R^2 of predictive models suggests that physical measurements such as particle TMR fractions retained on the PSPS would provide additional information for dairy ration formulation, especially for milk composition.

Key words: TMR, feed evaluation, particle size

881 Effect of supplementary concentrate type on energy balance and blood metabolites in early lactation dairy cows offered grazed pasture. K. M. Pierce*, S. J. Whelan, J. J. Callan, and F. M. Mulligan, *School of Agriculture, Food Science and Veterinary Medicine, University College Dublin, Belfield, Dublin 4, Ireland.*

This experiment evaluates the effect of supplementary concentrate type on energy balance and blood metabolites in early lactation dairy cows offered a perennial ryegrass pasture. Forty 8 cows of mixed parity were assigned to 1 of 4 concentrate types in a randomized block design. Cows received perennial ryegrass plus 3 kg twice daily of the following concentrate types: Hi-Pro (18% CP), Lo-Pro (14% CP), Lo-Pro+ Meth (14% CP, with added methionine) and Lo-Pro Maize (14% CP). Hi-Pro, Lo-Pro and Lo-Pro+ Meth contained rolled barley, whereas Lo-Pro Maize contained stone ground maize as the main starch source. Blood was collected on d 14, 21, 28 and 35 post-calving for analysis of urea, non esterified fatty acids (NEFA), β-hydroxy butyric acid (BHBA) and glucose (GL). Pasture DMI was determined on wk 6 and 10 post calving. Data was analyzed using PROC MIXED of SAS. Dietary energy intake (18.23 ± 0.054 UFL/d) was not affected ($P > 0.05$) by treatment. A greater ($P < 0.05$) portion of dietary energy was recovered in the milk for Lo-Pro+ Meth (0.638 ± 0.034 of UFL intake) vs. Hi-Pro (0.535 ± 0.034 of UFL intake); Lo-Pro and Lo-Pro Maize were not different ($P > 0.05$) from other treatments. BHBA was higher ($P < 0.05$) for Hi-Pro (0.73 ± 0.045 mmol/L) vs. Lo-Pro Maize (0.58 ± 0.045 mmol/L); Lo-Pro and Lo-Pro+ Meth were not different from other treatments. NEFA were lower ($P < 0.05$) for Lo-Pro Maize (0.39 ± 0.058 mmol/L) vs. other treatments (0.59 ± 0.058 mmol/L). GL was higher for Lo-Pro Maize (3.34 ± 0.051 mmol/L) vs. Hi-Pro (3.14 ± 0.051 mmol/L); Lo-Pro and Lo-Pro+ Meth were not different from other treatments. Blood urea (1.39 ± 0.108 mmol/L) was not affected by treatment. Reducing concentrate CP and offering supplementary methionine improved energy efficiency. Reduced concentrations of GL, NEFA and BHBA in Hi-Pro vs. Lo-Pro Maize may be due to better energy balance.

Key words: supplementary concentrates, blood metabolites, dairy cows

882 Effect of total mixed rations particle fractions retained on the Penn State Particle Separator on milk yield lactation curves using a random regression animal model. M. Caccamo*[1], J. D. Ferguson[2], R. F. Veerkamp[3], I. Schadt[1], R. Petriglieri[1], G. Azzaro[1], A. Pozzebon[1], and G. Licitra[1,4], *[1]CoRFiLaC, Regione Siciliana, Ragusa, Italy, [2]University of Pennsylvania, PA, [3]WageningenUR Livestock Research, Animal Breeding and Genomics Centre, Lelystad, the Netherlands, [4]DISPA, Catania University, Catania, Italy.*

Several studies reported influence of diet on milk production. As part of a larger project aiming to develop management evaluation tools

based on results from test-day (TD) models, the objective of this study was to estimate the effect of total mixed rations (TMR) particle fractions estimated using the Penn State Particle Separator (PSPS) on milk, fat, and protein yield curves. A random regression TD animal model was fitted to a full data set (134,579 test-day records) to obtain variance components. The model included parity, days in milk (DIM), age at calving, year and season at calving, days dry, calving interval and stage of pregnancy as fixed effects. The term DIM was modeled using 9-order Legendre polynomial. Animal, sire and maternal grand sire effects were modeled using 3-order Legendre polynomials. Model fitting was carried out using ASREML. Then, the same model with fixed variance components was used on a subset containing 46,531 TD milk yield records from 2006 through 2008 from 3,554 cows in 27 herds in southeastern Sicily where TMRs were sampled immediately before or right after the TD. In these herds, TMR samples were collected every 3 mo, sieved using a PSPS including 19 (upper), 8 (middle), and 1 (lower) mm sieves and an additional bottom pan and proportions were measured. All sieve proportions and their interaction with DIM were included in the model as fixed effects. Conditional Wald F statistic on fixed effects revealed significant effects ($P < 0.001$) for all sieves on milk, fat, and protein yield, except upper sieve on fat and lower sieve on protein production. In particular, pan and lower sieve proportions were negatively related whereas those retained on the middle sieve were positively related to fat production at the beginning of the lactation. Furthermore, the correlations between milk curve shape and middle and lower sieve proportions were positive and negative, respectively, throughout the whole lactation, suggesting that PSPS sieve fractions could represent an additional important parameter for the formulation of dairy rations.

Key words: particle size, test-day model, total mixed ration

Ruminant Nutrition: Mycotoxins – Prevalence, Impact, and Control Strategies in Ruminant Diets

883 Major mycotoxins in ruminant diets. D. E. Diaz*, *Novus International Inc., St. Charles, MO.*

Mycotoxins are undesirable, but mostly unavoidable, mold produced feed contaminants. The level of mycotoxins in foods and feed can fluctuate widely and vary significantly from year to year. These fluctuations depend on many factors, including adverse conditions that favor fungal invasion and growth either in the field or during storage. Apart from their threat to public health, mycotoxins are also associated with significant economic losses for both crops and animals. Although several hundred mycotoxins have been described in the scientific literature, less than 10 have been extensively studied since the discovery of aflatoxin in the early 1960s. Mycotoxins can increase disease incidence and reduce production efficiency in livestock. They can cause dermal toxicity, reproductive effects, carcinogenicity, neurotoxicity, teratogenicity, nephotoxicity and hepatoxicity. Additionally, mycotoxins may affect immune function and cause lipid peroxidation. In spite of current research advances, applied aspects of mycotoxicology are either limiting or difficult to extrapolate into the real world. This review will attempt to discuss some of the most common problems related to presence of mycotoxin in ruminant diets.

Key words: mycotoxins, ruminant

884 Impact of mycotoxins on the immune system. T. K. Smith*, *University of Guelph, Guelph, ON, Canada.*

Ruminant animals are generally considered to be more resistant to feed borne mycotoxins than monogastric animals because of the potential for rumen microorganisms to inactivate mycotoxins before they enter the blood stream. One symptom of mycotoxicoses that is sometimes observed in ruminants and monogastrics is immunosuppression. Lingering health problems in the herd, animals that do not respond to medications and failure of vaccination programs can be seen. Positive identification of mycotoxins as the causative factor is difficult because many conventional analytical techniques underestimate the degree of mycotoxin contamination of feedstuffs. This is further complicated by the fact that symptoms and lesions noted are not the classical lesions characteristic of mycotoxicoses. They are lesions caused by infections resulting from a mycotoxin-induced compromised immune system. The severity of immunosuppression can be further influenced by management systems. Environmental stresses arising from some management practices will also impart a degree of immunosuppression which may, therefore, appear to exaggerate mycotoxin-induced immunosuppression. The feeding of aflatoxin contaminated feeds to ruminants has been shown to lower disease resistance and to compromise vaccine-induced immunity. Several mechanisms of bovine immunosuppression by aflatoxin have been demonstrated in vitro including mitogen-induced stimulation of peripheral lymphocytes and inhibition of bovine lymphocyte blastogenesis. Recent studies in dairy cows demonstrated that feed naturally contaminated with *Fusarium* mycotoxins (mainly deoxynivalenol) can also affect immune function. Decreased serum IgA concentrations, depressed neutrophil phagocytosis and stimulated primary antibody response to ovalbumin immunization were seen. It can be concluded that ruminant animals can be subject to immunosuppression and decreased disease resistance when exposed to feed borne mycotoxins.

Key words: ruminants, mycotoxins, immunity

885 Prevalence of mycotoxins in feedstuffs. D. Taysom*, *Dairyland Laboratories Inc., Arcadia, WI.*

Each year molds and mycotoxins have a major economic impact on the feed industry and despite advances in analysis of the toxic metabolites produced by molds, they still prove to be difficult to measure and quantify. There are hundreds of unique mycotoxins in the environment; however, there are good analytical methods for approximately 15 – 25 toxins and depending on the sample matrix, most labs are proficient at testing 5 to 8 toxins. A variety of methods; ELISA, TLC, HPLC, HPLC/MS, HPLC/MS/MS are available with verifiable low detection limits on grains and meal product. However products that have undergone fermentation (corn silage) or are mixtures, (grain mixes, TMRs) are limited in number of methods available and must utilize higher detection limits. While complete "panels" of mycotoxin analysis are often recommended when trouble shooting mycotoxin contamination, there is a lack of evidence that this approach is more successful in determining the presence of mycotoxins when compared with analyzing for toxins commonly referred to as "markers." New research indicates that having samples identified for mycotoxin producing molds may also be an effective diagnostic tool. The most common approach for monitoring the prevalence of mycotoxins across a broad geographic region is to summarize data from laboratories performing mycotoxin analysis. While this is useful information, one should consider that most samples submitted for laboratory analysis are suspect in nature and laboratory summaries are not random sampling of products for mycotoxin contamination. There would be a great benefit to the feed industry for a mycotoxin monitoring program that included random sampling of products, accounted for seasonal differences and was implemented consistently over several years.

Key words: mycotoxins, prevalence, laboratory summary

886 Evaluation of feed additives for reducing mycotoxins. I. P. Oswald*, *INRA, ToxAlim Reseach Center, 31027 Toulouse Cedex 03, France.*

Mycotoxins are secondary metabolites elaborated by filamentous fungi and the contamination of food and feed with mycotoxins is a worldwide problem. These toxins have significant human and animal health, economic and international trade implications. The major mycotoxins of concern are aflatoxins, trichothecenes, ochratoxin, ergot alkaloids, zearalenone and fumonisins, most of which are highly toxic and some are carcinogenic in humans. With global warming, the threat from fungal invasion of crops is likely to increase. Every effort must be made to reduce the occurrence of mycotoxins. This is a complex task that require an integrated understanding of crop biology, agronomy, fungal ecology, harvesting methods, storage conditions, food or feed processing and detoxification strategies. The use of feed additives to alleviate nutrient deficiencies, increase product pigmentation, improve pellet quality and adsorb toxicants and toxins is a well established practice in the animal feed industry. A diverse variety of substances have also been investigated as potential mycotoxin-detoxyfying agents. Depending on their mode of action, these feed additives may act by reducing the bioavailability of the mycotoxins or by degrading them or transforming them into less toxic metabolites. We can define at least 2 main categories: (1) One of the strategies for reducing the exposure to mycotoxins is to decrease their bioavailability by including various

mycotoxin adsorbing agents in the compound feed, which leads to a reduction of mycotoxin uptake as well as distribution to the blood and target organs. (2) Another strategy is the degradation of mycotoxins into non-toxic metabolites by using biotransforming agents such as bacteria/fungi or enzymes. Substances that do not directly interact with mycotoxins, i.e., antioxidant agents, immunostimulatory agents, are not considered sensu stricto as mycotoxin-detoxifying agents. However, such compounds may be very efficient for reducing the toxicity of mycotoxins.

Key words: feed additive, mycotoxin, ruminants

Teaching/Undergraduate and Graduate Education

887 Perceptions of livestock practices by students entering introductory animal science courses. G. A. Holub*[1], C. T. Boleman[2], and S. W. Ramsey[1], *[1]Texas A&M University, College Station, [2]Texas AgriLife Extension, College Station.*

The purpose of this study is to determine attitudes of introductory animal science course students about common livestock management practices to alter teaching methods of the course based on the results. The IRB approved, anonymous survey was conducted for 3 Introductory Animal Science classes at Texas A&M University over the course of 2008 (n = 847). The study used an ex post facto approach and a correlational design. Quantitative data were analyzed using SPSS 15.0 for Windows software. Descriptive statistics were used to summarize data. Frequencies, percentages, central tendency measures, and variability measures were used to describe these data. The majority of respondents by category were male (63.0%), freshman (53.9%), less than 20 years of age (79.0%), and college of agriculture science students (50.7%). To determine the background of the students, they were asked to define where they were raised. The most frequent response was for "major city (over 100,000)" - 24.8%. This was followed closely by respondents from a "town (between 2,500 and 25,000)" – 22.2%, "rural" – 20.6%, "city (between 25,000 and 100,000)" – 18.9%, and "rural community (<2,500 population)" - 13.8%. Fourteen production practices were evaluated for acceptance by respondents The Likert scale used for acceptance was defined as 1 = Very Acceptable to 5 = Very Unacceptable. Seven of the 14 statements yielded mean values of less than 2.0. Six production practices yielded mean values between 2.0 and 3.0. Only one production practice yielded a mean value of greater than 3.0. The summary table shows the results of these analysis in order of acceptance by the students. Conclusions of the survey include half of the production practices are considered acceptable by the students before any teaching about the practices and half needed more emphasis by the instructor to enable students to have a more positive perception of the practice.

Table 1. Likert scale means for the acceptance of livestock production practices by introductory animal science students

Practices	N	Mean	SD
Vaccinate	845	1.21	0.54
Shearing	846	1.27	0.55
A.I.	846	1.61	0.85
Castration	842	1.83	1.03
Squeeze chutes	842	1.88	0.99
Ear notching	846	1.93	0.95
Dehorning	846	1.94	1.01
Feedlots	839	2.08	0.97
Auction market handling	840	2.09	0.93
Hot iron branding	846	2.13	1.09
Farrowing crates	839	2.54	0.90
Battery cages for laying hens	844	2.74	0.98
Separating calves/mothers	843	2.85	1.17
Debeaking	846	3.15	1.15

Key words: animal science, undergraduate, perceptions

888 Demographics and eating habits of students entering introductory animal science courses. G. A. Holub*[1], C. T. Boleman[2], and S. W. Ramsey[1], *[1]Texas A&M University, College Station, [2]Texas AgriLife Extension, College Station.*

The objectives were to determine the background and demographics and eating habits by protein sources (red meat, eggs, poultry and dairy) of students in introductory animal science classes to alter instruction for the semester based on the results. The study was conducted with 3 introductory Animal Science level classes at Texas A&M University in 2008 (n = 847). Frequencies, percentages, central tendency measures, and variability measures were used to describe these data. The majority of respondents by category were male (63.0%), freshman (53.9%), less than 20 years of age (79.0%), and college of agriculture science students (50.7%). Students were asked to define where they lived. The most frequent response was "major city (over 100,000)" - 24.8%, followed by "town (between 2,500 and 25,000)" – 22.2%, "rural" – 20.6%, "city (between 25,000 and 100,000)" – 18.9%, and "rural community (<2,500 population)" - 13.8%. Respondents were asked about their farming background, pet ownership, and eating habits. A total of 496 respondents (59.2%) were presently associated with farming and 93.1% had a family pet. With regard to eating habits, 96.7% classified themselves as meat eaters, while 3.3% classified themselves as either a vegetarian or vegan, but 757 respondents (89.7%) said there were no family members who were considered vegetarians. Respondents were asked to provide their consumption of animal food products by determining the number of servings they eat per week. The products included eggs, red meat, poultry, and dairy. For egg consumption, 455 (53.8%) respondents said they consume 1–2 servings per week, followed by 3–4 servings at 19.8%, and zero servings at 14.5%. Similar to egg consumption, dairy had a majority response where > 56% indicated they consume milk daily. Red meat and poultry were more evenly distributed as compared with eggs or dairy. A total of 268 (31.8%) respondents said they eat 3–4 servings of red meat per week and 222 respondents (26.2%) 5–6 servings per week. The leading category for poultry was 3–4 servings, 365 respondents (43.2%), followed by 253 respondents (30.0%) at 5–6 servings per week.

Key words: undergraduate, animal science, eating habits

889 Incorporating an issues survey assignment into an introductory animal science course. J. A. Sterle*, *Texas A&M University, College Station.*

Eighteen undergraduates enrolled in General Animal Science Honors course were required to develop, administer and interpret a survey about livestock industry issues. Objectives of the project were to 1) expose the students to scientific process, 2) investigate livestock issues in society, 3) increase understanding of interpretation of survey data, and 4) expose students to advocacy and agriculture education. Public perception of agriculture was discussed in-depth. Students responded as participants to a livestock production perception study, followed by discussion of each question's wording, possible misinterpretation, and overall bias. Students were allowed to choose survey topic, although exact duplicates were discouraged. Topics included livestock terminology, food safety, horse harvest, organic food, government grazing lands, gestation stalls, growth implants, and the general use of animals (pets and livestock) in society. Surveys varied in length and type of questions, although all had at least 10 questions. Students submitted several drafts before final printing. "Fact cards" was also developed

for each survey, consisting of 3–8 bullet points, educating respondents about the topic once survey was taken. One hundred copies of each survey were distributed. Students were allowed to determine audience and place of distribution. Students collected, recorded and analyzed data, and presented findings. They were also asked to present possible misinterpretations of results (i.e., by media or groups opposing livestock production). When surveyed about the project, students noted peer apathy about completing the survey. All students responded "a significant amount" when asked how much they learned by completing this project. Most students (75%) indicated a higher level of understanding of survey research, and 15/18 (83.33%) declared a preference to conduct the survey via internet. Students indicated that participants were concerned with answering the questions "correctly," even though they were asked opinions. Every student specified a "greatly improved" understanding of public perception of animal agriculture by completing the project.

Key words: teaching, issues, survey

890 Improving learning through integration of an upper division class with an introductory class in companion animals. J. P. McNamara*, *Washington State University, Pullman.*

To increase the depth and breadth of science understanding and application to animal nutrition and management, 2 courses at WSU: AS 205, Companion Animal Nutrition (General University Biology Course) taught to all classes and majors; and AS 464, Companion Animal Management, a primarily major course for seniors, have been used for the last 4 years in a project to integrate several levels of learning and application skills. The learning outcomes of the project were to increase scientific knowledge, media and information literacy, critical thinking across a wide spectrum, quantitative reasoning, working with groups to solve problems; and learning how to communicate to others. Lessons in the biology class investigated connections between nutritional chemistry, animal diversity, and practical decision making (use of pet food labels); or the biology behind the interaction of nutritional states and disease and their impacts on society. In the advanced class, students researched topics from the canine genome project and mechanisms of genetic diseases; to the human animal bond and how it affects economic and political decisions. Each advanced student then individually developed a teaching module on a broad topic to be used by the students in the introductory class. The course objectives in part read: To help you identify media and science concepts displayed in select videos and other media to relate media messages about scientific topics, or animals, to your own life and to society in general. To think critically about how media provides various messages, how they relate to animals and science, and how such messages and ads could influence others. Surveys (Likert Scale) from both classes over the last 3 years (60 students in advanced class; 450 students in introductory class; over 80% response rate) were approximately 78 to 85% positive on thinking critically, working on a team, improving information literacy and understanding interdisciplinary importance; and 90+ % on improving ability to "answer my own questions." Other faculty may be able to use such approaches to expand the role of Animal Sciences in overall university instruction and improve student learning.

Key words: companion animal, teaching, course integration

891 Internships and international collaboration in beef cattle reproductive management. K. G. Pohler*[1], D. A. Mallory[1], D. J. Patterson[1], M. F. Smith[1], J. L. M. Vasconcelos[2], R. F. G. Peres[3], and E. R. Vilela[4], *[1]University of Missouri, Columbia, [2]FMVZ - UNESP, Botucatu, SP, Brazil, [3]Agropecuária Fazenda Brasil, Barra do Garças, MT, Brazil, [4]Lageado Agricultural Consulting LTD, Mineiros, GO, Brazil.*

Recent advances in reproductive technologies in cattle (e.g., fixed-time artificial insemination [AI]) have created demand for qualified individuals capable of implementing these technologies. The University of Missouri developed a reproductive management internship in conjunction with Select Sires, Inc. (F. B. Miller Internship in Reproductive Management) to address this issue. Objectives of this internship include the following: 1) Provide undergraduate and graduate students with extensive practical training in the implementation of estrus synchronization (ES) and AI programs in beef and dairy herds, and 2) Provide students with the ability to solve "real world" reproductive management problems, both individually and as a team. Over the past 15 years, the internship provided opportunities for 156 students to work with over 190,000 heifers and cows in production settings in 12 states. Outcomes include the following: 1) Increased competency of students' reproductive management skills, 2) A deeper understanding of the US beef and dairy industries, and 3) A network of allied industry contacts, that expand career opportunities beyond the classroom. The internship was expanded in 2011 to provide graduate students with international experience in reproductive management. Objectives of this program include the following: 1) Gain extensive practical experience in implementing ES and AI protocols in large Brazilian herds, and 2) Provide students with knowledge of the Brazilian beef industry. Recently, 2 graduate students worked with over 20,000 beef heifers and cows located on more than 15 farms and ranches in 3 states in Brazil. A goal of the program is to promote future collaborations with Brazilian researchers and allied industry. Based on the placement of students into careers that involve implementation of reproductive management technologies (e.g., AI employees, veterinarians, extension specialists in reproduction, etc) the internship program has been successful. Supported by National Research Initiative Competitive Grant no. 2005–55203–15750 from the USDA Cooperative State Research, Education, and Extension Service

Key words: estrus synchronization, beef cattle, internship

892 Predictors of performance in an Animal Nutrition classroom. M. A. Soberon*, D. J. R. Cherney, and R. C. Kiely, *Cornell University, Ithaca, NY.*

Accurately identifying predictors of classroom performance better equips advisors to make course recommendations to undergraduate advisees as well as instructors striving to meet the needs of a diverse classroom. This research endeavors to discover predictive relationships between SAT scores, residency, transfer status, major, gender, grade in a recommended chemistry prerequisite (Chem) and performance in an animal nutrition course (Nutr; Cornell University). Data from a total of 443 students, representing 4 semesters (Fall 2007–2010) of Nutr students was collected from the CALS Registrar and analyzed using SAS 9.2. The instructor was the same and the class material was essentially unaltered during this time. All of the analyzed predictors were significant with the exception of major; this was affected by the low number of non-majors in the class. Final cumulative GPA was highly correlated with Nutr grade, indicating students with high grades in the course tend to also have a high cumulative GPA. The highest correlation for an analyzed predictor was Chem grade, with a significant Nutr grade difference for students who completed the Chem prerequisite (86.3 vs. 80.6). Twenty-nine percent of the students were transfer students. This research identified areas where predictors could be better

utilized for transfers. Although SAT scores are correlated with performance, they were not on record with CALS Registrar for 86.8% of transfer students. Moreover, transfers rarely take Cornell Chem. In a survey conducted for the fall 2010 class, students identified the following as influencing their grade in Nutr: study habits (81.2%), test taking (70.6%), transfer status (48% of transfers), animal experience level (27.1%), personal problems (24.7%) and class prerequisites (22.4%).

Table 1. Predictors of student performance in Animal Nutrition

Item		n	Grade	SE	*P*-value	r^2
GPA[1]		174	83.5	6.85	<0.001	0.450
SAT Math		299	84.4	7.83	<0.001	0.144
SAT Verbal		299	84.4	7.79	<0.001	0.152
Chemistry		227	86.3	5.90	<0.001	0.409
Residency	Resident	251	82.5	8.73	0.007	0.017
	Non-resident	192	84.8			
Transfer status	Four year	314	84.4	8.69	0.001	0.025
	Transfer	129	81.3			
Major	Animal Sci	403	83.5	8.80	0.854	0.00
	Non-major	40	83.8			
Gender	Male	107	79.0	8.42	<0.001	0.085
	Female	336	85.0			

[1]Graduated students only.

Key words: nutrition, predictors, teaching

893 Attitudes and knowledge of high school students about the department of animal industry of the University of Puerto Rico at Mayagüez. G. Ortiz-Colón*, J. M. Huerta-Jiménez, E. Jiménez-Cabán, and M. Pagán-Morales, *University of Puerto Rico at Mayagüez, Mayagüez, PR.*

The student enrollment in the College of Agricultural Sciences of the University of Puerto Rico at Mayagüez has been stagnant for at least the last 6 years. Within the College of Agricultural Sciences, the situation of the Department of Animal Industry (DAI) is not different. The DAI enrollment has declined in 7% over the last 6 academic years. The reasons for this phenomenon have not been previously investigated. We hypothesized that high school students of Puerto Rico did not understand the professional options a bachelor in Animal Industry has to offer. Surveys were developed to evaluate what knowledge high school students possessed about the DAI. Surveys (2,700) were distributed to 135 professionals (20 surveys /professional) of the Cooperative and Agricultural Extension Service who were assigned to visit at least one school in each of the 78 counties of Puerto Rico. A total of 726 surveys were returned representing students in 31 high schools representing 26 counties of Puerto Rico. Of the surveyed individuals, 75.8% were 15 to 16 years old and 57.6% were females. Most students (89%) were in 10th and 11th grade. The majority of the surveyed individuals (72.2%) had no experience in agriculture. Only 49.9% of the studied population could correctly define "animal industry." However, when students were asked to define the term "animal science," 78% did it correctly. Although only 7.4% of the surveyed population was interested in an animal industry academic program, 19.4% was interested in an animal science academic program. These data suggest that students do not understand the term animal industry and this could be limiting their interest in enrollment at the DAI. The data suggests that if the name of the DAI is changed to the Department of Animal Science more high school students might applied to this academic program.

Key words: Hispanic serving institutions, animal science, student recruitment

894 Mentoring underrepresented students through agricultural related research projects. J. S. Pendergraft*[1], R. M. Legere[1], and A. RodrÍguez[2], *[1]Sul Ross State University, Alpine, TX, [2]University of Puerto Rico, Mayaguez, PR.*

Sul Ross State University (SRSU) was awarded a Hispanic-Serving Institutional grant of $290,000 over a 4-year period to increase the number of underrepresented students entering and completing graduate school through developing a science-based mentoring program. To facilitate cross-cultural and cross-institutional collaboration, SRSU partnered with key personnel at the University of Puerto Rico at Mayaguez (UPRM). The research mentoring model allowed faculty to work with top graduate students to select a team of undergraduates that would work together on sustainable agricultural and biological research projects. Three projects were designed in the fall of 2010 to begin comparing student participation in the new research mentoring model with the successful managerial mentoring model at SRSU. These research projects were conducted utilizing 30 students, 3 faculty members, and 3 universities which included Eastern New Mexico University. Of the 30 participating students in the research projects 10 of them were underrepresented animal science students. This was a 50% increase in total participation and a 30% increase in minority participation compared with the projects conducted over 2 years in the managerial mentoring program. Notably, 2 of the 7 graduate mentors were Hispanic students. Thirty percent of the undergraduate participants were either freshmen or sophomores in classification and half of them were minority students. Undergraduate student participants represented 5 different Animal Science concentrations and Natural Resource Management degree programs. One of the mentors has been invited to attend veterinarian school at Kansas State University. The science-based research mentoring model developed at SRSU from the Hispanic Serving Institute grant will increase the quality of its postsecondary instruction while enhancing the educational equity for underrepresented students in agricultural programs. Acknowledgments: Dr. D. Smith, Eastern New Mexico University

Key words: Hispanic, experiential, mentoring

895 Graduate student course curriculum in animal science departments. R. F. Leuer*[1] and H. M. White[2], *[1]University of Minnesota, St. Paul, [2]Indiana University, Indianapolis.*

Graduate education in animal science is at a crossroads at many colleges and universities. As faculty numbers have dropped and research areas have become increasingly specialized, meeting all graduate student course needs has become increasingly difficult. An online survey was conducted during the summer of 2010 to assess the quality of graduate courses available within animal science departments. One-hundred respondents representing 34% MS and 66% PhD students studying nutrition, animal breeding and genetics, physiology, management and production systems, reproduction, and other areas, completed the survey. Only 50% of students were satisfied with the course curriculum offered within their department. Satisfaction was not affected ($P > 0.05$) by degree currently being pursued. Basic graduate courses were reportedly available to 72% of students and advanced courses were available to 61% of students. Dissatisfaction with the

basic course offerings tended ($P = 0.06$) to influence and dissatisfaction with advance course offerings influenced ($P < 0.05$) overall satisfaction. Students working with swine and equine species were less satisfied ($P < 0.05$) with overall course offerings than students working with beef, dairy, or poultry. The possibility of participation in internet-based courses to augment current classes appealed to 87% of students and PhD students were more supportive ($P < 0.05$) of this option. Support for online course options was higher ($P < 0.05$) among students who worked with beef, dairy, and swine compared with students working with equine, companion animals and small ruminants. Of 2 format options presented for online courses, more students indicated that they would prefer ($P < 0.05$) broadcasted live lectures compared with self-paced online tutorials (65 vs. 35%). These survey results indicate that graduate student course needs are not always being met and that gaps in course offerings in advanced subject areas influences overall course curriculum satisfaction. These results also suggest that future development of online courses, offered across universities, may augment current course curriculums.

Key words: graduate education, online courses, course curriculum

896 Increasing awareness of the Multimedia Educational Resource for Learning and Online Teaching (MERLOT) website.
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The objective of this abstract is to increase awareness of the Multimedia Educational Resource for Learning and Online Teaching (MERLOT) Web site and solicit materials for inclusion in the Animal Science section of the Agricultural and Environmental Sciences Community (www.merlot.org). MERLOT is a well-established reservoir of peer-reviewed free on-line teaching resources targeted for use in higher education. Its strategic goal is to increase the availability of quality online learning material and thereby improve the effectiveness of teaching. Materials found in MERLOT can be used for online course development as well as in web-enhanced face-to-face courses. Types of materials include animations, case studies, collections, drill and practice activities, learning objects, lectures, online courses, open textbooks, exams, reference material, simulations, tutorials, and training materials. Some ideas for using material found in Merlot include assigning supplemental readings, developing an assignment around a site, incorporating materials into presentations, and using online tools to complete assignments. The Agricultural and Environmental Sciences Editorial Board and online Community was established in 2010 and currently contains sections for the disciplines of Agriculture Education, Agriculture and Bio Engineering, Agriculture, Environment & Development Economics, Animal Sciences, Environment and Natural Resources, Food Science, and Plant Science. Online material is being solicited for all sections, including Animal Sciences. Submission of material for peer-review is open to all persons and easily accessed. Publishing materials on MERLOT offers the opportunity for faculty to contribute to the scholarship of teaching and learning.

Key words: MERLOT, teaching, online

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